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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1.MMSASRLAGTLIPAMAFISC.....SMNPEGTGTCGNQCATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4355	100.0	839	6	ABU04773 Human exp
2	4355	100.0	839	6	ABU04774 Human exp
3	4355	100.0	839	6	ABU04775 Human exp
4	4355	100.0	839	7	ADC78785 Human PRO
5	4355	100.0	839	7	ADD48826 Human PRO
6	4335.5	99.6	837	5	AAW86361 Human DNA
7	4335.5	99.6	837	5	AAE16102 Human DNA
8	4335.5	99.6	837	5	ABU04776 Human exp
9	4328.5	99.4	837	5	AAE16116 Human DNA
10	4178	95.9	808	8	ADOS7782 Chimpanze
11	4167	95.7	808	8	ADOS7785 Gorilla t
12	4164	95.6	808	8	ADOS7803 Chimpanze
13	4141	95.1	799	5	AAW86352 Human DNA
14	4141	95.1	799	5	AAE16093 Human DNA
15	4141	95.1	799	5	ABR83162 Human Tol
16	4141	95.1	799	6	ABR42963 Human Tol
17	4141	95.1	799	7	ABR39121 Human Tol
18	4141	95.1	799	7	ADP56656 Human Tol
19	4141	95.1	799	8	ADP48597 Human Tol
20	4040	92.8	801	8	ADOS7788 Gibbon to
21	3918	90.0	795	8	ADOS7791 Rhesus mo
22	3892	89.4	795	8	ADOS7800 Hamadryas
23	3819	87.7	801	8	ADOS7797 Squirlrel
24	3681.5	84.6	738	8	ADP29455 Human sec
25	3501	80.4	745	8	ADOS7794 White-fac

26	1090	25.0	208	3	AAV88059 Human Tol
27	919	21.1	178	8	ADN12270 IL-1R/TLR
28	785	18.0	179	7	ADC42707 Murine To
29	629.5	14.5	661	2	AAW28510 Product o
30	629.5	14.5	661	2	AAW87556 B cell bu
31	629.5	14.5	661	7	ADC38652 Human bec
32	629.5	14.5	661	7	ADP69098 Human MP5
33	628.5	14.4	650	3	AAV82527 Human RP1
34	615.5	14.1	661	2	AAW47274 Human B-C
35	603.5	13.9	784	2	AAW86350 Human DNA
36	603.5	13.9	784	5	AAE16091 Human DNA
37	603.5	13.9	784	5	ABR83161 Human Tol
38	603.5	13.9	784	8	ADN02005 Human Inf
39	602.5	13.8	784	2	AAV05869 Human Tol
40	602.5	13.8	784	6	ABU61956 Human Tol
41	602.5	13.8	784	7	ADL15005 Human Tol
42	602.5	13.8	784	8	ADP56652 Human Tol
43	602.5	13.8	784	8	ADP48593 Human Tol
44	602.5	13.8	784	8	ADP23787 PRO polyP
45	602.5	13.8	784	8	ADQ39727 Human myo

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
XX	ABU04773;	
AC	29-JAN-2003	(first entry)
XX		
DE	Human expressed protein tag (EPT) #1439.	
XX		
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
KW	protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
OS	Homo sapiens.	
XX		
PN	WO200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX		
XX	(ZYCO-) ZYCO INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
DR	WPI; 2003-040607/03.	
XX		
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX		
PS	Example 2; SEQ ID NO 1439; 134pp; English.	
CC	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	

Db 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKRLTFTS 360
Qy 361 NKGNAFSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLG 420
Db 361 NKGNAFSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLG 420
Qy 421 LEQLEHLDPQHSNLRKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Db 421 LEQLEHLDPQHSNLRKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Qy 481 NSFOENFLPDIPTFLRNLTFLDLISQCOLBOLSPTAFNSSLSQVLNMGSHNNPESLDTPPY 540
Db 481 NSFOENFLPDIPTFLRNLTFLDLISQCOLBOLSPTAFNSSLSQVLNMGSHNNPESLDTPPY 540
Qy 541 KCLNSLQVLDVSLNHIWTSKQELQHPSSSLAFNLITQNDPACTCEHOSFLQWIKDQRL 600
Db 541 KCLNSLQVLDVSLNHIWTSKQELQHPSSSLAFNLITQNDPACTCEHOSFLQWIKDQRL 600
Qy 601 LVEVERMECATPPSDKQMPVLSLNTTCOMKTIIGVSVLSVLVSVVAVLVYKFFHML 660
Db 601 LVEVERMECATPPSDKQMPVLSLNTTCOMKTIIGVSVLSVLVSVVAVLVYKFFHML 660
Qy 661 LAGCIKYGGENIYDAFYIYSSQDEDMVRNELVKNLEEGVPPFOLCLHYRDFIPGVAIAA 720
Db 661 LAGCIKYGGENIYDAFYIYSSQDEDMVRNELVKNLEEGVPPFOLCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVIVVVSQHPFIOGRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLR 780
Db 721 NIHEGFHRSKRVIVVVSQHPFIOGRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTVGTGCMQEAISI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTVGTGCMQEAISI 839

RESULT 4
ID ADC78785 standard; procein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DB Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN M02003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002MO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
XX
PT N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327bp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA:
Query Match 100.0%; Score 4355; DB 7; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSASRLAGTILPMAFLSCVRPESMPCVAVNNITVQCMELNPFYKIPDNLPEPTKXLD 60
Db 1 MMSASRLAGTILPMAFLSCVRPESMPCVAVNNITVQCMELNPFYKIPDNLPEPTKXLD 60
Qy 61 LSFNPLRLHLSGSEFSFPELQVLDLSRCEIQTIEDGAVQSLSHTLITGNPIQSLALG 120
Db 61 LSFNPLRLHLSGSEFSFPELQVLDLSRCEIQTIEDGAVQSLSHTLITGNPIQSLALG 120
Qy 121 AFSGLSLQKLVAVETNLASLENPPIGHLTKELVNAHNLISQPKLPEYFSNLTNLEHL 180
Db 121 AFSGLSLQKLVAVETNLASLENPPIGHLTKELVNAHNLISQPKLPEYFSNLTNLEHL 180
Qy 181 DLSNKTQSTYCTDPLVLRHQPMLNLSLIDSLNPMNFIQGAKEIRLHKLTLENNPSTL 240
Db 181 DLSNKTQSTYCTDPLVLRHQPMLNLSLIDSLNPMNFIQGAKEIRLHKLTLENNPSTL 240
Qy 241 NVMTKCIQGLAGLVHRLVIGEPFNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDI 300
Db 241 NVMTKCIQGLAGLVHRLVIGEPFNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDI 300
Qy 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKRLTFTS 360
Db 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKRLTFTS 360
Qy 361 NKGNAFSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLG 420
Db 361 NKGNAFSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLG 420
Qy 421 LEQLEHLDPQHSNLRKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Db 421 LEQLEHLDPQHSNLRKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Qy 481 NSFOENFLPDIPTFLRNLTFLDLISQCOLBOLSPTAFNSSLSQVLNMGSHNNPESLDTPPY 540
Db 481 NSFOENFLPDIPTFLRNLTFLDLISQCOLBOLSPTAFNSSLSQVLNMGSHNNPESLDTPPY 540
Qy 541 KCLNSLQVLDVSLNHIWTSKQELQHPSSSLAFNLITQNDPACTCEHOSFLQWIKDQRL 600
Db 541 KCLNSLQVLDVSLNHIWTSKQELQHPSSSLAFNLITQNDPACTCEHOSFLQWIKDQRL 600
Qy 601 LVEVERMECATPPSDKQMPVLSLNTTCOMKTIIGVSVLSVLVSVVAVLVYKFFHML 660
Db 601 LVEVERMECATPPSDKQMPVLSLNTTCOMKTIIGVSVLSVLVSVVAVLVYKFFHML 660
Qy 661 LAGCIKYGGENIYDAFYIYSSQDEDMVRNELVKNLEEGVPPFOLCLHYRDFIPGVAIAA 720
Db 661 LAGCIKYGGENIYDAFYIYSSQDEDMVRNELVKNLEEGVPPFOLCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVIVVVSQHPFIOGRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLR 780
Db 721 NIHEGFHRSKRVIVVVSQHPFIOGRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTVGTGCMQEAISI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTVGTGCMQEAISI 839

RESULT 5
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

DT 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAF05316, SEQ ID NO 14536.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 OS Unidentified.
 XX
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 XX
 PI Woolf C, D'Urso D, Refort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; AAF05316.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Example 1; Page: 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 839 AA;

Query Match 100.0%; Score 4355; DB 7; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSASRLAGTLIPMAFLSCVRPSMPCVEVPVITQCMELNPKYKIPDNLPTSTKRLD 60
 DB 1 MMSASRLAGTLIPMAFLSCVRPSMPCVEVPVITQCMELNPKYKIPDNLPTSTKRLD 60

QY 61 LSENPPLHLGSSYSPFPPELQVLDLSRCCEIQTEDAGYQSLSHSTLITGNPIQSLALG 120
 DB 61 LSENPPLHLGSSYSPFPPELQVLDLSRCCEIQTEDAGYQSLSHSTLITGNPIQSLALG 120
 QY 121 AFGSLSLQKLVAVETNLASLBNPPIGHLTKLKELVANHLIQLFQKPEVPSNLTNLEHL 180
 DB 121 AFGSLSLQKLVAVETNLASLBNPPIGHLTKLKELVANHLIQLFQKPEVPSNLTNLEHL 180
 QY 181 DLSGNKIQSIYCTDLRLVLAHQMPPLNLSTLSDLPNPNFIOGAFKXIRLKLTLNNPDSL 240
 DB 181 DLSGNKIQSIYCTDLRLVLAHQMPPLNLSTLSDLPNPNFIOGAFKXIRLKLTLNNPDSL 240
 QY 241 NVMKTCIQGLAGLEVHRLVLGEPFNGNLEKFDKSALEGLCNLTIEEFRLAYLDYDDI 300
 DB 241 NVMKTCIQGLAGLEVHRLVLGEPFNGNLEKFDKSALEGLCNLTIEEFRLAYLDYDDI 300
 QY 301 IDLFNCLTNVSSPSLVSVTIERVKDFSYNFGWHLVNCCKFGQFPTLKLSLRLEFTS 360
 DB 301 IDLFNCLTNVSSPSLVSVTIERVKDFSYNFGWHLVNCCKFGQFPTLKLSLRLEFTS 360
 QY 361 NKGNAFSEVDLSLEFLDLSRNGLSFKGCCSDPFGTSLKYDLSPNGVITWSSNFLG 420
 DB 361 NKGNAFSEVDLSLEFLDLSRNGLSFKGCCSDPFGTSLKYDLSPNGVITWSSNFLG 420
 QY 421 LEQLEHLDFQHSNKKQMSFVSLSLRLIYLDISHTHTVAENGISLSEVLKXAG 480
 DB 421 LEQLEHLDFQHSNKKQMSFVSLSLRLIYLDISHTHTVAENGISLSEVLKXAG 480
 QY 481 NSPOENFLPIFTELRLTLFLDSQCOLBOLSPFANSLISLOVLANSHNPFSLDTPPY 540
 DB 481 NSPOENFLPIFTELRLTLFLDSQCOLBOLSPFANSLISLOVLANSHNPFSLDTPPY 540
 QY 541 KCINSLQVLDYSLNHIMTSKKOELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKDQRL 600
 DB 541 KCINSLQVLDYSLNHIMTSKKOELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKDQRL 600
 QY 601 LVEVERMECATPSDKQMPVLSLNTTQNMKTIIIGVSVLVVSVVAVLYKKYFHLML 660
 DB 601 LVEVERMECATPSDKQMPVLSLNTTQNMKTIIIGVSVLVVSVVAVLYKKYFHLML 660
 QY 661 LAGCIRKGRBNITDARVIYSSODEMVRNLELVNKEGVPPOLCLHYRDFITGVALLA 720
 DB 661 LAGCIRKGRBNITDARVIYSSODEMVRNLELVNKEGVPPOLCLHYRDFITGVALLA 720
 QY 721 NIIEGFKSKRKYIVVVSQHFIOQRWCIFFEYLAQTQWPLSSRAGIIFIVLQKYEKTLRL 780
 DB 721 NIIEGFKSKRKYIVVVSQHFIOQRWCIFFEYLAQTQWPLSSRAGIIFIVLQKYEKTLRL 780
 QY 781 QQVELYRLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSMNPGVGTGCMQGEATSI 839
 DB 781 QQVELYRLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSMNPGVGTGCMQGEATSI 839

RESULT 6

AAW86361
 ID AAW86361 standard; protein; 837 AA.

AAW86361;

15-MAR-1999 (first entry)

Human DNAX toll-1-like receptor DTLR4.

DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 interleukin 1 receptor; phosphate metabolism; innate immunity response;
 modulate inflammatory function; morphological effect;
 immunological disorder.

Homo sapiens.

WO9805047-A2.

12-NOV-1998.

XX 07-MAY-1998; 98WO-US008979.
 XX
 XX 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX
 PA (SCHE) SCHERING CORP.
 PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
 XX WPI: 1999-059670/05.
 DR N-PSDB; AAV80675.
 PT Human DNX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 XX metabolism, modulate inflammatory function or innate immunity responses.
 PS Claim 3; Page 147-149; 171pp; English.
 XX
 CC The present invention specifically describes human DNX toll-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 CC
 SQ Sequence 837 AA;
 Query Match 99.6%; Score 4335.5; DB 2; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 2 MSASRLAGTLIPAMAFISCVPESMEPCVEVVPNITVOCMLNPKYKIDNLPSTKNL 61
 Db 1 MSASRLAGTLIPAMAFISCVPESMEPCVEVVPNITVOCMLNPKYKIDNLPSTKNL 59
 QY 62 SFNPLRLHLSGYSFSPFPELVLDLSRCEIQITIEDGAVYSLSTLITITGNPISLALGA 121
 Db 60 SFNPLRLHLSGYSFSPFPELVLDLSRCEIQITIEDGAVYSLSTLITITGNPISLALGA 119
 QY 122 FSGSLSLQKLVAVETNVLASLENFPIGHKTKLKEINVAHNLIOSTKLPBYFNSLNTLNEHLD 181
 Db 120 FSGSLSLQKLVAVETNVLASLENFPIGHKTKLKEINVAHNLIOSTKLPBYFNSLNTLNEHLD 179
 QY 182 LSSNKKIOSIYCTDRAVHOMPLNLSLISLNPNNFIOGAFKEIRLHKTLRLNPFPSLN 241
 Db 180 LSSNKKIOSIYCTDRAVHOMPLNLSLISLNPNNFIOGAFKEIRLHKTLRLNPFPSLN 239
 QY 242 VMKTCIOGLAGLEVHRLVLEGFNENGNLEKFKSALBGLCNLTIEEFLAYLDYLDII 301
 Db 240 VMKTCIOGLAGLEVHRLVLEGFNENGNLEKFKSALBGLCNLTIEEFLAYLDYLDII 299
 QY 302 DLFNCLTNVSSFSLSVSTIERVKOPSTNFGMQLHVLVNCFKGPPTLKLKSLKLTFTSN 361
 Db 300 DLFNCLTNVSSFSLSVSTIERVKOPSTNFGMQLHVLVNCFKGPPTLKLKSLKLTFTSN 359
 QY 362 KGGNASEVDLPSEFLDLSRNGSLSPKCCSQSPGTTSLKYLDLSFNGVITWMSNPLGL 421
 Db 360 KGGNASEVDLPSEFLDLSRNGSLSPKCCSQSPGTTSLKYLDLSFNGVITWMSNPLGL 419
 QY 422 EOLEHLDFOHNSLKNOMSEFVFLSLRNLIYDISHITRVAFNKGLSLEVLKMAGN 481
 Db 420 EOLEHLDFOHNSLKNOMSEFVFLSLRNLIYDISHITRVAFNKGLSLEVLKMAGN 479
 QY 482 SFQENFLPDIETELRNLTFLDLSQCLEQSPTAFNSLSLQVLNMGSHNNFFSLDTPPYK 541

Db 480 SFQENFLPDIETELRNLTFLDLSQCLEQSPTAFNSLSLQVLNMGSHNNFFSLDTPPYK 539
 QY 542 CLNSLOVLDYSLNINIMMSKQOELOHPPSSLAFLNLTQNDPACTCEHOSFLQWIDQROL 601
 Db 540 CLNSLOVLDYSLNINIMMSKQOELOHPPSSLAFLNLTQNDPACTCEHOSFLQWIDQROL 599
 QY 602 VEVERMECATPSPDQGNPVLSLNITTCOMNKTIIIGSVLSVLVSVVAVLVYKFFHMLL 661
 Db 600 VEVERMECATPSPDQGNPVLSLNITTCOMNKTIIIGSVLSVLVSVVAVLVYKFFHMLL 659
 QY 662 AGCIKTRGENTIDAFIYYSODEDWVRNELYKNLESGVPPQLCHYRDFIPGVAIAAN 721
 Db 660 AGCIKTRGENTIDAFIYYSODEDWVRNELYKNLESGVPPQLCHYRDFIPGVAIAAN 719
 QY 722 IIHGFKSRKVIYVVSQHFIOSRWCIFEYELAQTWQFLSSRAGIIFIVLOKVEKTLRQ 781
 Db 720 IIHGFKSRKVIYVVSQHFIOSRWCIFEYELAQTWQFLSSRAGIIFIVLOKVEKTLRQ 779
 QY 782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGSNNPEGTVGTCNMGEATS1 839
 Db 780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGSNNPEGTVGTCNMGEATS1 837
 RESULT 7
 ID AAE16102 standard; protein; 837 AA.
 AC AAE16102;
 XX 26-MAR-2002 (first entry)
 DT
 XX Human DNX Toll like receptor (DTLR) 4 #2.
 DE
 XX Human, DNX Toll like receptor; DTLR; therapy; immunological disorder;
 KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 KW Homo sapiens.
 OS
 XX W0200190151-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 23-MAY-2001; 2001WO-US016766.
 PF
 XX 25-MAY-2000; 2000US-0207558P.
 PR
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI: 2002-083085/11.
 DR N-PSDB; AAD26292.
 XX
 PT New DNX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS Claim 3; Page 41; 297pp; English.
 XX
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAE16116). However these sequences differ
 CC at several locations
 CC
 XX

XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 5; Length 837;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

2 MSASRLAGTLIPAAAFSCVAPESMEPCVEVVPNTTYQCMELNFKYKIPDNLPSTKNL 61
 1 MSASRLAGTLIPAAAFSCVAPESMEPCVE-VPNITTYQCMELNFKYKIPDNLPSTKNL 59
 62 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 60 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYOSLSHSLTLITGNPIQSLALGA 119
 122 FSGSLSLQKLVAVENNLASLENPFGHKTKELVANLILQSPFLPEYPSNLTNLEHLD 181
 120 FSGSLSLQKLVAVENNLASLENPFGHKTKELVANLILQSPFLPEYPSNLTNLEHLD 179
 182 LSSNKIQTCTDRLVHQPMLNLSLDPNPMNFIOGAFKELRLKLTLRNPFSLN 241
 180 LSSNKIQTCTDRLVHQPMLNLSLDPNPMNFIOGAFKELRLKLTLRNPFSLN 239
 242 VMKTCIQGLAGLEVRLVGEFRNEGNLEKFDKSLBGLCNLTIEEFLAVLDYLDII 301
 240 VMKTCIQGLAGLEVRLVGEFRNEGNLEKFDKSLBGLCNLTIEEFLAVLDYLDII 299
 302 DLFNCTIVWSSFLSVTVTERKQDSYVNGWQHELVNCKRGQPTTLKSLKRLTFPSN 361
 300 DLFNCTIVWSSFLSVTVTERKQDSYVNGWQHELVNCKRGQPTTLKSLKRLTFPSN 359
 362 KGGNAFSEVDLPSEFLFLSRNGLSFKGCGSDPGTTLKLYLDLSPFGVITMSNFTGL 421
 360 KGGNAFSEVDLPSEFLFLSRNGLSFKGCGSDPGTTLKLYLDLSPFGVITMSNFTGL 419
 422 EQLHLDFOHSNLSKQMESEVFLSLRLNLIYLDISHHTTRVAFNGIENGSLSEVLKMAGN 481
 420 EQLHLDFOHSNLSKQMESEVFLSLRLNLIYLDISHHTTRVAFNGIENGSLSEVLKMAGN 479
 482 SPQENFLPDITELRNLTFLDLISQCLHQLSPFANSLSLQVLMNSHNPFSLDTPPYK 541
 480 SPQENFLPDITELRNLTFLDLISQCLHQLSPFANSLSLQVLMNSHNPFSLDTPPYK 539
 542 CLNSIQVLDYSLNHNMTSKQELQHPSSLAFLNLTQNDPACTCHQSFLQWIKQORLL 601
 540 CLNSIQVLDYSLNHNMTSKQELQHPSSLAFLNLTQNDPACTCHQSFLQWIKQORLL 599
 602 VEVEEMECATSDKQGMFVLNLTQCNQAKTIIIGVSVLVVAVVAVLVYKFEYHMLL 661
 600 VEVEEMECATSDKQGMFVLNLTQCNQAKTIIIGVSVLVVAVVAVLVYKFEYHMLL 659
 662 AGCTKYGGENIYDAFVIYSSQDEDMVNEVLKNEEGVPPQCLAHYRDFPGVAIAAN 721
 660 AGCTKYGGENIYDAFVIYSSQDEDMVNEVLKNEEGVPPQCLAHYRDFPGVAIAAN 719
 722 IIHGPHSRKRVIVVVOHFTQSRWCIFEYEIAQWQGLSSAGIIFVLQKVEKTLILRO 781
 720 IIHGPHSRKRVIVVVOHFTQSRWCIFEYEIAQWQGLSSAGIIFVLQKVEKTLILRO 779
 782 QVELYRLRLSRNTYLEMEDSVLGRHIFWRRLKALLDGSKWNPDEGTGTCWQOEAISI 839
 780 QVELYRLRLSRNTYLEMEDSVLGRHIFWRRLKALLDGSKWNPDEGTGTCWQOEAISI 837

ID ABU04776 standard; protein; 837 AA.

XX ABU04776;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1442.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 XX cytochrome; protease inhibitor; transporter; cytoskeletal protein;

XX receptor; transcription factor; cancer; MHC;
 XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.

XX Example 2, SEQ ID NO 1442; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 XX fragment of a kinase, phosphatase, protease, or transcription factor. The
 XX transporter, cytoskeletal protein, receptor or transcription factor. The
 XX polypeptide is useful as an immunogenic composition for eliciting in a
 XX mammal an immunogenic response directed against any of the purified
 XX polypeptide. The purified polypeptide, or the antibody that binds to this
 XX polypeptide, is useful for treating cancer. The polypeptide is also
 XX useful for identifying compounds that binds to a naturally processed
 XX class I or class II MHC-binding polypeptide. The polypeptides and
 XX polynucleotides are particularly useful for treating or preventing
 XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 XX lymphoma or leukaemia. These are also useful for screening agents for
 XX treating the above mentioned diseases. This sequence represents an
 XX expressed protein tag (EPT) isolated from human tissue for translational
 XX profiling. Note: This sequence does not appear in the printed
 XX specification but was obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_ptc_sequences

XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 6; Length 837;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

2 MSASRLAGTLIPAAAFSCVAPESMEPCVEVVPNTTYQCMELNFKYKIPDNLPSTKNL 61
 1 MSASRLAGTLIPAAAFSCVAPESMEPCVE-VPNITTYQCMELNFKYKIPDNLPSTKNL 59
 62 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 60 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYOSLSHSLTLITGNPIQSLALGA 119

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QY 122 FSGLSLQKVAVAETNLASLENPPIGHLKTLKELNVAHNLIOSEFKLPEYFSNLTNLEHLD 181
XX 120 FSGLSLQKVAVAETNLASLENPPIGHLKTLKELNVAHNLIOSEFKLPEYFSNLTNLEHLD 179
QY 182 LSSNKKIOSICTDRLVHQMPNLNLSLDLSLNPNPFIOGPAFKELRLHKLTLRNPNPSLN 241
XX 180 LSSNKKIOSICTDRLVHQMPNLNLSLDLSLNPNPFIOGPAFKELRLHKLTLRNPNPSLN 239
QY 242 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEFLAYLDYLDII 301
XX 240 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEFLAYLDYLDII 299
QY 302 DLFNCLTNVSSFSLSVSTIERVKDPSYNFGMOHLELVNCKEFGQPTLKSLKRLTFTSN 361
XX 300 DLFNCLTNVSSFSLSVSTIERVKDPSYNFGMOHLELVNCKEFGQPTLKSLKRLTFTSN 359
QY 362 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTTSKLYLDLSPNGVITMSSNPLGL 421
XX 360 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTTSKLYLDLSPNGVITMSSNPLGL 419
QY 422 EQLHLDFOHNSNLKQMSSESVFLSLRNLTYLDISHTHTRVAFNGIFNGLSLEVLKMAGN 481
XX 420 EQLHLDFOHNSNLKQMSSESVFLSLRNLTYLDISHTHTRVAFNGIFNGLSLEVLKMAGN 479
QY 482 SFQENPLDPIFTELRLNLTFLDLSQCCQLEQLSPFANSLISLQVLMNSHNNFSLDTPPYK 541
XX 480 SFQENPLDPIFTELRLNLTFLDLSQCCQLEQLSPFANSLISLQVLMNSHNNFSLDTPPYK 539
QY 542 CLNSLOVLDVSLNIMTMSKQELQHPSSLAFLNLTONDFACCTEHOFSLOWITDOQL 601
XX 540 CLNSLOVLDVSLNIMTMSKQELQHPSSLAFLNLTONDFACCTEHOFSLOWITDOQL 599
QY 602 VEVRMCAFPSPDQKMPVLNLTCCQNKTIIGSVLSVLVAVLVYKFFHMLL 661
XX 600 VEVRMCAFPSPDQKMPVLNLTCCQNKTIIGSVLSVLVAVLVYKFFHMLL 659
QY 662 AGCIKYGRENITDAFYIYSSQDEDMVNLVKMLEGVPPQCLAHYRDFIPGVAIAAN 721
XX 660 AGCIKYGRENITDAFYIYSSQDEDMVNLVKMLEGVPPQCLAHYRDFIPGVAIAAN 719
QY 722 IIHGFHRSKRVIVVSOHPIQSRWCTFEYIAQTQWPLSRAGITFIYLOKVEKTLRLQ 781
XX 720 IIHGFHRSKRVIVVSOHPIQSRWCTFEYIAQTQWPLSRAGITFIYLOKVEKTLRLQ 779
QY 782 QVELYRLISRTTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGVCNMQOATS1 839
XX 780 QVELYRLISRTTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGVCNMQOATS1 837

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
AC AAE16116;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
KW Human, DNAX Toll like receptor; DTLR; therapy; immunological disorder;
XX interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 211
FT /label= Unknown
FT /note= "Encoded by AAY"
PN WO200190151-A2.
XX
XX 29-NOV-2001.

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XX 23-MAY-2001; 2001WO-US016766.
XX
XX 25-MAY-2000; 2000US-0207558P.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX WPI; 2002-083085/11.
XX DR N-PSDB; AAD26306.
XX
XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
XX conditions exhibiting abnormal expression of the receptors of their
XX ligands, particularly abnormalities manifested by immunological
XX disorders.
XX
XX Claim 3; Page 240-243; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
XX human DNAX Toll like receptor (DTLR) protein and their corresponding
XX nucleic acids. The DTLR is useful for treating conditions exhibiting
XX abnormal expression of the receptors of their ligands. Such abnormality
XX is manifested by immunological disorders. In particular, the DTLR is
XX useful for treating various disease or disorders associated with abnormal
XX expression or abnormal triggering of response to a ligand. The DTLR is
XX also useful as an immunogen for the production of antisera or antibodies
XX specific, e.g. capable of distinguishing between other interleukin (IL)-1
XX receptor family members, for the DTLR or its various fragments. The
XX purified DTLR can be used to screen monoclonal antibodies or antigen-
XX binding fragments. The antibodies are useful for screening expression
XX libraries for particular expression products. These are useful for
XX detecting or diagnosing various immunological conditions related to
XX expression of DTLR or cells that express it. The present sequence is
XX human DTLR4 protein, alternative version. The DTLR4 gene is located on
XX chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
XX be similar to the sequence shown in page 41 (AAE16102). However these
XX sequences differ at several locations
XX
XX Sequence 837 AA;
XX
XX Query Match 99.4%; Score 4328.5; DB 5; Length 837;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 836; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
XX
QY 2 MSASRLAGTLIPMAAFSCVRPSPWPCVENVNITYQCHELNFYKIPDLNLPSTKQLDL 61
XX 1 MSASRLAGTLIPMAAFSCVRPSPWPCVENVNITYQCHELNFYKIPDLNLPSTKQLDL 59
QY 62 SFNPLRHLSGSYSPFPELQVLDLSRCEIQTIEDGAYOSLSHLSLTITGNPIQSLALGA 121
XX 60 SFNPLRHLSGSYSPFPELQVLDLSRCEIQTIEDGAYOSLSHLSLTITGNPIQSLALGA 119
QY 122 FSGLSLQKVAVAETNLASLENPPIGHLKTLKELNVAHNLIOSEFKLPEYFSNLTNLEHLD 181
XX 120 FSGLSLQKVAVAETNLASLENPPIGHLKTLKELNVAHNLIOSEFKLPEYFSNLTNLEHLD 179
QY 182 LSSNKKIOSICTDRLVHQMPNLNLSLDLSLNPNPFIOGPAFKELRLHKLTLRNPNPSLN 241
XX 180 LSSNKKIOSICTDRLVHQMPNLNLSLDLSLNPNPFIOGPAFKELRLHKLTLRNPNPSLN 239
QY 242 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEFLAYLDYLDII 301
XX 240 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEFLAYLDYLDII 299
QY 302 DLFNCLTNVSSFSLSVSTIERVKDPSYNFGMOHLELVNCKEFGQPTLKSLKRLTFTSN 361
XX 300 DLFNCLTNVSSFSLSVSTIERVKDPSYNFGMOHLELVNCKEFGQPTLKSLKRLTFTSN 359
QY 362 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTTSKLYLDLSPNGVITMSSNPLGL 421
XX 360 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTTSKLYLDLSPNGVITMSSNPLGL 419

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QY 422 EOLEHLDPOHSLKMKSEPSVFLSLRNLIYLDISHTRVAFNGIFNGLSLEVLKMAGN 481
 Db 420 EOLEHLDPOHSLKMKSEPSVFLSLRNLIYLDISHTRVAFNGIFNGLSLEVLKMAGN 479
 QY 482 SPOENFLDIFTELNLTFDLISQCOLSPTANSLSLOVLMASHNPFSLDTPPYK 541
 Db 480 SPOENFLDIFTELNLTFDLISQCOLSPTANSLSLOVLMASHNPFSLDTPPYK 539
 QY 542 CLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNTQNDFACTCHOSFLQWIKDQRL 601
 Db 540 CLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNTQNDFACTCHOSFLQWIKDQRL 599
 QY 602 VEVERMECATPSDQKQMPVLSLNTTCQANKTIIGVSVLSVAVVAVLVKYPFHML 661
 Db 600 VEVERMECATPSDQKQMPVLSLNTTCQANKTIIGVSVLSVAVVAVLVKYPFHML 659
 QY 662 AGCIKYGGENTYDAFVLYSSODEDMVNEMLVKNLEEGVPPQCLAHYRDFPGVAIAAN 721
 Db 660 AGCIKYGGENTYDAFVLYSSODEDMVNEMLVKNLEEGVPPQCLAHYRDFPGVAIAAN 719
 QY 722 IIHGFFHKSRYIVVVSQHFQISRWCFEYELAQWQFSLSRAGIIFIVLOKVEKTLRQ 781
 Db 720 IIHGFFHKSRYIVVVSQHFQISRWCFEYELAQWQFSLSRAGIIFIVLOKVEKTLRQ 779
 QY 782 QVELYRLSRNTYLEMEDSVLGRHIFWRRLRXALIDGKSNPEGTGTCNMQEATSI 839
 Db 780 QVELYRLSRNTYLEMEDSVLGRHIFWRRLRXALIDGKSNPEGTGTCNMQEATSI 837

RESULT 10

ID ADO57782 standard; protein; 808 AA.
 AC ADO57782;

XX 12-AUG-2004 (first entry)
 Db Chimpanzee toll-like receptor 4 SEQ ID NO:3.
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 XX Pan troglodytes.
 OS MO2004042365-A2.
 PN 21-MAY-2004.
 PD 03-NOV-2003; 2003WO-US036247.
 PF 01-NOV-2002; 2002US-0423113P.
 PR (EVOLO-) EVOLUTIONARY GENOMICS LLC.
 XX Meslier W;
 PI WPI; 2004-400726/37.
 DR N-PSDB; ADO57780, ADO57781.
 XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX Example 1, SEQ ID NO 3; 11pp; English.
 XX The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the

CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.

XX Sequence 808 AA;

Query Match 95.9%; Score 4178; DB 8; Length 808;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 805; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 32 VVPIITTCQMEINLYKIPDNLPSTKNLDSFNPRLHIGSYSPSPPELQVLDLSRCEIQ 91
 Db 1 VVPIITTCQMEINLYKIPDNLPSTKNLDSFNPRLHIGSYSPSPPELQVLDLSRCEIQ 60
 QY 92 TIEDGAYOSLSHTLITGNPISLALGASGSLQKLVAVETNLASLNPPGHIXT 151
 Db 61 TIEDGAYOSLSHTLITGNPISLALGASGSLQKLVAVETNLASLNPPGHIXT 120
 QY 152 LKEINLVANHLIQSEPLPEYFENLTLNLEHLDLSNKKIOSIYCTDRLVHLQMPNLNLSLDS 211
 Db 121 LKEINLVANHLIQSEPLPEYFENLTLNLEHLDLSNKKIOSIYCTDRLVHLQMPNLNLSLDS 180
 QY 212 LNPANFTOPGAFKEIRLHKLTLRNPPSLNVMKTCIOGLAGLEVRLVLSFRRNEGLEK 271
 Db 181 LNPANFTOPGAFKEIRLHKLTLRNPPSLNVMKTCIOGLAGLEVRLVLSFRRNEGLEK 240
 QY 272 FDKSALBGLCNLTTEBFLAYLDYLDITDLEFCLTNVSSFSLSVSTIEVKPFSYVFG 331
 Db 241 FDKSALBGLCNLTTEBFLAYLDYLDITDLEFCLTNVSSFSLSVSTIEVKPFSYVFG 300
 QY 332 WOHLIELVNCKEGQEPPTLKLKSLKRLFTSNKNGNAFSEVDLPSEFLDLSHNGLSFKGCC 391
 Db 301 WOHLIELVNCKEGQEPPTLKLKSLKRLFTSNKNGNAFSEVDLPSEFLDLSHNGLSFKGCC 360
 QY 392 SOSDFGTTSLKYLDLSRNGVITMSSNFGLEQLEHLDPOHSLKMKSEPSVFLSLRNLIY 451
 Db 361 SOSDFGTTSLKYLDLSRNGVITMSSNFGLEQLEHLDPOHSLKMKSEPSVFLSLRNLIY 420
 QY 452 LDISHTRVAFNGIFNGLSLEVLKMAAGNSFOENPLPDFTELRNLTFDLISQCOLBQL 511
 Db 421 LDISHTRVAFNGIFNGLSLEVLKMAAGNSFOENPLPDFTELRNLTFDLISQCOLBQL 480
 QY 512 SPTAFNSLSLOVLMASHNPFSLDTPPYKCLNSLOVLDYSLNHIMTSKQELQHPSSLS 571
 Db 481 SPTAFNSLSLOVLMASHNPFSLDTPPYKCLNSLOVLDYSLNHIMTSKQELQHPSSLS 540
 QY 572 AFLNLTONDFACTCHOSFLOWIKDQROLLEVERMECATPSDQKQMPVLSLNTTCQANK 631
 Db 541 AFLNLTONDFACTCHOSFLOWIKDQROLLEVERMECATPSDQKQMPVLSLNTTCQANK 600
 QY 632 TIIGSVLSVLSVAVVAVLVKYPFHMLLAGCIKYRGENTYDAFVLYSSODDDWANE 691
 Db 601 TIIGSVLSVLSVAVVAVLVKYPFHMLLAGCIKYRGENTYDAFVLYSSODDDWANE 660
 QY 692 LVKNLEEGVPPQCLAHYRDFPGVAIAANIIEHGFHKSRYIVVVSQHFQISRWCFEY 751
 Db 661 LVKNLEEGVPPQCLAHYRDFPGVAIAANIIEHGFHKSRYIVVVSQHFQISRWCFEY 720
 QY 752 EIAQWQFSLSRAGIIFIVLOKVEKTLRQVELYRLSRNTYLEMEDSVLGRHIFWRRL 811
 Db 721 EIAQWQFSLSRAGIIFIVLOKVEKTLRQVELYRLSRNTYLEMEDSVLGRHIFWRRL 780
 QY 812 RKALLDGKSNPEGTGTCNMQEATSI 839
 Db 781 RKALLDGKSNPEGTGTCNMQEATSI 808

RESULT 11

ID ADO57785 standard; protein; 808 AA.
 AC ADO57785;

XX 12-AUG-2004 (first entry)
XX Gorilla toll-like receptor 4 SEQ ID NO:6.
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; gorilla.
OS Gorilla gorilla.
XX MO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003WO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Messier W;
XX WPI; 2004-400726/37.
XX N-PSDB; ADOS7783; ADOS7784.
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX Example 1; SEQ ID NO 6; 111pp; English.
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents gorilla TLR4.
XX
XX Sequence 808 AA;
XX
XX Query Match 95.7%; Score 4167; DB 8; Length 808;
XX Best Local Similarity 99.4%; Pred. No. 0;
XX Matches 803; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
QY 32 VVNNITVQCMELNFKYKIPDNLPSTKNLDSFNPLRHIGSYSPSPPELQVLDLSRCEIQ 91
Db 1 VVNNITVQCMELNFKYKIPDNLPSTKNLDSFNPLRHIGSYSPSPPELQVLDLSRCEIQ 60
QY 92 TIEBGAYOSLSHSLTLLITGNPIOSLALGAFSGSLQKLVAVETNLASLENPIGHLKT 151
Db 61 TIEBGAYOSLSHSLTLLITGNPIOSLALGAFSGSLQKLVAVETNLASLENPIGHLKT 120
QY 152 LKEINLVANHILQSFRLPEYFSNLTNLEHLDSNKKIOSYCTDRLVHQMPLNLSDLS 211
Db 121 LKEINLVANHILQSFRLPEYFSNLTNLEHLDSNKKIOSYCTDRLVHQMPLNLSDLS 180
QY 212 LNPNNFTOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVLSFRNENLEK 271
Db 181 LNPNNFTOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVLSFRNENLEK 240
QY 272 FDKSALBGLCNLTIEBRLAVLDYLDIIDLFNCLTNVSSFSLSVVTIERKXDFSYNFG 331
Db 241 FDKSALBGLCNLTIEBRLAVLDYLDIIDLFNCLTNVSSFSLSVVTIERKXDFSYNFG 300
QY 332 MOHLELVNCKRGOPPTLKLSIKLTFPSNKGNAFSDVLPSEFLDLSNGLSPFGCC 391
Db 301 MOHLELVNCKRGOPPTLKLSIKLTFPSNKGNAFSDVLPSEFLDLSNGLSPFGCC 360

QY 392 SOSDFGTTSLKYLDLSFNGVITMSSNFLAGLEHLDFOHNLKOMSEFSVFLSLRNLIY 451
Db 361 SOSDFGTTSLKYLDLSFNGVITMSSNFLAGLEHLDFOHNLKOMSEFSVFLSLRNLIY 420
QY 452 LDISHTHTRAVFNQIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSOCQLEQL 511
Db 421 LDISHTHTRAVFNQIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSOCQLEQL 480
QY 512 SPTAFNSLSLQVLANMHNHNFSDTPEYKCLNSLOVLDYSLNIMTSKQELQHPSSL 571
Db 481 SPTAFNSLSLQVLANMHNHNFSDTPEYKCLNSLOVLDYSLNIMTSKQELQHPSSL 540
QY 572 AFLNLTONDFACTCEHOSFLQWIKDORQLVVEYRMECATPSDQGNPVLSTNTQMNK 631
Db 541 AFLNLTONDFACTCEHOSFLQWIKDORQLVVEYRMECATPSDQGNPVLSTNTQMNK 600
QY 632 TIIGSVLSVLVSVAVLVYKFFHMLLAGCIRYGRGENIYDAFVIYSSQDEDDWRNE 691
Db 601 TIIGSVLSVLVSVAVLVYKFFHMLLAGCIRYGRGENIYDAFVIYSSQDEDDWRNE 660
QY 692 LVKNLEEGVPPFQCLHYRDPFPGVALAANIHEGFHKSRRVYVVSQHFIOGRWCIFEX 751
Db 661 LVKNLEEGVPPFQCLHYRDPFPGVALAANIHEGFHKSRRVYVVSQHFIOGRWCIFEX 720
QY 752 EIAQWQFLSSRAGIIFIVLOKYEKTLRQOVELYRLSNRYLEWEDSVLGRHIFWRRL 811
Db 721 EIAQWQFLSSRAGIIFIVLOKYEKTLRQOVELYRLSNRYLEWEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNMPEGTGTGCNMOEATSI 839
Db 781 RKALLDGKSNMPEGTGTGCNMOEATSI 808
XX
XX RESULT 12
XX ID ADOS7803 standard; protein; 808 AA.
XX AC ADOS7803;
XX 12-AUG-2004 (first entry)
XX Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX Pan troglodytes.
XX MO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003WO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Messier W;
XX WPI; 2004-400726/37.
XX N-PSDB; ADOS7801, ADOS7802.
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX Disclosure; SEQ ID NO 24; 111pp; English.
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey

comparing comparing the TLR4 polynucleotide sequence of the Old World monkey with corresponding TLR4 polynucleotide sequence of a human. The method of the invention has antibacterial, immunosuppressive, and antiasthmatic activity. The method is useful in identifying a nucleotide change in a TLR4 polynucleotide sequence of an Old World monkey where the change may be associated with reduced sensitivity to Gram-negative bacterial infection. The methods, agents and composition are useful in treating sepsis, severe sepsis or septic shock and asthma. The present sequence represents chimpanzee TLR4.

Sequence 808 AA;

Query Match 95.6%; Score 4164; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

32 VPPNTTCMELNPKTIDNLPSTKNDLSPNPLRHGVSFFSPPELQVLDLSRCEIQ 91
1 VPPNTTCMELNPKTIDNLPSTKNDLSPNPLRHGVSFFSPPELQVLDLSRCEIQ 60
92 TIEBGAYOSLSHSLTLITGNPIQSLALGAFSGSLSLQKLVAVETNLASLENFPIGHKT 151
61 TIEBGAYOSLSHSLTLITGNPIQSLALGAFSGSLSLQKLVAVETNLASLENFPIGHKT 120
152 LKEILNVAHNLQSEFLPEYFSNLNLNLEHLDSSNKIQSIYCTDLRVLHQMPLNLSDLS 211
121 LKEILNVAHNLQSEFLPEYFSNLNLNLEHLDSSNKIQSIYCTDLRVLHQMPLNLSDLS 180
212 LNPMPFLOPGAPKEIRLHKLTLRNNPDSLNWKTICIQLAGLHVRLVGEFRNGNLEK 271
181 LNPMPFLOPGAPKEIRLHKLTLRNNPDSLNWKTICIQLAGLHVRLVGEFRNGNLEK 240
272 FDKSALBEGJLNLTEEFRLAYLDYLDIIDLFCNLTVNSPFLSVTIERKQDSYNGF 331
241 FDKSALBEGJLNLTEEFRLAYLDYLDIIDLFCNLTVNSPFLSVTIERKQDSYNGF 300
332 WQHELVNCKFGQFPFLKLKSLKRLTFTSNKGNASEVDLPSLEFLDLSRNGLSFKGCC 391
301 WQHELVNCKFGQFPFLKLKSLKRLTFTSNKGNASEVDLPSLEFLDLSRNGLSFKGCC 360
392 SOSDPTGTSLSKTYLDSFNGVITMSNFIQGLBOLHLDQHSNLSKMSFVSPLSRNLIT 451
361 SOSDPTGTSLSKTYLDSFNGVITMSNFIQGLBOLHLDQHSNLSKMSFVSPLSRNLIT 420
452 LDISHTHRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIPTLRLNLFELDLSQQLBOL 511
421 LDISHTHRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIPTLRLNLFELDLSQQLBOL 480
512 SPFAENSLSSLOVLMNSHNPFSLDTPPYKCLNSLOVLDYSLNHMTSKOELQHPSSL 571
481 SPFAENSLSSLOVLMNSHNPFSLDTPPYKCLNSLOVLDYSLNHMTSKOELQHPSSL 540
572 APLNLTQNDPACTCHOSFLOMFKQROLVVEVMECATPSDKGMEVLSLNTTCQNNK 631
541 APLNLTQNDPACTCHOSFLOMFKQROLVVEVMECATPSDKGMEVLSLNTTCQNNK 600
632 TIIGSVSVSVVAVAVLVYKFFHMLAGCICYGGENYDFAFVYSSODEDWMVNE 691
601 TIIGSVSVSVVAVAVLVYKFFHMLAGCICYGGENYDFAFVYSSODEDWMVNE 660
692 LVKNLEBVPFQOLCLHYRDFIPGVALANIIHGBFHSRKVIVVSOHFIQSRWCIFEY 751
661 LVKNLEBVPFQOLCLHYRDFIPGVALANIIHGBFHSRKVIVVSOHFIQSRWCIFEY 720
752 EIAQTWQSLSRAGIIFIVLOKVEKTLRQVVELYRLSRNTYLEWESVUGRAHFWRL 811
721 EIAQTWQSLSRAGIIFIVLOKVEKTLRQVVELYRLSRNTYLEWESVUGRAHFWRL 780
812 RKALLDGKSNPEGTAVTGCMQOATS 839
781 RKALLDGKSNPEGTAVTGCMQOATS 808

RESULT 13
AAW86352
ID AAW86352 standard; protein; 799 AA.
XX
AC AAW86352;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human DNAX toll-like receptor DTLR4.
XX
KW DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
interleukin 1 receptor; phosphate metabolism; innate immunity response;
modulate inflammatory function; morphological effect;
immunological disorder.
XX
OS Homo sapiens.
XX
PN WO9850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
XX
FI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
DR WPI; 1999-059670/05.
XX
DR N-PSDB; AAV80666.
XX

Human DNAX toll-like receptor, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate immunity responses.
Example; Page 115-117; 171pp; English.
The present invention specifically describes human DNAX toll-like receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate immunity responses or morphological effects. The DTLR proteins can be used in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. These abnormalities are typically manifested by immunological disorders

Sequence 799 AA;
Query Match 95.1%; Score 4141; DB 2; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

41 MELNFKYKIPDNLPTSTKNLDSFNPRLHLSGVSFFSPPELQVLDLSRCEIQTIEBGAQS 100
1 MELNFKYKIPDNLPTSTKNLDSFNPRLHLSGVSFFSPPELQVLDLSRCEIQTIEBGAQS 60
101 LSHSLTLITGNPIQSLALGAFSGSLSLQKLVAVETNLASLENFPIGHKTLEILNVAH 160
61 LSHSLTLITGNPIQSLALGAFSGSLSLQKLVAVETNLASLENFPIGHKTLEILNVAH 120
161 LIQSFKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQMPLNLSDLSLNPNPFIOP 220
121 LIQSFKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQMPLNLSDLSLNPNPFIOP 180
221 GAFFKIRLHKLTLRNNPDSLNWKTICIQLAGLHVRLVGEFRNGNLEKFDKSALEGL 280

Db 181 GAFKEIRLHKLTLRNNFSLNVMKTCIOGLAGLEVHRLVIGEPFNEGULEKFDKSALEGL 240
Qy 281 CNLTIEEFRLAYLDYLDIIDLFCNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNC 340
Db 241 CNLTIEEFRLAYLDYLDIIDLFCNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNC 300
Qy 341 KFGQFPTLKLSKRLFTTSNKGNAFSEVDLPSELFDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPTLKLSKRLFTTSNKGNAFSEVDLPSELFDLSRNGLSFKGCCSQSDFGTTS 360
Qy 401 LKYLDLSFNGVITWSSNFIJGLEHLDFOHSHNLKQMSSEFVLSLRLNYLDISHHTR 460
Db 361 LKYLDLSFNGVITWSSNFIJGLEHLDFOHSHNLKQMSSEFVLSLRLNYLDISHHTR 420
Qy 461 VAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLNLTFLDLSQCEQLSPRAFNSLS 520
Db 421 VAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLNLTFLDLSQCEQLSPRAFNSLS 480
Qy 521 SLOVLNASHNPFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSIAFLNLQND 580
Db 540 SLOVLNASHNPFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSIAFLNLQND 540
Qy 581 FACTCEHOSFLOWIKDORQLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 640
Db 541 FACTCEHOSFLOWIKDORQLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 600
Qy 641 VLVSVVAVLVYKFFHMLLAGCIKYRGENTYDAFVYSSODEDWVRNELYKNEBGV 700
Db 601 VLVSVVAVLVYKFFHMLLAGCIKYRGENTYDAFVYSSODEDWVRNELYKNEBGV 660
Qy 701 PPFLQCLHYRDPITGVAIANIIHGFYKSKRVIVVSOHFIQSRWCIFEYELIAQTWQFL 760
Db 720 PPFLQCLHYRDPITGVAIANIIHGFYKSKRVIVVSOHFIQSRWCIFEYELIAQTWQFL 720
Qy 761 SSRAGIIFIVQKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFMRRLRKALLDQKS 820
Db 721 SSRAGIIFIVQKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFMRRLRKALLDQKS 780
Qy 821 WNPBGTVGTGCMQOEATSI 839
Db 781 WNPBGTVGTGCMQOEATSI 799

RESULT 14
AAE16093
ID AAE16093 standard; protein; 799 AA.
XX
AC AAE16093;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW Human: DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW interluekin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX WPI; 2002-083085/11.
DR N-PSDB; MAD26283.

XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
PS Claim 1; Page 35; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interluekin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ Sequence 799 AA;
Query Match 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 MELNFKYKIPDLNLPSTYKNDLSFNPLRHLSYSFSPPELOVLDLSRCEIQTIEDGAYQS 100
Db 1 MELNFKYKIPDLNLPSTYKNDLSFNPLRHLSYSFSPPELOVLDLSRCEIQTIEDGAYQS 60
Qy 101 LSHLSTLITGNPQISALAFSGLSLOKLVANETMLASLENPIHKLTKELNVAHN 160
Db 61 LSHLSTLITGNPQISALAFSGLSLOKLVANETMLASLENPIHKLTKELNVAHN 120
Qy 161 LIQSFKLPEYFNSNLTNLEHLDLSNKKIQSIYCTDLRYLHQWPLNLTSLDLSLPMNFLOP 220
Db 121 LIQSFKLPEYFNSNLTNLEHLDLSNKKIQSIYCTDLRYLHQWPLNLTSLDLSLPMNFLOP 180
Qy 221 GAFKEIRLHKLTLRNNFSLNVMKTCIOGLAGLEVHRLVIGEPFNEGULEKFDKSALEGL 280
Db 181 GAFKEIRLHKLTLRNNFSLNVMKTCIOGLAGLEVHRLVIGEPFNEGULEKFDKSALEGL 240
Qy 281 CNLTIEEFRLAYLDYLDIIDLFCNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNC 340
Db 241 CNLTIEEFRLAYLDYLDIIDLFCNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNC 300
Qy 341 KFGQFPTLKLSKRLFTTSNKGNAFSEVDLPSELFDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPTLKLSKRLFTTSNKGNAFSEVDLPSELFDLSRNGLSFKGCCSQSDFGTTS 360
Qy 401 LKYLDLSFNGVITWSSNFIJGLEHLDFOHSHNLKQMSSEFVLSLRLNYLDISHHTR 460
Db 420 LKYLDLSFNGVITWSSNFIJGLEHLDFOHSHNLKQMSSEFVLSLRLNYLDISHHTR 420
Qy 461 VAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLNLTFLDLSQCEQLSPRAFNSLS 520
Db 421 VAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLNLTFLDLSQCEQLSPRAFNSLS 480
Qy 521 SLOVLNASHNPFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSIAFLNLQND 580
Db 540 SLOVLNASHNPFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSIAFLNLQND 540
Qy 581 FACTCEHOSFLOWIKDORQLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 640
Db 541 FACTCEHOSFLOWIKDORQLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 600
Qy 641 VLVSVVAVLVYKFFHMLLAGCIKYRGENTYDAFVYSSODEDWVRNELYKNEBGV 700

Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEDMWRNELVKNLEBGV 660

Qy 701 PPOLCLHYRDFIPGVAIAANI IHGFKRSKRVIVVVSQHFIQSRCIFEEYIAQTWQFL 760

Db 661 PPOLCLHYRDFIPGVAIAANI IHGFKRSKRVIVVVSQHFIQSRCIFEEYIAQTWQFL 720

Qy 761 SSRAGIIFIVLQKVEKTLRQOVELYRLLSRNTYLEMDESVLGRHIFRRRLKALLDGS 820

Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLLSRNTYLEMDESVLGRHIFRRRLKALLDGS 780

Qy 821 WNPETVGTGCMQOEATSI 839

Db 781 WNPETVGTGCMQOEATSI 799

RESULT 15

ABB83162

ID ABB83162 standard; protein; 799 AA.

XX ABB83162;

AC ABB83162;

XX ABB83162;

DT 09-AUG-2002 (first entry)

XX 09-AUG-2002 (first entry)

DE Human Toll-like receptor-4, Tlr4.

XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;

KM cytosolic; immunostimulatory; scavenger receptor; Toll receptor;

KM respiratory tract infection; Toll-like receptor; Tlr4.

XX Homo sapiens.

OS Homo sapiens.

PN WO200235236-A1.

PD 02-MAY-2002.

XX 26-OCT-2001; 2001WO-FR003352.

BE 26-OCT-2001; 2001WO-FR003352.

XX 27-OCT-2000; 2000FR-00013883.

PR 27-OCT-2000; 2000FR-00013883.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX Jeanin P, Magistrelli G, Herbault N, Bonnefoy J;

PI WPI; 2002-383586/41.

DR N-PSDB; AEN83318.

XX N-PSDB; AEN83318.

PT Identifying agent that binds to scavenger receptors and signals through a

PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a

PT cytotoxic T cell response.

XX

XX Disclosure; Page 58-60; 71pp; French.

PS

XX The present invention relates to a method for identifying new therapeutic

CC compounds (I) by selecting molecules that bind to scavenger receptors and

CC signal through a Toll receptor. The present sequence is the protein

CC sequence for human Toll-like receptor-4, Tlr4, which was used to

CC illustrate the method of the invention. (I) are useful as carriers and/or

CC adjuvants in prophylactic or therapeutic vaccines, particularly where the

CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or

CC tumour cell, especially a pathogen that causes respiratory tract

CC infection, also more generally for inducing an immune response. (I) can

CC also be used for specific targeting of active agents (antigens etc.) to

CC antigen-presenting cells (especially immature dendritic cells), for

CC subsequent internalisation by these cells

XX

SO Sequence 799 AA;

Query Match 95.1%; Score 4141; DB 5; Length 799;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MEINFKYKPDNLPTSTKNDLSFNPRLHLSGYSFFSPPELOVLDLSRCEIOTIEDGAYOS 100

|||||

Db 1 MEINFKYKPDNLPTSTKNDLSFNPRLHLSGYSFFSPPELOVLDLSRCEIOTIEDGAYOS 60

Qy 101 LSHLSTLILTNPIQSIALGAFSGLSLQKLVAVETNLASLENPIGHLTKLKEINVAHN 160

Db 61 LSHLSTLILTNPIQSIALGAFSGLSLQKLVAVETNLASLENPIGHLTKLKEINVAHN 120

Qy 161 LIQSFKLPEYSNLTNLEHDLSSNKIQSITCTDLRYLHOMPLNLSIDLINPNFQOP 220

Db 121 LIQSFKLPEYSNLTNLEHDLSSNKIQSITCTDLRYLHOMPLNLSIDLINPNFQOP 180

Qy 221 GAFKEIRLHKLTLENNPDLNWMKTCIQGLAGLEVHRLVLGEFNNEGULEKFDKSALEGL 280

Db 181 GAFKEIRLHKLTLENNPDLNWMKTCIQGLAGLEVHRLVLGEFNNEGULEKFDKSALEGL 240

Qy 281 CNLTIIEFRRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVDFSYNFGMOHLELVNC 340

Db 241 CNLTIIEFRRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVDFSYNFGMOHLELVNC 300

Qy 341 KFGQPTLKLSLRRLFTSNKGNAPSEVDLPSLEFLDLSRNLGSLFKGCCSQSDFGTTS 400

Db 301 KFGQPTLKLSLRRLFTSNKGNAPSEVDLPSLEFLDLSRNLGSLFKGCCSQSDFGTTS 360

Qy 401 LKYLDLSPNGVITMSSNPLGLEOLEHLDFOHSNLSKOMSESVFLSLRNLITLDSHTHTR 460

Db 361 LKYLDLSPNGVITMSSNPLGLEOLEHLDFOHSNLSKOMSESVFLSLRNLITLDSHTHTR 420

Qy 461 VAFNGIFNGLSLSEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCLQSLPTAFNSLS 520

Db 421 VAFNGIFNGLSLSEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCLQSLPTAFNSLS 480

Qy 521 SLQVLANSHNNFSLDTPPYKCLNSLOYLDYSLNHNMTSKQOELOHPSSLAFLNLTOND 580

Db 481 SLQVLANSHNNFSLDTPPYKCLNSLOYLDYSLNHNMTSKQOELOHPSSLAFLNLTOND 540

Qy 581 FACTCEHOSFLOWKDQROLIVEYERMECAPSPDKQGPVLSLNTCOMNKTIIIGSVYLS 640

Db 541 FACTCEHOSFLOWKDQROLIVEYERMECAPSPDKQGPVLSLNTCOMNKTIIIGSVYLS 600

Qy 641 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEDMWRNELVKNLEBGV 700

Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEDMWRNELVKNLEBGV 660

Qy 701 PPOLCLHYRDFIPGVAIAANI IHGFKRSKRVIVVVSQHFIQSRCIFEEYIAQTWQFL 760

Db 661 PPOLCLHYRDFIPGVAIAANI IHGFKRSKRVIVVVSQHFIQSRCIFEEYIAQTWQFL 720

Qy 761 SSRAGIIFIVLQKVEKTLRQOVELYRLLSRNTYLEMDESVLGRHIFRRRLKALLDGS 820

Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLLSRNTYLEMDESVLGRHIFRRRLKALLDGS 780

Qy 821 WNPETVGTGCMQOEATSI 839

Db 781 WNPETVGTGCMQOEATSI 799

Search completed: March 12, 2005, 19:54:56

Job time : 97.4 secs

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OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds

(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-2

Perfect score: 4355

Sequence: 1 MMSASRLAGTILPAMAFISC.....SWNEGTIVGTCNNQEAATSI 839

Scoring table: BLOSUM62

Searched: Gapex 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4197	96.4	844	4	US-09-949-016-9438
2	629.5	14.5	661	1	US-08-514-014-4
3	629.5	14.5	661	1	US-08-833-823-4
4	599.5	13.8	784	4	US-09-982-308B-23
5	539	12.4	775	4	US-09-949-016-8799
6	316	7.3	605	3	US-09-063-950-5
7	305	7.0	623	4	US-09-949-016-10995
8	303	7.0	605	1	US-08-190-802A-49
9	303	7.0	605	3	US-08-477-346-49
10	303	7.0	605	3	US-08-473-089-49
11	303	7.0	605	4	US-08-487-072A-49
12	303	7.0	605	4	US-09-538-092-1087
13	299.5	6.9	662	4	US-09-538-092-1325
14	299.5	6.9	662	4	US-09-949-016-6619
15	299.5	6.9	662	4	US-09-949-016-10710
16	299	6.9	1525	3	US-09-191-647-2
17	299	6.9	1525	3	US-09-540-245A-2
18	299	6.9	1525	3	US-09-540-153-2
19	296	6.8	603	1	US-08-190-802A-50
20	296	6.8	603	3	US-08-477-346-50
21	296	6.8	603	3	US-08-473-089-50
22	296	6.8	603	4	US-08-487-072A-50
23	292.5	6.7	907	4	US-09-170-496D-264
24	292.5	6.7	907	4	US-09-170-496D-278
25	289.5	6.6	1112	3	US-09-353-585-3
26	289	6.6	1112	3	US-09-312-283C-396
27	286	6.6	1112	3	US-09-353-585-2

28	285	6.5	1523	3	US-09-182-024A-2	Sequence 2, Appli
29	283.5	6.5	1166	4	US-10-101-464A-900	Sequence 900, App
30	281	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
31	278	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
32	275	6.3	620	4	US-09-907-784A-73	Sequence 73, Appli
33	275	6.3	620	4	US-09-905-125A-73	Sequence 73, Appli
34	275	6.3	620	4	US-09-902-775A-73	Sequence 73, Appli
35	275	6.3	620	4	US-09-906-700-73	Sequence 73, Appli
36	275	6.3	620	4	US-09-903-603A-73	Sequence 73, Appli
37	275	6.3	620	4	US-09-904-920A-73	Sequence 73, Appli
38	275	6.3	620	4	US-09-905-064-73	Sequence 73, Appli
39	275	6.3	620	4	US-09-905-381A-73	Sequence 73, Appli
40	275	6.3	620	4	US-09-906-618-73	Sequence 73, Appli
41	272	6.2	1480	3	US-09-191-647-7	Sequence 7, Appli
42	272	6.2	1480	3	US-09-540-245A-7	Sequence 7, Appli
43	272	6.2	1480	3	US-09-540-153-7	Sequence 7, Appli
44	272	6.2	1480	5	PCT-US91-09055-2	Sequence 2, Appli
45	271	6.2	1139	4	US-09-513-505-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9438

Query Match 96.4%; Score 4197; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 EVVNNITVQCMEINLFYKIPDNLPSTKNLDLSPFPLHLHLSYSFSPPELOVLSRCEI 90
DB 36 EVVNNITVQCMEINLFYKIPDNLPSTKNLDLSPFPLHLHLSYSFSPPELOVLSRCEI 95
QY 91 QTIEDGAYOSLSHSLTILITGNPIQSIALGAFSGLSLQKVAETNIAASLENPIGHK 150
DB 96 QTIEDGAYOSLSHSLTILITGNPIQSIALGAFSGLSLQKVAETNIAASLENPIGHK 155
QY 151 TKELVANHLIQSFKLPEYFSNLTNLEHLDLSSNKIOSITYCTDLRYVHQMPILNLSIDL 210
DB 156 TKELVANHLIQSFKLPEYFSNLTNLEHLDLSSNKIOSITYCTDLRYVHQMPILNLSIDL 215
QY 211 SLNMFNITIOGAFETIRLHKLTLPNPNDSLNWKTCTOGLAGLEVHVLVGEFNEGNLE 270
DB 216 SLNMFNITIOGAFETIRLHKLTLPNPNDSLNWKTCTOGLAGLEVHVLVGEFNEGNLE 275
QY 271 KFDKSALEGCNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSVLTERRVDFSYNF 330
DB 276 KFDKSALEGCNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSVLTERRVDFSYNF 335
QY 331 GWOHLIELVNCFOQPTLKLSLKRLLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGC 390
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Db 336 GMDHLELVNCKRGQPPYLKLSKLTITSNKGAFSEVDLPSEFLDLSNGISFGKC 395
Qy 391 CSQSDFGTTSKYLDLDSFNGVITWSSNFGLEOLEHLDFOHNLKOMSEFSVFLSLRMI 450
Db 396 CSQSGFGTTSKYLDLDSFNGVITWSSNFGLEOLEHLDFOHNLKOMSEFSVFLSLRMI 455
Qy 451 YLDSHTHTTRVAFNGIFNGLSLEVLKXAGNSFOENFLPDIPTELRNLTPLDLSQCQLEQ 510
Db 456 YLDSHTHTTRVAFNGIFNGLSLEVLKXAGNSFOENFLPDIPTELRNLTPLDLSQCQLEQ 515
Qy 511 LSPFAFNSLSLOYLNMSHNPFSLDTPPYKCLNSLOYLDYSLNIMTSKQELQHPSS 570
Db 516 LSPFAFNSLSLOYLNMSHNPFSLDTPPYKCLNSLOYLDYSLNIMTSKQELQHPSS 575
Qy 571 LAFNLTONDPACTCEHOSFLOMIDKORQLVEVERMECATPSPDKQMPVLSLNTTCOMN 630
Db 576 LAFNLTONDPACTCEHOSFLOMIDKORQLVEVERMECATPSPDKQMPVLSLNTTCOMN 635
Qy 631 KTIIGSVLSLVVSVAVLVYKFFHMLLAGCIRYGRGENIYDAFVIYSSQEDWVRN 690
Db 636 KTIIGSVLSLVVSVAVLVYKFFHMLLAGCIRYGRGENIYDAFVIYSSQEDWVRN 695
Qy 691 ELVKNLESGVPPFOLCHYRDPFPGVAITANIHEGFKSRKVIVVSOHPTOSRWCFE 750
Db 696 ELVKNLESGVPPFOLCHYRDPFPGVAITANIHEGFKSRKVIVVSOHPTOSRWCFE 755
Qy 751 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRQOVELYRLSNRYLLEWEDSVLGRHIFWR 810
Db 756 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRQOVELYRLSNRYLLEWEDSVLGRHIFWR 815
Qy 811 LRKALLDGKSNPBGCTVGTGCMQEAISI 839
Db 816 LRKALLDGKSNPBGCTVGTGCMQEAISI 844

RESULT 2
US-08-514-014-4
/ Sequence 4, Application US/08514014
/ Patent No. 5707829
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John
/ APPLICANT: Kelleher, Kerry
/ APPLICANT: Carlin, McKeough
/ TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
/ STREET: 87 Cambridgepark Drive
/ CITY: Cambridge
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02140
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/514,014
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brown, Scott A. 32,724
/ REFERENCE/DOCKET NUMBER: G16000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 876-8224
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

Query Match 14.5%; Score 629.5; DB 1; Length 661;
Best Local Similarity 29.7%; Pred. No. 5:36-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

Qy 25 SWEP-CYEVVPNLTYOCMEINFYKIPDNLPESTKNLDSFPLRHLDSYSEFSPELQVL 83
Db 23 SWDMCKIEKANKTYNCBNGLSLIPDLPYTFLEFSFPLTINRFRSLMANLTF 82
Qy 84 DLSRCEIQTIEDGAYQSLSHLSTLITGNPFIQSLALGAFSGLSLQKLVAVETIASLEN 143
Db 83 DLTRCQINWTHIEDFQSHHQSLTVLGNPLIFMAEISLNGPKSLKHLFLIGTISNLEF 142
Qy 144 PFIHLKTLKELVANHNLQSFKLPYFYSNLTNLEHLDLSNKKIQSIYCTDLRVLHQMPL 203
Db 143 IPVHNLNLSLSLYGSHNISIKFPKDFP-ARNIKVLDFOGNAIHYISREDMRSLQ--A 199
Qy 204 LNLSDLSLPMNFIQGAPEIRLHLKTLRNPDLSLNMKTCIQGLAGLEVHGLVGEF 263
Db 200 LNLSDLSLPMNFIQGAPEIRLHLKTLRNPDLSLNMKTCIQGLAGLEVHGLVGEF 255
Qy 264 RNEGULEKPKSALEGLCNLTIEEFRLAYLDYLDIID-LFNCLTVVSSFSVSVTIER 322
Db 256 EDIDD-EDISSAMKGCCEMSVBSLNQ--EHRSDISSTTFQCFQLOGLDLATHTLKG 312
Qy 323 VKDPSYFNGWOHELVN-----CKF--GQFPTL-----KLKSLKRLTFTSN 361
Db 313 LPS-----GKGLNLILKLVLSVNHFPQLQISANPSPSLTHLYIRGNVKKLHLGVGLE 367
Qy 362 KGNAPSEVDLPSEFLDLSRNGLSFKGCCSQSGFQTSKYLDLSFNGVITWSSN-FLG 420
Db 368 KLGN-----LQTDLSHNDIEASDCCSLQKNLSHQTLNLSNEBGLQSOAFKE 418
Qy 421 LEQLEHLDFOQ-----HSLNKOMSEFS--VFLSLRMIY--LDISHTHTTRVAFNGIFNGLS 472
Db 419 CPQLELDLDAFTRHIAAPQ--SPQNLHFLQVNLITCFDLSNQH-----LLAALPV 470
Qy 473 LEVIXKAGNSFOENFL--PDIPTELRNLTPLDLSQCQLEBOLSPFAFNSLSLOYLNMSHN 530
Db 471 LRHLNKGNHFOGTIKTYMLQTVGSLVLISSCGILSIDQAFHSLGKMSHVDLSHN 530
Qy 531 NFF--SLDTPPY-----KCLNSLOYLDYSLNIMTSKQELQHPSSLAFLNTQND 581
Db 531 SLTCDSDLSHLKGIYLNLAANSINISPRLLPTL-----SQOSTNLSHNPL 579
Qy 582 ACTCEHOSFLOMIDKORQLVEVERMECATPSPDKQMPVLSLNTTCOMNTIIGSVLSV 641
Db 580 DCTCSNIHFLTWYKENHKLGESEETTCANPSPILRGVGLSDVLSGCI--TAIGIFPLIV 637
Qy 642 LVYSVAVLVY 652
Db 638 FLV-LIALLLF 647

RESULT 3
US-08-833-823-4
/ Sequence 4, Application US/08833823
/ Patent No. 5969093
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John
/ APPLICANT: Kelleher, Kerry
/ APPLICANT: Carlin, McKeough
/ TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs

```

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 14.5%; Score 629.5; DB 2; Length 661;
Best Local Similarity 29.7%; Pred. No. 5,3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CVEVENVITYQCHELNFYKIPDNLPSTKNLDSFNDLRHLSGYSFSPPELOVL 83
23 SWDQCIKKEANKTYNCENLGLSEIPDLPTTEFLERSFNLPTIHRFSLNMLTFL 82
84 DLSRCEIQIEDGAQVSLSHSTLITGNPIOSLALGAFSGLSLOKLVAVETNLSLEN 143
83 DLRQIWMIHEDTQSHHQJSTLVLTGNPLIFMAETSLNGSKSLKHVFLQIGSINLEF 142
144 PPIGHLTKLKELVANHLIOSFKLPEYFSNLTNLEHLDSKSIQSIYCTDLRVVHOMPL 203
143 IPVNLLEWLESYLGSNHISIKFKDPR-ANLKVDFONNAIYISREDKRSLEQ--A 199
204 LNLSDLSINPMNFIQPGAFKEIRLHKLTLRNNPDSLNVMTCTIOGLAGLEVHRLVLEGF 263
200 INLSINFGNNVKGIELGAFDSTVFSQ--NFGDTPLSVIFNGLQNSTTQSLMLGNF 255
264 RNEGULEKFDKSALEGLCNLTIEEFLRLAYLDYLDIID-LFNCITNVSBSLSVTIER 322
256 EDIID-EDISSAMKGLCEMSVESLNLQ--EHRFSDISSTTFQCTOQELDLTATHKKG 312
323 VKDFSYNGFQWHLIELVN-----CKP--GQPTL-----KLKSLKRLTPTSN 361
313 LPS-----GMKGLNLKLVLSVNHFDQLQISANFSLTHTLYRGNVKKLHLGVCLE 367
362 KGNNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDGTTSLKYLDSFNGVITMSSN-FLG 420
368 KLGN-----LQTLDSHNDIEASDCCSLQKNLHLOTNLNSHBPLGLSQQAKKE 418
421 LEQLEHLDFO-----HSNLKQMSSEF--VFLSLRNLIY--LDISHTHTVAENGINGSS 472
419 CPQELDLAFLRLHINAPO--SPFQNHFLQVNLTYCFDLDSNH-----LIAGLPLV 470
473 LEVLKAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLSOLSPRTAFNSLSLQVNMGSN 530
471 LRHLNLKGNHPODGIITKTNLQTYGSLFVLISSCGLISITQQAFLHSGKSHVDLSHN 530
531 NFF--SLDTFPY-----KCLNSLQVLDVLSLHIMTISKQELQHPSSLAFLNLTONDF 581

531 SLTCDISLHSLKGIYLNLANSNINIISPLPLT-----SQOSTINISHNP 579
582 ACTCEHQSFLQWIKDQOLLEVERMECATSDSKQMPVLSINTCCNNKTIIGSVLSV 641
580 DTCGSHFLTWYKENLHKLHKGSEBETCANPPLRGVLSYKSCGI--TAIGIFPLIV 637
642 LVSVVAVLVY 652
638 FLV-LTALILF 647

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Dalia, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavadny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: J06010C
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 13.8%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 4.1e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPTSTKNLDSFNDLRHLSGYSFSPPELOVLDSRCEIQIEDGAQVSLSHSTL 107
46 IPSGLTERVKSLLDSNNRITYISNSDLQRCVNLQALVLTNGINTIEEDSFSSLSLEHL 105
108 ILTGNPIOSLALGAFSGLSLOKL-----VAFTNLASLENPIGHLKT----- 151
106 DLSYVLSNLSMSPFKPLSLTIFNLGNPKYKTIGETSLSFHLTKQLLRGNMDTFPKI 165
152 -----LKELVANHLIOSFKLPEYFSNLTNLEHLDSK-----I0SI 190
166 QKDFAGLTFLBELEIDASDLQSYE-PKSLKSIGNVSHLHMKHILILEIPVDVTSV 224
191 YCTDLRVVHOMPLANLSDLSINPMNFIQPGAFKEIRLHKLTLRN--NFDLS-NVMK 244
225 ECLER-----DITDLDTFHSSELSYGTSTNSL-ICKTFRVNKKYIDESLFOVMK 271
245 TC--IOGLAGLEVHRLVY--GEFRNNGNLEKFPKSLALEGLCNLTIEEFLRLA--YLDVYL 297
272 LNLQISGLLEBEFDCTLNGVGNFRASDNDRAVIDPGKVE--TITIRLHLPFYLFY-- 326
298 DDIIDLFNCLTNVSSFSLSVYTIERYVDPSYNGFQWHLIELVNCCKFGQFPTLKLSLRLT 357
327 -DLSTLYSLTERVK-----RITVENSKV-----LVPCLLSQ----- 357
358 FTSKNGNAFSEVDLPSEFLDLSRN-----GLSFKCCSQSDGTTSLKYLDSFNGVI 412
358 -----HKSLEVIDLSENLMVEEYLKNSAC-----EDAMPBLOTLILRON--- 397

QY 413 TMSNPLGLBQLEHLDPOHSNLSKMSFSPVLSLNLITLDISTHTHTRVAFNGIPNGLS 472
| : : : : :
Db 398 -----HL-----ASLEKTBG--TLLTLKNLTNIDISK----- 422
QY 473 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCOLEBOLS---PTAFNSLSLQVLANMSH 529
| : : : : :
Db 423 -----NSFHS--MPEICQWPERKMKYLNLSSTRHISVTCGP-----KTLIELIDVSN 466
QY 530 N--NPFSLD-----TFP--YKCLNSLQVLDYSLNHIMTSKQELQHPFSSL 571
| : : : : :
Db 467 NNLNLFSLNLPOLKELYSIRNKLMTLPDASLLPMLVLKISRNALITTSKEQLDSF--HTL 525
QY 572 AFLNLTQNDPACTGCHOSFLOMIDQOROLVAV-----ERMECATPSDKQGMPLSLNIT 626
| : : : : :
Db 526 KTLBAGGNPFCSCBFLSFTQ---EQQALAKVLIDWPANYLCSPSHVRGOQVQDVRLS 581
QY 627 ---COMNKTIIGVSLVSVVAVVAVLYKFX--FHLMLAGCIKYGK-----GENI-Y 674
| : : : : :
Db 582 VSECHRIALVSGMCALFLILITLTVGLCHRHGMLWMMAMWLQAKRPRKAPSRNICY 641
QY 675 DAFVYSSQDEBDWVNEVLVKNLEEGVPPQOLCLHYRDFIPGVALANIIHGGFHSRKVI 734
| : : : : :
Db 642 DAFVYSERDAVWVENLWVQELFNPNPFKCLHKKRDFIPGKWIIDNII--DSIEKSHKTV 700
QY 735 VVVSQHFIQSRKCFEYELAQTMQFSLBAGIIFIVLQKVEKTLRQO--VELYRLSRNT 793
| : : : : :
Db 701 FVLSNFVKSCKYELBDFSHRFLPDENNDAILILBIEBKALPQRFCKLRKIMNTKT 760
QY 794 YLEWEDSVLGRHIFWRRLRKAL 815
| : : : : :
Db 761 YLEWPMDEARQREGFWVNLRAAL 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application us/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 2007012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 12.4%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 1,66-40;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;

QY 48 IPDNLPESTKNDLSFNPRLHLSYSPFPELQVLDLSRCEIQITIDGAYQSLSHLSTL 107
| : : : : :
Db 81 IPSGITEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTNSGINTIEEDSFSLGLEHL 140
QY 108 ILTGNPISLALGASGSLQK-----VAVENTLASLENFPGLHKT--- 151
| : : : : :
Db 141 DLSYVLTSLSSSWKPLSLFLNLGNPKYKTLGSETLSFSLTLQILRAGNMDTFKI 200
QY 152 -----LKELVAVANHLIOSFKLPEYFSNLTLBHLDSNKK-----IQSI 190
| : : : : :
Db 201 QKRPAGLTFPELELIDASDLQSYE--PKSLKSIGQVSHLILHMKQHILLLEIFVDVYTSV 259

QY 191 YCTDLRVLHQPLNLNLSLDSLNPMNF--IQPGAFKERILHKLTLRN--NFDSL-NVMK 244
| : : : : :
Db 260 ECLER-----DTELDPHFHSELSSTGETNSL-ICKFTRRWVKITDESILFYVMK 306
QY 245 TC--IQAGLEVARLV-----GEFRNNGNLEKPKKSMLEGCNLTIEFRLA--YLDVYL 297
| : : : : :
Db 307 LLNOISGLELEFPDCTLNGVGNFRASDNDRVIDPGKE--TLTIRRLHIFRELYF-- 361
QY 298 DDIIIDFNCCLTNVSSFSVSVTIERVDPSYNGFQMOHLELVNCKFGQFPPLKLSLRLT 357
| : : : : :
Db 362 -DLSTIVSLTERVK-----RTVENSRYF-----LVPCLLSQ----- 392
QY 358 FTSNKGNAFSEVDLPSELEFLDSRN-----GLSFKGCSSQSDGTTSLKYLDSFNGVI 412
| : : : : :
Db 393 -----HKSLEYLDLSENMVBEYILKNSAC--EDAWPSLQTLILIRON--- 432
QY 413 TMSNPLGLBQLEHLDPOHSNLSKMSFSPVLSLNLITLDISTHTHTRVAFNGIPNGLS 472
| : : : : :
Db 433 -----HL-----ASLEKTBG--TLLTLKNLTNIDISK----- 457
QY 473 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCOLEBOLS---PTAFNSLSLQVLANMSH 529
| : : : : :
Db 458 -----NSFHS--MPEICQWPERKMKYLNLSSTRHISVTCGP-----KTLIELIDVSN 501
QY 530 N--NPFSLD-----TFP--YKCLNSLQVLDYSLNHIMTSKQELQHPFSSL 571
| : : : : :
Db 502 NNLNLFSLNLPOLKELYSIRNKLMTLPDASLLPMLVLKISRNALITTSKEQLDSF--HTL 560
QY 572 AFLNLTQNDPACTGCHOSFLOMIDQOROLVAV-----ERMECATPSDKQGMPLSLNIT 626
| : : : : :
Db 561 KTLBAGGNPFCSCBFLSFTQ---EQQALAKVLIDWPANYLCSPSHVRGOQVQDVRLS 616
QY 627 ---COMNKTIIGVSLVSVVAVVAVLYKFX--FHLMLAGCIKYGK-----GENI-Y 674
| : : : : :
Db 617 VSECHRIALVSGMCALFLILITLTVGLCHRHGMLWMMAMWLQAKRPRKAPSRNICY 676
QY 675 DAFVYSSQDEBDWVNEVLVKNLEEGVPPQOLCLHYRDFIPGVALANIIHGGFHSRKVI 734
| : : : : :
Db 677 DAFVYSERDAVWVENLWVQELFNPNPFKCLHKKRDFIPGKWIIDNII--DSIEKSHKTV 735
QY 735 VVVSQHFIQSRKCFEYELAQTMQFSLBAGIIFIVLQKVEKTLRQO--VELYRLSRNT 794
| : : : : :
Db 736 FVLSNFVKSCKYELBDFSHRFLPDENNDAILILBIEBKALPQRFCKLRKIMNTKT 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application us/09063950C
; Patent No. 6225085

; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.3%; Score 316; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 4,1e-20;
Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

QY 33 VPNTIYQCMELNFKYIPDNLPESTKNDLSFNPRLHLSYSPFPELQVLDLSRCEIQ 92
| : : : : :
Db 53 VNELSVFCSSRNLRTRLDGIPGTQALWLDSSNLSIPPAFRULSLATPLNLOGGOLGS 112


```

QY 93 IEDGAYQSLSHSTLITGNPIQSIALGAFS-----GLSSL 128
DB 113 LEPOALLGLENLCHLHLEBNOLRLSLAVGTFAATPALALLGSSNNRLSLREDELPEGLCNL 172
QY 129 OKLAVETNLASLENFPIGHLKTLKELVANHLIOSFLLPEFSNLTNLEHLDSNNIO 188
DB 173 WDLNIGMNSLAVLPDPAFRGLGGLRELVLAGNRL-AYIOPALFSGLAELRELDSSRNALR 231
QY 189 SIYCTDLRVLHOMPLNLISLDSLNPMNFIOGAFKEIR-LHKLTLRNPFDSINVKTCI 247
DB 232 AI-----KANVAPQLPRLQ-KLYIDRLILAAVAGALGLKALRWLDLSHN-RVAGLLEDTF 286
QY 248 OGGLAGLEVHRLVLEFRNEGNLEKPKSALBEGLCNLTIEFRLAYDYLDIIDLFNCL 307
DB 287 PGLGLRLVRL-----SHNAIASLRPTFEDL-----HFLEEL----- 319
QY 308 TNVSSFSLVSTIERVKDPSYNGWHLVLVNCCKGQFPPLKLSKRLTFTS--NKGN 365
DB 320 -----QLGHNRIROLAERSFE-GLGQLEVLTLDHNOQEVKGAFLGLTNVAVMNLSGN 372
QY 366 AFSEVDLPSEFLDLNR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITMSSNFL 419
DB 373 CLR--NLPEQVFRGLKLSHLBESSCLGRIRPHFAGLSGRIRFLKNDGLVIGIEBSL 430
QY 420 -GLEQLHLDPQHSNLMKMSSESVFLSLRNLIYDISHHTRVAFNGIPLNGSLLEVLKM 478
DB 431 WGLLELLELDLTNSQL-----THLP--HQLFOGLKLEYLL 465
QY 479 AGNSQENFLP-DIFTELRLNLTFLDLSOCOLBOLSPAFNSLSLOVNMSSNPFSLDT 537
DB 466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEALGSLASLGRIRLYLNLRN--SLRT 520
QY 538 FPKYCLNSLOVLDVSLNHTSKOELQHPSSLAFLNLTONDFACTCEHOS----- 589
DB 521 FTPQ-----PGLERLWLBEGNPMWCSCLKALRDPALON 554
QY 590 -----FLQMT--KQORQLVEVERMECATPSPDKQMPVLUSL 623
DB 555 PSAVRPFOALICEGDDCOPPYTYNNITCASPEVAGLDRDL 597

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10995

Query Match 7.0%; Score 305; DB 4; Length 623;
Best Local Similarity 24.3%; Pred. No. 4,4e-19;
Matches 171; Conservative 96; Mismatches 260; Indels 178; Gaps 28;

QY 4 ASRLA-----GLIPNAFLSCVR--PESWE-----PCV-----EVVPMIT 37
DB 16 ACRMLARKGIALALLLSWALGPRSLGADPGTGGABGAPCAPACVCSYDDADELS 75

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QY 38 YQCEMLNPFYKIPDNLPRSTKNLDSFNPRLHLSGYSFSPPELOVLDLSRCEIOTIEDGA 97
DB 76 VFCSSRNILTRLPDVGQTOALMDGNLSSVPAAAFONLSLGLFNLQCGOLGSLPEQA 135
QY 98 YQSLSHSTLITGNPIQSIALGAFS-----GLSSLQKVA 133
DB 136 LIGLENLCHLHLEBNOLRLSLAVGTFAATPALASGLSNNRLSRLEDGLFEGISLMDNLT 195
QY 134 VETNLASLENFPIGHLKTLKELVANHLIOSFLLPEFSNLTNLEHLDSNNIOIYCT 193
DB 196 GMSNLAVLPDPAFRGLGGLRELVLAGNRL-AYIOPALFSGLAELRELDSSRNALRAT--- 251
QY 194 DLRYLHOMPLNLISLDSLNPMNFIOGAFKEIR-LHKLTLRNPFDSINVKTCIOGLAG 252
DB 252 KANVAPQLPRLQ-KLYIDRLILAAVAGAFGLKALRWLDLSHN-RVAGLLEDTFPGILG 309
QY 253 LEVRLVLEFRNEGNLEKPKSALBEGLCNLTIEFRLAYDYLDIIDLFNCLTNVSS 312
DB 310 LRVRL-----SHNAIASLRPTFEDL-----HFLEEL----- 337
QY 313 FSLVSTIERVKDPSYNGWHLVLVNCCKGQFPPLKLSKRLTFTS--NKGNVAFSEV 370
DB 338 -QLGHNRIROLAERSFE-GLGQLEVLTLDHNOQEVKGAFLGLTNVAVMNLSGNCLR-- 393
QY 371 DLPSEFLDLNR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITMSSNFL-GLEQ 423
DB 394 NLPEQVFRGLKLSHLBESSCLGRIRPHFAGLSGRIRFLKNDGLVIGIEBSLMLGAE 453
QY 424 LEHDPQHSNLMKMSSESVFLSLRNLIYDISHHTRVAFNGIPLNGSLLEVLKMGNSF 483
DB 454 LLELDLTNSQL-----THLP--HQLFOGLKLEYLLSRRL 488
QY 484 QENFLP-DIFTELRLNLTFLDLSOCOLBOLSPAFNSLSLOVNMSSNPFSLDTPPYKC 542
DB 489 AE--LPADALGPLQRAFWLDVSHNRLEALGSLASLGRIRLYLNLRN--SLRTFTQ- 542
QY 543 LNSLOVLDVSLNHTSKOELQHPSSLAFLNLTONDFACTCEHOSFLQMTK- 596
DB 543 -----PGLERLWLBEGNPMWDCGP--LKALRDPALONP 573

RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: 265
; CURRENT APPLICATION NUMBER: US/08/190,802A
; PRIOR FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

QY 597 ---QROLVEVERMECATPSPDKQMPVLISNITCOMKTIIGVSV 638
DB 574 SAVRPFOALICEGDDCOPPAYTN-----NITCASPEVAGLDRDL 612

```

NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 7.0%; Score 303; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIDPNLPSTKNLDSFNPRLHLSYSFSPPELQVLDLSRCIEQTEDGAYQ 99
DB 60 CSSRNLTRLPDGVGGTQALMDGNLSSVPPAFQNLSSLGFLNLQGGQGSLEPQALL 119
QY 100 SLSHLSTLLTGNPIQSIALGAFS-----GLSLQKLYAVE 135
DB 120 GLENLCHLHERNQRLSLATGTPAHTPALASLGNNRSLRLBDGLFEGSLMDNLGW 179
QY 136 TNLASLENPIGHLKTLKELVANHLIOSFKLPEYFSNLTNLEHLDSNNKIOSICTDL 195
DB 180 NSLAVLPDPAFRGSGSLRELVLVAGNRL-AVLQPALFSGLAELREIDLSRNALRAI---KA 235
QY 196 RVLHOMPLNLSDLSINPMNFIOPGAFKEIR-LHKLTLRNPSLNMTKTCIGLAGLE 254
DB 236 NVFVQLPRLO-KLYIDRLIAVAPGAFGLKALRLWLDLSHN-RVAGLLEDTFPGILGLR 293
QY 255 VHRVLVGFNENGNLEKFDKSLBGLCNLTIEFRRLAYLDYLDIDLFNCLTNVSSFS 314
DB 294 VLR-----SHNAIASLRPTFKD-----HLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGMHLVNCCKFGQPTLKLSLKLTFPS--NRGNAPSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLITLDHNQLOEVYAGAFGLITVNAVNNLSGNCIR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDPGTTSLKXYLDLSFNGVITMSSNFL-GLBQLE 425
DB 378 PEQVFRGLGKLSHLBSSCLGRIRPTFTGSLGRLLFLKONGLVGIEBOSLWGLAELL 437
QY 426 HLDFOHSLKQMSSEFVFLSLRNLITLDISHTTRVAFNGIFNGLSLSEVLKMAAGNSFOE 485
DB 438 ELDTLSNQL-----THLP-----HRLFGIGKLEYLLBRNRAE 472
QY 486 NFLP-DLFTELRNITFLDLSQCLBOUSPTVFNLSLSIQVIMSHNNFSLDTTPYKCLN 544
DB 473 --LPADLGLPQRAFWLDVSHNRLEALPNSLAPLGRIRYLSLRNN--SLRTFPQ--- 524
QY 545 SLOVLDSYLNHIMTSKKQELHFPSSLAFNLITNDPACTCEHOSFIOWIMD----- 596
DB 525 -----PPGLERLWLBGNPMDGCP-----LKALDFALQNPFA 557
QY 597 -QROLIVERMECATSDKQMPVLSLNITCOMNKTIIGSV 638
DB 558 VPRFVQALCEBGDCQPAYTYN-----NITCASPREVVGIDL 594

RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIDPNLPSTKNLDSFNPRLHLSYSFSPPELQVLDLSRCIEQTEDGAYQ 99
DB 60 CSSRNLTRLPDGVGGTQALMDGNLSSVPPAFQNLSSLGFLNLQGGQGSLEPQALL 119
QY 100 SLSHLSTLLTGNPIQSIALGAFS-----GLSLQKLYAVE 135
DB 120 GLENLCHLHERNQRLSLATGTPAHTPALASLGNNRSLRLBDGLFEGSLMDNLGW 179
QY 136 TNLASLENPIGHLKTLKELVANHLIOSFKLPEYFSNLTNLEHLDSNNKIOSICTDL 195
DB 180 NSLAVLPDPAFRGSGSLRELVLVAGNRL-AVLQPALFSGLAELREIDLSRNALRAI---KA 235
QY 196 RVLHOMPLNLSDLSINPMNFIOPGAFKEIR-LHKLTLRNPSLNMTKTCIGLAGLE 254
DB 236 NVFVQLPRLO-KLYIDRLIAVAPGAFGLKALRLWLDLSHN-RVAGLLEDTFPGILGLR 293
QY 255 VHRVLVGFNENGNLEKFDKSLBGLCNLTIEFRRLAYLDYLDIDLFNCLTNVSSFS 314
DB 294 VLR-----SHNAIASLRPTFKD-----HLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGMHLVNCCKFGQPTLKLSLKLTFPS--NRGNAPSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLITLDHNQLOEVYAGAFGLITVNAVNNLSGNCIR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDPGTTSLKXYLDLSFNGVITMSSNFL-GLBQLE 425

Db 378 PEQVFRGKGLSHLBSGCLGRIRPHFTFTGLSGRLFLKONGLVGIEBOSLWGIAELL 437
Qy 426 HLDFOHNLKQMSFVSFLSLRNLIYLDISHHTVAVANGIENGSLSEVLKMGANSFOE 485
Db 438 ELDTLSNQL-----THLP---HRLFOGKLELYLLSNRLAE 472
Qy 486 NFLP-DITFELRNLTFLDLSOCQLESPAFNSLSLQVIMSHNPFSLDTPPYKCLN 544
Db 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRIRYLSLRNN---SLRTFTPO--- 524
Qy 545 SLQVLDYSLNIMTMSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOWIKD----- 596
Db 525 -----PGLERLMLBGNPMDCCP---LKAALDFALQNPBA 557
Qy 597 -QROLLEVERMECATPSDKQGMPLSLNITQNMKTIIGSV 638
Db 558 VPRFVQALCEGDDCOPPAYTVN-----NITCASPEVVGDL 594

RESULT 10

US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; HYDROTHERMAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
Qy 40 CMLNFKYKPNLPPSTKQLDLSFPLRLHLSYSFSPPELQVLDLSRCEITIDGAYQ 99
Db 60 CSSRMILTRLPDGVPGTQALWLDGNLSSVPPAFQNLSSLGFLNLQGGQLSLPQALL 119

Qy 100 SLSHLSTLLIINGNBIOSIALGAFS-----GLSSLOKLVAVE 135
Db 120 GLENLCHLHERNQLRSIALGTFAHTPALASGLNNRLSRLEDGLFEGGLSLMDLNLGW 179
Qy 136 TNLASLENFPILGHKTLKELVANVNLIOSFCLPEYFSNTLNLHLDLSSNNIQLSYCDL 195
Db 180 NSLVLDPAPAFRGGLSRELVLAENRL-AVQPALFSGLABLRELDLSRNALRL--KA 235
Qy 196 RVLQMPPLNLSLDLSNPMFIOGAFKEIR-LHKLTLRNPFSLNVMKTCIOGLAGLE 254
Db 236 NVFQQLPRLQ-KLVLDRLIAAVALGAPLGLKALRWLDLSN-RVAGLEBTPFGLGLGR 293
Qy 255 VHRVLGFERNGLERKEDKSLGCLNLTIEFRFLAYLDYDIDLDFNCLTNVSSFS 314
Db 294 VLRL-----SHVAIASLRRTFKDL-----HFLBEL-----Q 320
Qy 315 LVSTYTERVQPSYFNGQHLVNCCKFGQPTLKLSLRKLTFS--NRGNAFSEVDL 372
Db 321 LGHNRIRQLARSEF-GIGQLEVLTLDNQLOEVKAGAFGLGTLVVAVNNLSGNCIR-NL 377
Qy 373 PSLFELDSL-R-NGLSFKGCC-----SOSDFGTSLKYLDLSFNGVITWSSNFL-GLBOLE 425
Db 378 PEQVFRGKGLSHLBSGCLGRIRPHFTFTGLSGRLFLKONGLVGIEBOSLWGIAELL 437
Qy 426 HLDFOHNLKQMSFVSFLSLRNLIYLDISHHTVAVANGIENGSLSEVLKMGANSFOE 485
Db 438 ELDTLSNQL-----THLP---HRLFOGKLELYLLSNRLAE 472
Qy 486 NFLP-DITFELRNLTFLDLSOCQLESPAFNSLSLQVIMSHNPFSLDTPPYKCLN 544
Db 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRIRYLSLRNN---SLRTFTPO--- 524
Qy 545 SLQVLDYSLNIMTMSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOWIKD----- 596
Db 525 -----PGLERLMLBGNPMDCCP---LKAALDFALQNPBA 557

RESULT 11

US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPFSTKNLDSFNPLRHLSYSFFSPPELQVLDLSRCEIQTIEDGAYQ 99
Db 60 CSSRNLTFLPDGVPGTQALWLDGNLSSVPPAFAQNLSSLGFLNLQGGQLSGLEPQALL 119
QY 100 SLSHLSTLITLGNPISQALGAFS-----GLSLQKLVAVE 135
Db 120 GLEMLCHLHLEBNQRLSLALGTFAHTPALASLGLSNNRLSRLEBDGLFEGLSLMDNLGW 179
QY 136 TNLASLNFPIGHLKTLKELNVANHLIQSFKLPEYFSNLTNLEHLDLSNKTQSIYCTDL 195
Db 180 NSLAVLPAAFRGLSRLVLAQNRLLAYIQPALFSLAELRELDSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSLNPNNFIOPGAFKEIR-LHKLTLRNPFSLNVMKTCIOGLAGLE 254
Db 236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLEBDTPFGLGLR 293
QY 255 VHRVLGEFRNEGNLEKDKSALBGLCNLTIEFRRLAYLDYDIDILFNCLTNVSSFS 314
Db 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGWQHLELVNCKFGQFPPTLKLSLKRITFTS--NKGNAFSEVDL 372
Db 321 LGHNRIRQLARSPF-GIGQLEVLTLDNQLOEVKAAFLGLITNVAVMNLSGNCIR--NL 377
QY 373 PSLEFLDLR-NGLSFKGCC-----SQSDFGTTSLSKYLDLSFNGVITMSSNFL-GLGLE 425
Db 378 PEQVFRGLKHLSHLESGSCGRIRPHFTGLSGLRRLFLKONGLVGIEBQSLMGLABLL 437
QY 426 HLDFOHSLKQMSSESVLSRLNLIYLDISHTTRVAENGIFNGLSLEVLKMAGNSFOE 485
Db 438 ELDTLSNQL-----THLP--HRLFOGLGLELYLLSRNLAE 472
QY 486 NFLP-DIFTELRLNLTFLDLSOCQLEOLSPTAFNSSLOVLMNSHNNPFSLDTPPYKCLN 544
Db 473 --LPADALGPLORAFMDVSHNRLEALPNSLLAPGRIRYLSLRNN--SLRTFTPO--- 524
QY 545 SLOVLDVSLNHNIMTSKKQELQHPSSLAFLNLTONDFACEHOSFLOWIKD----- 596
Db 525 -----PPGLERLWLEGNPMDCCP---LKALRDFALQNPNSA 557
QY 597 -QROLVVERMECATPSDKQGMFVLSLNTTCQNMKTIIGSV 638
Db 558 VPRFVQALCEGDDCQPPAYTYN-----NITCASPPEVVGIDL 594

RESULT 12
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gloc, Loic
; APPLICANT: Manesfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatler Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPFSTKNLDSFNPLRHLSYSFFSPPELQVLDLSRCEIQTIEDGAYQ 99
Db 60 CSSRNLTFLPDGVPGTQALWLDGNLSSVPPAFAQNLSSLGFLNLQGGQLSGLEPQALL 119
QY 100 SLSHLSTLITLGNPISQALGAFS-----GLSLQKLVAVE 135
Db 120 GLEMLCHLHLEBNQRLSLALGTFAHTPALASLGLSNNRLSRLEBDGLFEGLSLMDNLGW 179
QY 136 TNLASLNFPIGHLKTLKELNVANHLIQSFKLPEYFSNLTNLEHLDLSNKTQSIYCTDL 195
Db 180 NSLAVLPDAAFRGLSRLVLAQNRLLAYIQPALFSLAELRELDSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSLNPNNFIOPGAFKEIR-LHKLTLRNPFSLNVMKTCIOGLAGLE 254
Db 236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLEBDTPFGLGLR 293
QY 255 VHRVLGEFRNEGNLEKDKSALBGLCNLTIEFRRLAYLDYDIDILFNCLTNVSSFS 314
Db 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGWQHLELVNCKFGQFPPTLKLSLKRITFTS--NKGNAFSEVDL 372
Db 321 LGHNRIRQLARSPF-GIGQLEVLTLDNQLOEVKAAFLGLITNVAVMNLSGNCIR--NL 377
QY 373 PSLEFLDLR-NGLSFKGCC-----SQSDFGTTSLSKYLDLSFNGVITMSSNFL-GLGLE 425
Db 378 PEQVFRGLKHLSHLESGSCGRIRPHFTGLSGLRRLFLKONGLVGIEBQSLMGLABLL 437
QY 426 HLDFOHSLKQMSSESVLSRLNLIYLDISHTTRVAENGIFNGLSLEVLKMAGNSFOE 485
Db 438 ELDTLSNQL-----THLP--HRLFOGLGLELYLLSRNLAE 472
QY 486 NFLP-DIFTELRLNLTFLDLSOCQLEOLSPTAFNSSLOVLMNSHNNPFSLDTPPYKCLN 544
Db 473 --LPADALGPLORAFMDVSHNRLEALPNSLLAPGRIRYLSLRNN--SLRTFTPO--- 524
QY 545 SLOVLDVSLNHNIMTSKKQELQHPSSLAFLNLTONDFACEHOSFLOWIKD----- 596
Db 525 -----PPGLERLWLEGNPMDCCP---LKALRDFALQNPNSA 557
QY 597 -QROLVVERMECATPSDKQGMFVLSLNTTCQNMKTIIGSV 638
Db 558 VPRFVQALCEGDDCQPPAYTYN-----NITCASPPEVVGIDL 594

RESULT 13
US-09-538-092-1325
; Sequence 1325, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gloc, Loic

APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurabSeqFormatter Version 0.9
SEQ ID NO 1325
LENGTH: 662
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q14392
US-09-538-092-1325

Query Match 6.9%; Score 299.5; DB 4; Length 662;
Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVVPITTYQCEMELNFKYIPDNLPSTKNLDSFNPRLHLSYSPFSFPELQVLDLSR 87
DB 25 PCRWVKKVVS--CQVIGLQVPSVLPPTETLDSGNDRLSIASPLGPTATLRHLDST 82
QY 88 CEIQTIEDGAYQSLSHTLITGNPIQSIALGAFSGSLQKLVAVETNLAS-----LE 142
DB 83 NEISFLQGAFOALTHEHLSLANHRLAMATLASAGGGLPRTVSLDSGSLVSGLE 142
QY 143 NPIGLHTLKELVANHLIOSFKLPEY-FSNLTNLEHLDSSNKGISICTDLAVLHOM 201
DB 143 RL-IGEAPSLHTLSLAENSLT--RLTRHTFRDMPALBQDLHSNVLMDIEDGAFGLPRL 199
QY 202 PLNLIS-----LDLSLNPNNFI-----QPGAKEIRLHKLTLRNN----- 236
DB 200 THINLSRNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQQA--EFQLTWLDLRNKLIH 257
QY 237 FDSLAVMKTCTIOGLAGLEVHRLVIGEFPN-----EGNLEKFDKSL 277
DB 258 FPDLAALRLIYLNLSNNLIRLPPTGPQDSKGIAHPSGKMSLPLASBSGMSGRPLSL 317
QY 278 EGLCNLTIEFRFLAVLDYLDIIDL-----NCLTNVSSFSLSVITERYKDPSPYNG 331
DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCPNLNSRNCLETFEARRLSLPCIMLDLSHN-A 374
QY 332 MOHLELVNCKFGQFPTLKLSIKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGI 385
DB 375 LETLELGRALGSLRTLLQ-----GNLRLDLPPTANLASLQGLNLSQGRV 422
QY 386 S-----FKGCCSGSDFGTSLKYLDLSFNGVITWSSNFLGLEOLEHLDFOHSNLKQ 436
DB 423 SPCGPDPEPGSGCAFS--GITSLSLSLIVNEI-----ELRAGAFLLTPPLE 470
QY 437 MSEFVFLSLRNLYLDISHTTRVAFNGIFNGI--SSLEVLKMAGNSPQ--ENFLPDLFT 493
DB 471 -----LDLSSNPGLEVATGALGSLASLEVIALQNGLMVLDVDPFCIC 515
QY 494 ELRNLTFLDLSQCQLEQSPFAFNSLSLOVLNMSHNNFSLDTPPYKCLNSLOVLDYSI 553
DB 516 ----LKRINLAENRISHL--PAWTOAVSLEVDL--RNNSSFSL--LPGSMGLB----- 560
QY 554 NHIMTSKQOELQHPSSLAFLNLTQNDPACTCEHOSFLOWIKQ--ROLLVAYERME--C 609
DB 561 -----TSLRRLYLQGNPLSC--CGN-----GMLAAQLHOGRVVDATQDCLIC 600
QY 610 ATPSDKQGPVLSLNTIT-----CONN--KTIIGSVLSVLSVAVLVYKFFHMLLAG 663
DB 601 RFSOBE-----VSLSHVRPEDECKGGLKNNILITITFLVSAITL-----LTTTLA 647

QY 664 C 664
DB 648 C 648

RESULT 14
US-09-949-016-6619
Sequence 6619, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6619
LENGTH: 662
TYPE: PRT
ORGANISM: Human
US-09-949-016-6619

Query Match 6.9%; Score 299.5; DB 4; Length 662;
Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVVPITTYQCEMELNFKYIPDNLPSTKNLDSFNPRLHLSYSPFSFPELQVLDLSR 87
DB 25 PCRWVKKVVS--CQVIGLQVPSVLPPTETLDSGNDRLSIASPLGPTATLRHLDST 82
QY 88 CEIQTIEDGAYQSLSHTLITGNPIQSIALGAFSGSLQKLVAVETNLAS-----LE 142
DB 83 NEISFLQGAFOALTHEHLSLANHRLAMATLASAGGGLPRTVSLDSGSLVSGLE 142
QY 143 NPIGLHTLKELVANHLIOSFKLPEY-FSNLTNLEHLDSSNKGISICTDLAVLHOM 201
DB 143 RL-IGEAPSLHTLSLAENSLT--RLTRHTFRDMPALBQDLHSNVLMDIEDGAFGLPRL 199
QY 202 PLNLIS-----LDLSLNPNNFI-----QPGAKEIRLHKLTLRNN----- 236
DB 200 THINLSRNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQQA--EFQLTWLDLRNKLIH 257
QY 237 FDSLAVMKTCTIOGLAGLEVHRLVIGEFPN-----EGNLEKFDKSL 277
DB 258 FPDLAALRLIYLNLSNNLIRLPPTGPQDSKGIAHPSGKMSLPLASBSGMSGRPLSL 317
QY 278 EGLCNLTIEFRFLAVLDYLDIIDL-----NCLTNVSSFSLSVITERYKDPSPYNG 331
DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCPNLNSRNCLETFEARRLSLPCIMLDLSHN-A 374
QY 332 MOHLELVNCKFGQFPTLKLSIKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGI 385
DB 375 LETLELGRALGSLRTLLQ-----GNLRLDLPPTANLASLQGLNLSQGRV 422
QY 386 S-----FKGCCSGSDFGTSLKYLDLSFNGVITWSSNFLGLEOLEHLDFOHSNLKQ 436
DB 423 SPCGPDPEPGSGCAFS--GITSLSLSLIVNEI-----ELRAGAFLLTPPLE 470
QY 437 MSEFVFLSLRNLYLDISHTTRVAFNGIFNGI--SSLEVLKMAGNSPQ--ENFLPDLFT 493
DB 471 -----LDLSSNPGLEVATGALGSLASLEVIALQNGLMVLDVDPFCIC 515
QY 494 ELRNLTFLDLSQCQLEQSPFAFNSLSLOVLNMSHNNFSLDTPPYKCLNSLOVLDYSI 553
DB 516 ----LKRINLAENRISHL--PAWTOAVSLEVDL--RNNSSFSL--LPGSMGLB----- 560

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Qy 554 NHMTSKQELQHPSSIAFLNTQNDFACTCEHOSFLQWIKQ-RQLLVEVERME---C 609
Db 561 -----TSLRRLYLQGNPLSC-CGN-----GMLAQHQGRVDVDAATQDLIC 600
Qy 610 ATPSDKQAMPVLSINIT-----COMN--KTIIGVSVLSVYVAVLVYKRYFPHMLLAG 663
Db 601 RFSQOE---VLSHVRPDECEKGKLNINLIIITLFIIVSAIL-----LTTLLA 647
Qy 664 C 664
Db 648 C 648

RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10710
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10710

Query Match 6.9%; Score 299.5; DB 4; Length 665;
Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

Qy 28 PCVEVENITTYQCEHLENKYKIPDNLPSTKNDLSFNPRLHLSYSPFSPPELOVLDISR 87
Db 28 PCXWVDKVS--COVLGLQVPSVLPPTETLIDSGNQLRSILASPLGFYATLRHLDIST 85
Qy 88 CEIQTIEDGAYOSLSHTLITGNPIOSLALGAFSGLSLOKLVAVETNLAS-----LE 142
Db 86 NEISFLOQGAFOALTHEHLSLAHNRILAMATALSAGLGPLRVTSLDLSGNSLSYGLLE 145
Qy 143 NPIGHLTKLKELVANHLIOSFKLPXY-FSNLTNLEHLDLSNKOISICTDLRVLHQ 201
Db 146 RL-LGEAPSLHTLSLAENSLT-RLTRHTFRDMALBQDLHSNVLMIDEDGAFEGLPRL 202
Qy 202 PLNLS-----LDLSNPMNFI---QGAFKYIRLHKLTLRNN--- 236
Db 203 THLMISNSLTCISDFSLQQLRVLDLSGNSIEAFQASQPOA--BFQLTWLDLRENKLIH 260
Qy 237 FDSLNVKTCIQGLAGLEVHRLVIGEPN-----EGNLEKFDKSA 277
Db 261 FPDLAALPRLIYLNLSNNLIRLPTGPQDSKGIHAPSEGSALPLSAPSGNASGRPLSQ 320
Qy 278 EGLCNLTIEEFRLAYLDYDIDLF-----NCLTNVSSFSVSVTIERVKDFSYNFG 331
Db 321 LNL-DLSYNEIEL-IPDSFLEHLSLCLTNLSRNCIRTFEARRLGSLPCLMLDLSHR-A 377
Qy 332 WQHLVYVCKFGQFPPTLKLSKRLTFTSNKGNAPSEV-----DPLSEFLDLSRNGI 385
Db 378 LETLELGARALGSLRTLLQ-----GNALRDLPTYTFANLASLQRLNLOGRNV 425
Qy 386 S-----FKGCCSQSDPFGTSLKYLDSLFGVYITMSNPLGLEQLEHLDPOHSNLIKQ 436

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Db 426 SPCCGPDEPBGSGCVAFS--GITSLSLSLVNDIEI-----ELLRAGAFIHTPLTE 473
Qy 437 MSEFSVFLSLRNLIYLDISHTRFVAFNGIFNGI-SSLEVLKMAAGNSFO--ENFLPDIFT 493
Db 474 -----LDLSNPGLEVATGALGIEASLEVIALQNGMLMWLQVLDLPCFIC 518
Qy 494 ELRNLTLDLSQCEQLSPLAFNSLSLOYLNMHNNPFSLDTPPYKCLNSLOVLDYSL 553
Db 519 ---LKRINLAENRLSHL--PAWQAVSLLEVLDL-RNNSFSL--LPGSAMGGL----- 563
Qy 554 NHMTSKQELQHPSSIAFLNTQNDFACTCEHOSFLQWIKQ-RQLLVEVERME---C 609
Db 564 -----TSLRRLYLQGNPLSC-CGN-----GMLAQHQGRVDVDAATQDLIC 603
Qy 610 ATPSDKQAMPVLSINIT-----COMN--KTIIGVSVLSVYVAVLVYKRYFPHMLLAG 663
Db 604 RFSQOE---VLSHVRPDECEKGKLNINLIIITLFIIVSAIL-----LTTLLA 650
Qy 664 C 664
Db 651 C 651

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Search completed: March 12, 2005, 19:58:48
Job time : 27.0639 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 74.2496 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAF...SNPEGTGTCNMQEATSI 839

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 1396920 seqs, 32984858 residues
Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	4141	95.1	799	14	US-10-128-166-7
4	4141	95.1	799	16	US-10-732-563-8
5	4141	95.1	799	16	US-10-732-796A-8
6	663	15.2	661	15	US-10-038-854-135
7	663	15.2	661	13	US-10-037-417-107
8	629.5	14.5	661	15	US-10-114-893-10
9	629.5	14.5	661	15	US-10-038-854-134
10	603.5	13.9	784	15	US-09-950-041-4
11	603.5	13.9	784	15	US-10-456-947-46
12	602.5	13.8	784	14	US-10-095-627-12
13	602.5	13.8	784	16	US-10-732-563-4

14	602.5	13.8	784	16	US-10-732-796A-4	Sequence 4, Appli
15	602.5	13.8	784	17	US-10-741-600-1390	Sequence 1390, Ap
16	602.5	13.8	784	17	US-10-741-600-1391	Sequence 1391, Ap
17	599.5	13.8	784	13	US-10-145-014-23	Sequence 23, Appl
18	590.5	13.3	1032	10	US-09-954-987B-192	Sequence 192, App
19	580.5	13.3	1032	14	US-10-272-502A-31	Sequence 31, Appl
20	580.5	13.3	1032	15	US-10-407-952-32	Sequence 32, Appl
21	567	13.0	1050	10	US-09-954-987B-175	Sequence 175, Appl
22	567	13.0	1050	14	US-10-272-502A-22	Sequence 22, Appl
23	567	13.0	1050	15	US-10-407-952-26	Sequence 26, Appl
24	534	12.3	1032	9	US-09-950-041-37	Sequence 37, Appl
25	534	12.3	1032	10	US-09-864-761-38325	Sequence 38325, A
26	534	12.3	1041	10	US-09-954-987B-184	Sequence 184, App
27	534	12.3	1041	10	US-09-954-987B-186	Sequence 186, App
28	534	12.3	1041	14	US-10-272-502A-26	Sequence 26, Appl
29	534	12.3	1041	15	US-10-407-952-28	Sequence 28, Appl
30	534	12.3	1041	16	US-10-732-563-16	Sequence 16, Appl
31	534	12.3	1041	16	US-10-732-796A-16	Sequence 16, Appl
32	533	12.2	1041	9	US-09-168-978-3	Sequence 3, Appli
33	533	12.2	1041	9	US-09-168-978-3	Sequence 3, Appli
34	533	12.2	1041	9	US-09-978-295A-498	Sequence 498, App
35	533	12.2	1041	9	US-09-978-697-498	Sequence 498, App
36	533	12.2	1041	9	US-09-978-192A-498	Sequence 498, App
37	533	12.2	1041	9	US-09-999-832A-498	Sequence 498, App
38	533	12.2	1041	10	US-09-978-189-498	Sequence 498, App
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41	533	12.2	1041	10	US-09-978-191A-498	Sequence 498, App
42	533	12.2	1041	10	US-09-978-403A-498	Sequence 498, App
43	533	12.2	1041	10	US-09-978-564A-498	Sequence 498, App
44	533	12.2	1041	10	US-09-999-833A-498	Sequence 498, App
45	533	12.2	1041	10	US-09-981-915A-498	Sequence 498, App
					US-09-978-824-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26

Sequence 26, Application US/09950041
Publication No. US20030032090A1

GENERAL INFORMATION:

APPLICANT: Hardiman, Gerard T.

APPLICANT: Rock, Fernando L.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kaestlein, Robert A.

APPLICANT: Ho, Stephen W.K.

APPLICANT: Liu, Yong-Jun

TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

FILE REFERENCE: DX0724XK1

CURRENT APPLICATION NUMBER: US/09/950, 041

PRIOR FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/728, 540

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 60/207, 558

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/073, 363

PRIOR FILING DATE: 1999-06-05

PRIOR APPLICATION NUMBER: 60/044, 293

PRIOR FILING DATE: 1997-05-07

PRIOR APPLICATION NUMBER: 60/072, 212

PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: 60/076, 947

PRIOR FILING DATE: 1998-03-05

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 837

TYPE: PRT

ORGANISM: Homo sapiens

US-09-950-041-26

Query Match

99.6%; Score 4335.5; DB 10; Length 837;

Best Local Similarity 99.9%; Pred. No. 0; Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MSASRLAGTLIPAMAFISCVPRESMEPCVE VPNIITVQCEMLNFYKIPDNLPFSTKXLDL 59
QY 62 SPNPLRHGYSYFSPPELQVLDLSRCEIQTIEDGAYQSLSHLSLTLITGNPIQSALGA 121
Db 60 SPNPLRHGYSYFSPPELQVLDLSRCEIQTIEDGAYQSLSHLSLTLITGNPIQSALGA 119
QY 122 FSGLSISQKVAVAVTNLASLENFPIGHLKTLKELVANAHLIQSFKEPPEYSNLTNLEHLD 181
Db 120 FSGLSISQKVAVAVTNLASLENFPIGHLKTLKELVANAHLIQSFKEPPEYSNLTNLEHLD 179
QY 182 LSSNKIOSICTDRLVHOMPLNLSLDLSLNPNNFIOPGAFKEIRLHKLTLRNPFSLN 241
Db 180 LSSNKIOSICTDRLVHOMPLNLSLDLSLNPNNFIOPGAFKEIRLHKLTLRNPFSLN 239
QY 242 VMKTCIOGLAGLEVHRLVGLGEPNENGLKEFKDSALBGLCNLTIEFRLAYLDYDDII 301
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QY 302 DLFNCLTNVSSFSIVSTIERVKDPSYNGMOMELVNCCKGSPPTLKISLKLTFSTN 361
Db 300 DLFNCLTNVSSFSIVSTIERVKDPSYNGMOMELVNCCKGSPPTLKISLKLTFSTN 359
QY 362 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKYLDLSFNGVITWSSNFG 421
Db 360 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKYLDLSFNGVITWSSNFG 419
QY 422 EOLEHLDFOHNSLKQMBSEFVLSLRNLIYLDISHTHTRAVNGIFNGLSLEVLKMAGN 481
Db 420 EOLEHLDFOHNSLKQMBSEFVLSLRNLIYLDISHTHTRAVNGIFNGLSLEVLKMAGN 479
QY 482 SPOENFLPDI FTELRLNLTFLDLSQCELOESPTAFNSLSLQVLMASHNNEFSLDTPYK 541
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QY 542 CLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNLTONDFACTCEHOSFLQWIMDQRL 601
Db 540 CLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNLTONDFACTCEHOSFLQWIMDQRL 599
QY 602 VEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVAVLYKFFPHMLL 661
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QY 722 IIHGFKRSKRVIVVVSQHFQSRMCIFEYELAQTMQFLSSRAGIIFVILQKVEKTLRLQ 781
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QY 782 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQOATS 839
Db 780 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQOATS 837

RESULT 2
US-09-950-041-8
Sequence 8, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
APPLICANT: Liu, Yong-Jun
TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1

CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-8

Query Match 95.1%; Score 4141; DB 10; Length 799;
Best Local Similarity 100.0%; Pred. No. 0; Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 101 LSHLSTLITGNPIQSALGAFSGLSLQKLVAVENTLASLENFPIGHLKTLKELVANA 160
Db 61 LSHLSTLITGNPIQSALGAFSGLSLQKLVAVENTLASLENFPIGHLKTLKELVANA 120
QY 161 LIOSFKLPEYSNLTNLEHLDLSNKKIOSICTDRLVHOMPLNLSLDLSLNPNNFIOP 220
Db 121 LIOSFKLPEYSNLTNLEHLDLSNKKIOSICTDRLVHOMPLNLSLDLSLNPNNFIOP 180
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Db 181 GAFKEIRLHKLTLRNPFSLNWKTCIOGLAGLEVHRLVGLGEPNENGLKEFKDSALBGL 240
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Db 241 CNLTIEFRLAYLDYDDIIDLPCNLTNVSFSLSVSTIERYKDSYNGMOMELVNC 300
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Db 421 VARENGITNGLSLEVLKMAGNSFOENFLPDI FTELRLNLTFLDLSQCELOESPTAFNSLS 480
QY 521 SLOVLMASHNNEFSLDTPYKCLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNLTOND 580
Db 481 SLOVLMASHNNEFSLDTPYKCLNSLOVLDYSLNHIMTSKQELQHPSSLAFLNLTOND 540
QY 581 FACTCEHOSFLQWIMDQRLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 640
Db 541 FACTCEHOSFLQWIMDQRLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 600
QY 641 VLVSVVAVLYKFFPHMLLAGCTKYRGENTYDAFVIYSSQDEDMWRNELYKMLEG 700
Db 601 VLVSVVAVLYKFFPHMLLAGCTKYRGENTYDAFVIYSSQDEDMWRNELYKMLEG 660
QY 701 PPOLCLHYRDEIPGVAIAANIIHGFHRSKRVIVVVSQHFQSRMCIFEYELAQTMQFL 760
Db 661 PPOLCLHYRDEIPGVAIAANIIHGFHRSKRVIVVVSQHFQSRMCIFEYELAQTMQFL 720

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Qy 761 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 820
Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 780
Qy 821 WNPETVGTGCMQOEATSI 839
Db 781 WNPETVGTGCMQOEATSI 799

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US2003007729A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDAN K
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Query Match          95.1%; Score 4141; DB 14; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MEINFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYOS 100
Db 1 MEINFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYOS 60

Qy 101 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKEINVAHN 160
Db 61 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKEINVAHN 120

Qy 161 LIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQMPLNLSLDLSLNMNFIOP 220
Db 121 LIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQMPLNLSLDLSLNMNFIOP 180

Qy 221 GAFKEIRLHLKLTNNPDSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 280
Db 181 GAFKEIRLHLKLTNNPDSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 240

Qy 281 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFSGYNGMOHLELYNC 340
Db 241 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFSGYNGMOHLELYNC 300

Qy 341 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy 401 LKTYLDSFNGVITMSSNFIQLEHLDPOHSNKKOMSESVFLSLRNLYLIDISHHTHR 460
Db 361 LKTYLDSFNGVITMSSNFIQLEHLDPOHSNKKOMSESVFLSLRNLYLIDISHHTHR 420

Qy 461 VAFNGIENGSLSEVLKMAGNSFOENFLPDITFELRNLTFLDLSQCCOLEQSPAPFNSLS 520
Db 421 VAFNGIENGSLSEVLKMAGNSFOENFLPDITFELRNLTFLDLSQCCOLEQSPAPFNSLS 480

Qy 521 SLOVYANSHANNFSLDTPPYKCLNSLOYLDVSLNHNIMTSKKQELQHPSPSIAPFNLITOND 580
Db 481 SLOVYANSHANNFSLDTPPYKCLNSLOYLDVSLNHNIMTSKKQELQHPSPSIAPFNLITOND 540

Qy 581 FACTCEHOSFLQWKDQROLIVVERMECATPSPDKQMPVLSLNTQOMKTIIGVSVLS 640

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Db 441 FACTCEHOSFLQWKDQROLIVVERMECATPSPDKQMPVLSLNTQOMKTIIGVSVLS 600
Qy 641 VLWVSVAVLVYKFFPHMLLAGCIKYGRGENIVDAVIYSSODEDWVRYNLEBEGV 700
Db 601 VLWVSVAVLVYKFFPHMLLAGCIKYGRGENIVDAVIYSSODEDWVRYNLEBEGV 660
Qy 701 PPFCULHYRDFIPGVAIAANIIEGFKRSKRVIVVVSQHFISQRCIFEYELAQWQPL 760
Db 661 PPFCULHYRDFIPGVAIAANIIEGFKRSKRVIVVVSQHFISQRCIFEYELAQWQPL 720

Qy 761 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 820
Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 780
Qy 821 WNPETVGTGCMQOEATSI 839
Db 781 WNPETVGTGCMQOEATSI 799

RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 5818300003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

Query Match          95.1%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MEINFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYOS 100
Db 1 MEINFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYOS 60

Qy 101 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKEINVAHN 160
Db 61 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKEINVAHN 120

Qy 161 LIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQMPLNLSLDLSLNMNFIOP 220
Db 121 LIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQMPLNLSLDLSLNMNFIOP 180

Qy 221 GAFKEIRLHLKLTNNPDSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 280
Db 181 GAFKEIRLHLKLTNNPDSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 240

Qy 281 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFSGYNGMOHLELYNC 340
Db 241 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFSGYNGMOHLELYNC 300

Qy 341 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy 401 LKTYLDSFNGVITMSSNFIQLEHLDPOHSNKKOMSESVFLSLRNLYLIDISHHTHR 460
Db 361 LKTYLDSFNGVITMSSNFIQLEHLDPOHSNKKOMSESVFLSLRNLYLIDISHHTHR 420

Qy 461 VAFNGIENGSLSEVLKMAGNSFOENFLPDITFELRNLTFLDLSQCCOLEQSPAPFNSLS 520

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Db 421 VAFNGIFNGSLSEVLKMAGNSFOENFLPDIIFTELRLNLTFLDLSQCLEQSPPTAFNSLS 480
Qy 521 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNTQND 580
Db 481 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNTQND 540
Qy 581 FACTCEHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 640
Db 541 FACTCEHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 600
Qy 641 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDMVRNELYKNLEEGV 700
Db 601 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDMVRNELYKNLEEGV 660
Qy 701 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRMCIFEYELAQTWQFL 760
Db 661 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRMCIFEYELAQTWQFL 720
Qy 761 SSRAGIIFIVLOKYEKTLRQOVELYRLSLRNTYLEWEDSVLGRHIFWRRLKALLDGKS 820
Db 721 SSRAGIIFIVLOKYEKTLRQOVELYRLSLRNTYLEWEDSVLGRHIFWRRLKALLDGKS 780
Qy 821 MNPEGTVGTGCNNQOEATSI 839
Db 781 MNPEGTVGTGCNNQOEATSI 799

RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732.796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRN
; ORGANISM: Homo sapiens
; US-10-732-796A-8

Query Match 95.1%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MEINFYKIPNLPSTKNDLDSFNPLRHLGYSFFSPPELOVLDLSRCEIQTIEDGAYQS 100
Db 1 MEINFYKIPNLPSTKNDLDSFNPLRHLGYSFFSPPELOVLDLSRCEIQTIEDGAYQS 60
Qy 101 LSHLSTIILTGNPIQSIALGAFSGLSLOKLVAVETNLASLENPPIGHLTKLKELVAAH 160
Db 61 LSHLSTIILTGNPIQSIALGAFSGLSLOKLVAVETNLASLENPPIGHLTKLKELVAAH 120
Qy 161 LIOSFKLPEYFSLNLTNLEHDLDSNKTOSTYCTDILRHLQMPPLNLSLDLSINPMFTOP 220
Db 121 LIOSFKLPEYFSLNLTNLEHDLDSNKTOSTYCTDILRHLQMPPLNLSLDLSINPMFTOP 180
Qy 221 GAFKEIRLHKLTLRNNDSLANVMTCTIOGLAGLEVHRLVGEPEENENLEKFPKSALEGL 280
Db 181 GAFKEIRLHKLTLRNNDSLANVMTCTIOGLAGLEVHRLVGEPEENENLEKFPKSALEGL 240
Qy 281 CNLTIEFRILAYLDYDIIDILFNCLTNVSSFSVLVTTIERVDFSYNGWQHLIELVNC 340
Db 241 CNLTIEFRILAYLDYDIIDILFNCLTNVSSFSVLVTTIERVDFSYNGWQHLIELVNC 300
Qy 341 KPGQFTLKLSLRLFTSNKGNASEVDLPSEFLDLSRNGLSFGKCCSODPCTTS 400

Db 301 KPGQFTLKLSLRLFTSNKGNASEVDLPSEFLDLSRNGLSFGKCCSODPCTTS 360
Qy 401 LKTYDLSFNGVITMSSNPLGLLEQLEHDPQSHNLKOMSEFSVFLSLRNLTYLDLSHTHTR 460
Db 361 LKTYDLSFNGVITMSSNPLGLLEQLEHDPQSHNLKOMSEFSVFLSLRNLTYLDLSHTHTR 420
Qy 461 VAFNGIFNGSLSEVLKMAGNSFOENFLPDIIFTELRLNLTFLDLSQCLEQSPPTAFNSLS 520
Db 421 VAFNGIFNGSLSEVLKMAGNSFOENFLPDIIFTELRLNLTFLDLSQCLEQSPPTAFNSLS 480
Qy 521 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNTQND 580
Db 481 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNTQND 540
Qy 581 FACTCEHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 640
Db 541 FACTCEHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 600
Qy 641 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDMVRNELYKNLEEGV 700
Db 601 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDMVRNELYKNLEEGV 660
Qy 701 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRMCIFEYELAQTWQFL 760
Db 661 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRMCIFEYELAQTWQFL 720
Qy 761 SSRAGIIFIVLOKYEKTLRQOVELYRLSLRNTYLEWEDSVLGRHIFWRRLKALLDGKS 820
Db 721 SSRAGIIFIVLOKYEKTLRQOVELYRLSLRNTYLEWEDSVLGRHIFWRRLKALLDGKS 780
Qy 821 MNPEGTVGTGCNNQOEATSI 839
Db 781 MNPEGTVGTGCNNQOEATSI 799

RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vermet, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malynkar, Uriel M
; APPLICANT: Shinkete, Richard A
; APPLICANT: Tchernyev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kerkuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimiro Y
; APPLICANT: Gangoili, Beba A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine B
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038.854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258, 928
; PRIOR FILING DATE: 2000-12-29

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;; PRIOR APPLICATION NUMBER: 60/259,415
;; PRIOR FILING DATE: 2001-01-02
;; PRIOR APPLICATION NUMBER: 60/259,785
;; PRIOR FILING DATE: 2001-01-04
;; PRIOR APPLICATION NUMBER: 60/269,814
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/279,832
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/279,833
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/279,863
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/283,889
;; PRIOR FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: 60/284,447
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: 60/286,683
;; PRIOR FILING DATE: 2001-04-25
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 411
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 135
;; LENGTH: 661
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-038-854-135

Query Match      15.2%; Score 663; DB 15; Length 661;
Best Local Similarity 28.7%; Pred. No. 4.1e-44;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY 14 AMAFLSC-VRPESWPCVAVVNNITYQCMELNFYKIPDNLPSTKNLDLSFNPJRHLSGY 72
DB 12 ALFLASCATSSDQCKIEKVNKTNCENGLNBIPTGLNFTCEFSFNVLPITQNT 71
QY 73 SFPSFPELQVLDNRCEIQTIEDGAYQSLSHLSTLITLGNITQSLALGAFGLSLQKLY 132
DB 72 TFSRLINFTFLDRLRCQIYWHEDIPQSHRLDVLVLNPLIFMAETALSGPKALKTLF 131
QY 133 AVETNLASLENPFIHGLTKLKELVANHLIOSFKLPEYFSLVTNLEHDLSSNKKIOSIYC 192
DB 132 FIOGIGISSIDRPLHNOKTLSLYGSHHISIKLPKFPF-EKLVKVDLFOONALHYISK 190
QY 193 TDLFVLHQMPLNLISLDSINPMNFIOGAFKEIRLHLKTLRNFDLSNWKTCIOGLAG 252
DB 191 EDMSSLOQ--ATNLSLNLNGNDIAGIEBGAFDSAVFQSL---NFGGQNLVLVFKGLKN 244
QY 253 LEVRLVIGFRNRGNLEKPKSALBGLCNLTIEFRLAYDYIIDLIIFNCLTNVSS 312
DB 245 STIOSLWGTFTEDMD-EDISPAVEEGLCENSVESINL-QKHYPFNISSTFHGFS--- 298
QY 313 FSLSVTTERVYKDSYNGMQLLELVNCKFCQFPT--LKLKSLKRLFTSNKGN--AFS 368
DB 299 -----GLOELDTATNLSHLPSGLVGLSTLKKLVLSANKFENLCOIS 340
QY 369 EVDLPSEF-----LDSRNLGSLFKGCCSQSDFTGTSKY 403
DB 341 ASNPSTLTHLSIKNCKTRELGTGCLLENLRELDISHDDIETSDCCNLQRLNLSHLS 400
QY 404 LDSFNGVITMSSN-FLGLEDEHLDPQHSNLKOMSESVLSLRNLTYLDISHTHRYA 462
DB 401 LNLSPNEPLSLKTAPEKCPQLELDLAFTRLKYVDAQSPQONHLKVLNLSHLDIS 460
QY 463 FNGIFNGLSLEVLKMGANSFOENFL--PDIFTELRLNLTFLDLSOCOLBOLSPTAFNLS 520
DB 461 SEQIFDGLPALQHNILQGNHFPKGNIOQTNSLOTLGRLEILVLSFCULSDIDQAFYSLK 520
QY 521 SLQVLNASHNNFSLDLPFYKCLNSLO--VLDSYNHIMTSKQELQHPSSLAFL--- 574
DB 521 MNNHVDLSHNR---LTSSISALSHLKIGIYLNLSNHSIT-----LPDLPLLSQOR 570
QY 575 --NLTONDFACTCHOSFLOWIKQOROLLVERRECECTPBDKQGMPLVLSNITTCQNMKT 632
DB 575 --NLTONDFACTCHOSFLOWIKQOROLLVERRECECTPBDKQGMPLVLSNITTCQNMKT 632
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DB 571 TINRQNPDLCTCSNIYFLENYKENMOKLEDTEDTLCENPPLNGVRLSDVTLSCSMAV 630
QY 633 IIGVSLVSLVSVAVLVYKFY 655
DB 631 GIFPLVPLVFPALLIFAVKXF 653

RESULT 7
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verner, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyanekar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Query Match      15.2%; Score 663; DB 15; Length 661;
Best Local Similarity 28.7%; Pred. No. 4.1e-44;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY 14 AMAFLSC-VRPESWPCVAVVNNITYQCMELNFYKIPDNLPSTKNLDLSFNPJRHLSGY 72
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; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match      14.5%; Score 629.5; DB 13; Length 661;
Best Local Similarity 29.7%; Pred. No. 2e-11;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

12 ALPLASCAATTSSPQCKICEKVENKTYNCENGLNEIPGLTNPSTCELFSEFNVLPITQNT 71
QY SFFSPPELVQVLDLSCEIQITEDGAYOSLSHSTLILGNPIQSLALGAFGLSLQVLY 132
Db TFSRLINLTFDLTRCQIYWHEDTFQSHRDITLVLANPIFAEFLGAPKALKHLF 131
QY 133 AVEFNLSLENFPIGHLTKLELVANHLIOSFKLPEYFSLNLTNLEHDLSSNKIOSIYC 192
Db 132 FIQGISIDPLPLHNOQKTESLYGSHISSIKLPKFPF--EKLVKVDLFGNNAIHYLSK 190
QY 193 TDRLVHOMPLINSLDLSLAMPNFIOGAKKEIRLHKLTLRNNPDSLANKTKCIQGLAG 252
Db 191 EDMSSLQO--ATNLSLNLNGNDIAGIEPAPDAVFOSL---NFGTQNLVIFKGIKN 244
QY 253 LEVRLVGFEPNNEGNEKFPKSALEGCNLTIEEFLAYLDYLDIIDLFNCLTNVSS 312
Db 245 STISLWLTGEDMD--EDISPAVEGLCEMSVESLNQ--QKHFFNISNTFHCFS---- 298
QY 313 FSLVSVTIERVYKDPFSYNGMQLBELVNCFGQFPF--LKLKSLKRLTFTSNKGN--AFS 368
Db 299 -----GLQELDLTATHLSLPSGLVGLSTLKKLVLSANKFENLQGIS 340
QY 369 EVDLPSELF-----LDLSRNLSTRGCCSOSDFTTSLKY 403
Db 341 ASNPFSLTHTLSIKQNTKRLGLGTGCLLENLRELDISHDIIETSDCCNLQLRNLSHQ 400
QY 404 LDLSFNGVITYSN--FLGLEQLEHLDFOHSLKQMSFVSFLSLNLTLYDISHTRVA 462
Db 401 LNLVSNBELSLKTAFFKCPQLELDLDAFLRLKYKDAQSPFONHLVLYLSHSLDIS 460
QY 463 FNGJFNGJLSLEVLKMAGNSFOENFL--PDIFTELRLNLTFLDSQCQLEQSPFAFNSLS 520
Db 461 SEQFDFGLPALQHLNLQGNHFPKGNIOKTNLSIQTLGRLEILVLSFCDDLSIDQAFSLK 520
QY 521 SLQVLSNHNFPFLSDTPPYKCLASLQ--VLDYSLNHTMSKKQELQHPSSLAFL---- 574
Db 521 MNHNVLDISHNR---LTSSISALSHLKGILYLNLSNHSII-----LPSILTLISQOR 570
QY 575 --NLTONDFACTCHOSFLQWIKDORQLVEVERMECATPSDKOGMPVLSLNTCOMNKT 632
Db 571 TINLRQNPDLCTCSNIYLEWYKEMQKLEBDEDTLTCENPLLKGVRISDVTLSCMAAV 630
QY 633 IIGVSLVSLVSVVAVLVYKPY 655
Db 631 GIFPLVLVFLVAILLIPAVKXF 653

RESULT 8
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Meberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OR INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCES: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114, 893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match      14.5%; Score 629.5; DB 13; Length 661;
Best Local Similarity 29.7%; Pred. No. 2e-11;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CYEVVPNTTYQCEMLNFKIPDNLPESTKNLDSLNPRLHLCYSFSPPELV 83
Db 23 SWDMCKICEKANKTYNCENGLSEIPDLTPNTEFFLESFNFPLPTINRKFSLMNTLPL 82
QY 84 DLRSCEIQITEDGAYOSLSHSTLILGNPIQSLALGAFGLSLQVAVETNLASLEN 143
Db 83 DLTRCQIYWHEDTFQSHQSLTVLTGNPLIFAEFLSLNGPSLKLFLIQTISNLEF 142
QY 144 FPIGHLTKLELVANHLIOSFKLPEYFSLNLTNLEHDLSSNKIOSIYCTDLRVLHQMPL 203
Db 143 IPVHNLNLSLYGSHISSIKFPKDFP--ARNLKVLDPONNAIHYISREDMSLEQ--A 199
QY 204 LNLSDLSLAMPNFIOGAKKEIRLHKLTLRNNPDSLANKTKCIQGLAGELRVLYGSF 263
Db 200 INLSLNFNGNNVKGIEGAPDSVFOSL---NFGTQNLVIFNGLQNSTTOSLWLTGF 255
QY 264 RNEGNEKFPKSALEGCNLTIEEFLAYLDYLDIIDLFNCLTNVSSFSVSVTIER 322
Db 256 EDIDD--EDISSAMTKGLCEMSVESLNQ--EHRPSDISSTTFQCFTQLOELDLTATHLKG 312
QY 323 VKDFSYNGMQLBELVN-----CKF--GQFPFL-----LKLKSLKRLTFTSN 361
Db 313 LPS-----GKKGLNLTCLKLVSVNHPDQLQISANPFSLTHTYIRGNVKKHLGVGCL 367
QY 362 KGNASEVLDPLSEFLDLSRNLGSLFKGCCSOSDFTTSLKYDLSNGVITYMSN--FLG 420
Db 368 KLGK-----LQTLDLSHNDIEASDCCSLQKNLSHQTLNLSNEBLSGISOAFKE 418
QY 421 LEQLEHDFQ---HNSLKQMSFVS--VPLSLRLYI--LDISHTRVAFNGJFNGJSS 472
Db 419 CPQLELDLDAFLRLHITAPQ--SPFONHLFQVNLNLTICFLDTSNQH-----LLAGLPV 470
QY 473 LEVLKMAGNSFOENFL--PDIFTELRLNLTFLDSQCQLEQSPFAFNSLSLQVLSNHN 530
Db 471 LRHLNKGHNFQDQITKTNMLQTVGSLVLYLSSCGSLSDQGAFFSLGMSHVDISHN 530
QY 531 NFF--SLDTPPY-----KCLNSLOVLDYSLNHTMSKKQELQHPSSLAFLNLTQNDP 581
Db 531 SLTCDSDLSLSHUKGIYLNLAANSINITISPLLPIT-----SQOSTINLSHNP 579
QY 582 ACTCEHOSFLQWIKDORQLVEVERMECATPSDKOGMPVLSLNTCOMNKTIIIGSVLYSV 641
Db 580 DCTCSNHFPLTWKKNHKLGESEFTTCANPRLRGVLSDVLSGCI--TAIGIFPLIV 637
QY 642 LVSVVAVLVY 652
Db 638 FLV-LTALILF 647

RESULT 9
US-10-038-854-134
; Sequence 134, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vermet, Corine
; APPLICANT: Bisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Urfel M
; APPLICANT: Shmukets, Richard A
; APPLICANT: Tchiernev, Velizar

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APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangolli, Bsha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glendene
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US/10/038,854
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
REMAINING Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 134
LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-854-134

Query Match 14.5%; Score 629.5; DB 15; Length 661;

Best Local Similarity 29.7%; Pred. No. 2e-41; Indels 89; Gaps 24;

Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWBP-CVEVFNITTYQCMELNPFYKAPDNLPSSTKNULDSFNDLRHLGYSVSPFDELQVL 83
23 SWDMCIRKANKNTYCNENLGLSEIPDLPNTTEPERSFNFLPIIHRTRSRMLNLTFL 82
84 DLRSCEIOTIEDGAYQSLSHSLTLLTGNPIOSIALGAFSGLSLQKLVAVETNLASLEN 143
83 DLTRQIWMIHEDTFQSHQSLTTLVTGNPLIFMAETSLNGPKSKLFLIQGTGSLNEF 142
144 FPIGHLTKLKLAVANHLIQLSPKLPREYSNLTNLEHLDLSKQISICTDRLVLAHQPL 203
143 IPVHLEMLJESILYIGSNHISISIKFKDPP-ANLKLVLDFONNAHYIISREDMRSLEQ--A 199
204 LNLSDLSLNPNNFLOPAGFKEIRLHLKTLRNPFSLNMVMTKICQGLAGLEVHRLVLSGF 263
200 INLSLNPNGNVKGIELAFDSTVQSL---NFGSTRPLSTIPNGLQNSTTQSLMLGTG 255
264 RNEGKLEFKDSALEGLCNLTTEPRFLAYLDYLDIID-LFNCLTNVSSPGLVSVTTIER 322

256 EDIDD-EDISSAMKGLCEMSVBSLNIQ--EHRPSDISSTTPQCFOTLOEILDRLATHIKG 312
323 VKDFSYNGMOHLELVN-----CKF--GQFPTL-----KLKSLKRLTPTSN 361
313 LPS-----GKGLNLKLVLSVNHFPQLOISANPSSLHLVIRGVNKKLHLGVGCL 367
362 KGNAPSEVDLPSEIFDLRSNGLSPFKCCSQSPGTTSTLKYLDLSENGVITMSN-FLG 420
368 KLGN-----LQTLDSLNDIEASDCCSLQKLNLSHLQTLNLSHNEPIGLQSQAFKE 418
421 LEQLEHLDFQ--HSNLKQSEFS--VELSLRLIY--LDISHTHRRVANRNGIFNGLSS 472
419 CPQLELDLAFTRHLINAPQ--SPQNHFLQVNLVTCFLDTSNQH-----LLAGLPV 470
473 LEVLMAGNSPQENFL--PDIFTELRLTFDLDSQCOLEQSPFAFNSLSSLOVLMNSHN 530
471 LRHLNKGNNHQDGTITKTNLQTVGSLSEVLILSSCGLSLIDQAFHSLGKSHVDLSHN 530
531 NFF--SLDTPPY-----KCLNSLOVLDVSLNHNIMTSKQELQHPSSLAFLNITONDF 581
531 SLTCDSDISLSHLKGIYLNLAANSINITSPRLPIL-----SQQSTINLSHNP 579
582 ACTCEHQSFLOWIDQQLVVERMGCATPSDQGMPEVLSLNTTCMNKTLIGSVLSV 641
580 DCTSNHFLTWYKENLHKLGESEETTCANPSSLRGVLSVVKLSGCI--TAIGIFPLIV 637
642 LVSVVAVLVY 652
638 FLV-LIALLP 647

RESULT 10
US-09-950-041-4
Sequence 4, Application US/09950041
Publication No. US20030032090A1

GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.

APPLICANT: Rock, Fernando L.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kastelein, Robert A.

APPLICANT: Liu, Yong-Jun

TITLE OF INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS

FILE REFERENCE: DK0724XK1

CURRENT APPLICATION NUMBER: US/09/950,041

PRIOR FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/728,540

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 60/207,558

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/073,363

PRIOR FILING DATE: 1999-06-05

PRIOR APPLICATION NUMBER: 60/044,293

PRIOR FILING DATE: 1997-05-07

PRIOR APPLICATION NUMBER: 60/072,212

PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: 60/076,947

PRIOR FILING DATE: 1998-03-05

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 784

TYPE: PRT

ORGANISM: Homo sapiens

US-09-950-041-4

Query Match 13.9%; Score 603.5; DB 10; Length 784;

Best Local Similarity 27.0%; Pred. No. 3.1e-39; Indels 219; Gaps 38;

Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPSSTKNULDSFNDLRHLGYSVSPFDELQVLDSRCEIOTIEDGAYQSLSHSL 107
46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSGINTIEDSPSSISLSLH 105

RESULT 12
US-10-095-627-12
Sequence 12, Application US/10095627
Publication No. US20030027260A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
Gowerski, Paul J.
Gurney, Austin
Mark, Melanie
Yang, Ruy-Bing
TITLE OF INVENTION: Human Toll Homologues
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,627
FILING DATE: 11-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,413A
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: 60/083322
FILING DATE: 28-Apr-1998
APPLICATION NUMBER: 60/065311
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: 60/062250
FILING DATE: 17-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marchang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1154-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12
Query Match 13.8%; Score 602.5; DB 14; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

245 TC--IQGLAGLEVRHLV---GFRPNEGKLPKSALEGKCNLTIEFRILA--YLDYLL 297
Db 272 LINOISGLELEFPDCTINGVGNFRASDNDVDPGRKE---TLTIRLAIHPRFLFY-- 326
Qy 298 DDIIIDFNCLENNVSSFSVSVTIERVKDFSNFGQHELVNCKRGQPFLLKSLKRLT 357
Db 327 -DLSTLYSLTERVK---RLTVENSKVF-----LVPCLLSQ----- 357
Qy 358 FTSNKGNAFEEVDLPSEPLDLSRN-----GLSEKGCSSODFCTSLKYLDLSPNGVI 412
Db 358 -----HKSLFVLDLSENLWVEYLKNSAC---EDAWPDLQTLILNQ--- 397
Qy 413 TWSSNFGLEQLLEHLDFQHSNLKQMSSEFVLSRLNLIYLDI SHTRVVAENGINGLSS 472
Db 398 -----HL-----ASLEKGE--TLTLTKNLTNIDISK----- 422
Qy 473 LEVLKMGNSFOENLPDIFTELNLFTLDSQQLBOLS---PFAFNSLSLOYLNMSSH 529
Db 423 -----NSFHS--MPETQMPKMKYLNLSSTRHSVTGCIIP-----KLEILDVSN 466
Qy 530 N--NFFSLD-----TFP--YKCLNSLOYLDVSLNHIIMTSKKQELQHPPSL 571
Db 467 NNALFSLNLPLQKELYISRNKMLTLPDASLLPMLVLKISRNATITTSKQDLSF--HTL 525
Qy 572 AFLNLTQNDPACTCEHOSFLOMIDQRLAVEV-----ERNECATPSDKQMPVLSLNT 626
Db 526 KLEAGNNFICSCFELSFTQ---EQQALAKVLIDWPANYLCSPSHYRGQOVDRVLS 581
Qy 627 ---CQMKTIIGVSLVSVVSVVAVLVYKRY--PHMLLAGCIYKGR-----GENI-Y 674
Db 582 VSECHRTALVSGMCCALFLLLTGLCHRGHLMYMMAMWADAKKPRKAPSRNICY 641
Qy 675 DAFVYVSQDDWVWNEVLVKNLEBGPPOCLYHRDPIPGVALIANTIHBEFHSRKVY 734
Db 642 DAFVYSERDAYWVENLMVQLENNPPFKCLHGRDIPGMIIDNII--DSIEKSHKV 700
Qy 735 VVVSQHFTQSRWCIFEXEIAQTWOLFSSRAGIIFIVLQKVEKTLIRQO--VELYRLSRNT 793
Db 701 FVLSNFVSEMKVEYLDPSHFRLEDDNDAIILLEPIEKKAIPQFCFKLRKIMNTYT 760
Qy 794 YLEWEDSVLGRHIFPRKRLAL 815
Db 761 YLEWPMDEAQREGEFVNLRAAI 782
RESULT 13
US-10-732-563-4
Sequence 4, Application US/10732563
Publication No. US20040132079A1
GENERAL INFORMATION:
APPLICANT: Gupta, Shalley K.
APPLICANT: Ghosh, Tarun K.
APPLICANT: Fink, Jason R.
TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
FILE REFERENCE: 58183WO003
CURRENT APPLICATION NUMBER: US/10/732,563
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-10-732-563-4
Query Match 13.8%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPSTKRLDLSFNLRLHSGSFFSPFELQVLDLSRCRQITIEGAYQSLSLSTL 107
Db 46 IPSGLTBAVKSLDLSNNRITTYISNSDLQRCVNLQALVLTSGINGINTEBDSFSSLSLEHL 105

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QY      108 ILTGNPIQSIALGAFSGLSLQKL-----VAETNLASLENFPIGHLKT--- 151
      106 DLSYNYLSNLSSSWFKPLSLTFLNLGNPKYKLGESLFSHLTKQLIRVGNMDTFYKI 165
QY      152 -----LKENLVANHLIQSFKLPEYFNSNLTNLHLDLSNKK-----IOSI 190
      166 QKQPAQGLTLEELFEIDASDQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDYTVSSV 224
QY      191 YCTDLRVLHQWPLNLTLSDLSINPMNF--IOPGAFKEIRLHKLTLRN--NFDSL-NVMK 244
      225 ECLLEIR-----DTLDLDFHFSELSTGETNSL- IKKFTFRVVKITDBSLFQVYK 271
QY      245 TC--IQGIAGLEVHRLV---GEFRNENLEKFKDSALEGICNLTIIEFRLLA--YLDYYL 297
      272 LNLQISGLELEFPDCTLNGVGNFRASDNDIVIDPKAYE--TLTIRRLHIPRYLFY-- 326
QY      298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSNFQWQHLELVNCKRGQFPYLKLSKLRLT 357
      327 -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLLSQ----- 357
QY      358 FTSNKGNAFSEVDLPSELFLDLSRN-----GLSFKGCSSQSDPGTSLKLYLDLSFNGVI 412
      358 -----HLKSLLEYLDISENLWVEEYLKNSAC---EDAWPSLQTLILRQN--- 397
QY      413 TMSNFIAGLEBQLEHLDFOHSLNKKOMSEFVFLSIRNLIYLDISHTTRVAFNGIFNGLSS 472
      398 -----HL-----ASLEKIGE--TLTLTKNLTNIDISK----- 422
QY      473 LEVLKMGNSFOENFLPDIETELRNLTFLDLSQOQLEQLS---PTAFNSLSLQVLYNMSH 529
      423 -----NSFHS--MBETCOMPEKMKYLNLSSTRHSVTGCP-----KTLEILDVSN 466
QY      530 N--NFFSLD-----TFP--YKCLNSIQVLDVSLNHNIMTSKQOELQHPFSSL 571
      467 NNLNLPFLNLPLQKELYISRNKMLTLPDASLPLMLLVLKISRNAITTFSEKQDLSF--HTL 525
QY      572 AFLMLTQNDPACTCEHOSFLOWIKDQRLVYV-----ERMECATPSDKQMPVLSLNTIT 626
      526 KTLFAGGNFICSCFELSFQ-----EQALAKVLIDWPANYLCSPSHVGRQOVYRLS 581
QY      627 ---CQMKTIIGVSVLVSVAVLYVKEY--FHLMLAGCIKYGR-----GENI-Y 674
      582 VSECHRTALVSGMCCALFLILLTGLVCHRPHGLMTMMWAMWIAQAKKPKKADSRNICY 641
QY      675 DAFVIYSSODEDWARNELVKNLEEGVPEPQLCHYRDFIPGVAIAANIHHGFHKSRRVI 734
      642 DAFVYSERDAYWVENIMVOELENPNPFKLCCHKRDFIPGKMIIDNII--DSIEKSHKTV 700
QY      735 VVVSQHFIQSRWCIFEYELIAQWQFLSRAGIIFIVLOKVEKTLIRQO--VELYRLLSRNT 793
      701 FVLSENFWKSEWCKEYELDFSHFRLEFDENNDAAIILILEPIEKKAIPQRFCKLRKIMNTKT 760
QY      794 YLEWEDSVLGRHIFMRRLKAL 815
      761 YLEWPMDEAQRBGFWVNLRAAI 782
      Db
RESULT 14
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OR INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCES: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732, 796A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
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      ; LENGTH: 784
      ; TYPE: PRS
      ; ORGANISM: Homo sapiens
      US-10-732-796A-4
Query Match 13.8%; Score 602.5; DB: 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 3,76-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;
      108 ILTGNPIQSIALGAFSGLSLQKL-----VAETNLASLENFPIGHLKT--- 151
      106 DLSYNYLSNLSSSWFKPLSLTFLNLGNPKYKLGESLFSHLTKQLIRVGNMDTFYKI 165
QY      152 -----LKENLVANHLIQSFKLPEYFNSNLTNLHLDLSNKK-----IOSI 190
      166 QKQPAQGLTLEELFEIDASDQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDYTVSSV 224
QY      191 YCTDLRVLHQWPLNLTLSDLSINPMNF--IOPGAFKEIRLHKLTLRN--NFDSL-NVMK 244
      225 ECLLEIR-----DTLDLDFHFSELSTGETNSL- IKKFTFRVVKITDBSLFQVYK 271
QY      245 TC--IQGIAGLEVHRLV---GEFRNENLEKFKDSALEGICNLTIIEFRLLA--YLDYYL 297
      272 LNLQISGLELEFPDCTLNGVGNFRASDNDIVIDPKAYE--TLTIRRLHIPRYLFY-- 326
QY      298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSNFQWQHLELVNCKRGQFPYLKLSKLRLT 357
      327 -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLLSQ----- 357
QY      358 FTSNKGNAFSEVDLPSELFLDLSRN-----GLSFKGCSSQSDPGTSLKLYLDLSFNGVI 412
      358 -----HLKSLLEYLDISENLWVEEYLKNSAC---EDAWPSLQTLILRQN--- 397
QY      413 TMSNFIAGLEBQLEHLDFOHSLNKKOMSEFVFLSIRNLIYLDISHTTRVAFNGIFNGLSS 472
      398 -----HL-----ASLEKIGE--TLTLTKNLTNIDISK----- 422
QY      473 LEVLKMGNSFOENFLPDIETELRNLTFLDLSQOQLEQLS---PTAFNSLSLQVLYNMSH 529
      423 -----NSFHS--MBETCOMPEKMKYLNLSSTRHSVTGCP-----KTLEILDVSN 466
QY      530 N--NFFSLD-----TFP--YKCLNSIQVLDVSLNHNIMTSKQOELQHPFSSL 571
      467 NNLNLPFLNLPLQKELYISRNKMLTLPDASLPLMLLVLKISRNAITTFSEKQDLSF--HTL 525
QY      572 AFLMLTQNDPACTCEHOSFLOWIKDQRLVYV-----ERMECATPSDKQMPVLSLNTIT 626
      526 KTLFAGGNFICSCFELSFQ-----EQALAKVLIDWPANYLCSPSHVGRQOVYRLS 581
QY      627 ---CQMKTIIGVSVLVSVAVLYVKEY--FHLMLAGCIKYGR-----GENI-Y 674
      582 VSECHRTALVSGMCCALFLILLTGLVCHRPHGLMTMMWAMWIAQAKKPKKADSRNICY 641
QY      675 DAFVIYSSODEDWARNELVKNLEEGVPEPQLCHYRDFIPGVAIAANIHHGFHKSRRVI 734
      642 DAFVYSERDAYWVENIMVOELENPNPFKLCCHKRDFIPGKMIIDNII--DSIEKSHKTV 700
QY      735 VVVSQHFIQSRWCIFEYELIAQWQFLSRAGIIFIVLOKVEKTLIRQO--VELYRLLSRNT 793
      701 FVLSENFWKSEWCKEYELDFSHFRLEFDENNDAAIILILEPIEKKAIPQRFCKLRKIMNTKT 760
QY      794 YLEWEDSVLGRHIFMRRLKAL 815
      761 YLEWPMDEAQRBGFWVNLRAAI 782
      Db
RESULT 15
US-10-741-600-1390
; Sequence 1390, Application US/10741600
```

```
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1390
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-600-1390

Query Match      13.8%; Score 602.5; DB 17; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

QY      48  IPDNLPSTKNLDLSENPRLHLSYSPFSPPELQVLDLRCEIQTIEDGAYOSLSHLSTL 107
DB      46  IPSGLTEAVKSLDLNNRTIYSNSDLQRCVNLQALVLTNSGINITIEBDSFSSLSLEHL 105
QY      108  ILTGNPISLALGAFSGSLLOKL-----VAVEINLASLENFPGLHKT--- 151
DB      106  DLSYNYLTLSSSSWFKPLSLTFPLNLGNPYKTLGTSLSFSLTKLQILRVGNMDFTYKI 165
QY      152  -----LKELVANVLLOSFKLPEYFSNLTNLEHDLSSNK-----IQSI 190
DB      166  QKQDPAGLTFLEBELIDASDLQSYE-PSKLSIQNVSHLILHMKOHLILLEIFVDVTSSV 224
QY      191  YCTDLRVLHQMPLNLSIDLINPMNF--IQGAFKEIRLHKLTLRN--NFDST-NVMK 244
DB      225  ECLER-----DTDLDTFHFSLSSTGETNSL-IKFTFRNVKITDESILFQYMK 271
QY      245  TC--IQGLAGLEVHRLV--GEPRNENLEKFKDSALEGLCNLTIEFRILA--YLDYYL 297
DB      272  LNLQISGLLELEFDDCTLNGVNFPRASDNDRVIDPKVE--TLTIRRLHIPRYLFY-- 326
QY      298  DDIDLFNCLTNVSSFSLSVTVIERVKDPSYVFGWQHLELVNCKFGQFPPLTKLSIKRLT 357
DB      327  -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLLSQ----- 357
QY      358  FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKGCCSOSDFGTTSLKYLDLSPNGVI 412
DB      358  -----HKSLEYLDLSNLMWBEYLKNSAC---EDAMPISQTLILRN--- 397
QY      413  TMSNFFLGLEQLEHLDFOHSNLKQMSPEVSFLSNLIYLDISHTHTRVAENGINGLSS 472
DB      398  -----HL-----ASLEKTGE--TLTLTKNLTNIDISK----- 422
QY      473  LEVLKMGNSFOENLPDIFTELRLTLFLDSQCQLEOLS---PFAFNSLSLOLVNLSH 529
DB      423  -----NSFRHS--MPETCOMPERMKYLNLSSTRIHSVTGCP-----KTLKILDVSN 466
QY      530  N--NFFSLD-----TFP--YKCLNSLOVLDYSLNHIIMTSKQELQHPSSLT 571
DB      467  NNLMNLFSLNLPQLKLYLSRNKMLTLPDASLLPMLLVKLSRNALITTSKQELDSF-HTL 525
QY      572  AFLNLTONDPACTCEHQSFLQWIKQORQLVEV---ERMECATPSDKQGNPVLNLNIT 626
DB      526  KTLKNGGNPFICSCHEFLSFTQ---EQQALAKVLIDWPANYLCDPSHYRGGQOVQDVRLS 581
QY      627  ---COMNTIIGVSLVSLVSVAVLVYKPY--PHMLLAGCICYR-----GENI-Y 674
DB      582  VSECHRTALVSGMCCALFLILTLTGVLCHRFHGLMYMGMAMALQAKRKRKAPSRNICY 641
QY      675  DAFVLYSSQDSDWVNNELVKNLEBGPFPOLCLAYRDEPIPGVAIANIIEHGFHRSRKYI 734
DB      642  DAFVYSERDAYVWENLWQELENFNPFPKCLCHKRDPFGKWIIDNII--DSIEKSHKTV 700
QY      735  VVSGHFIQSRWCIFEYELAQTWQFLSRAGIIFIVLOKEKTLIRQO--VBLVRLLSRNT 793
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```
DB      701  FVLSNFVYSWECKYELDFSHFRLLFDENNDAIILILEPIEKKAIPORFCKLRKIMNTYK 760
QY      794  YLEWEDSVLGRHIFPRRLRKAL 815
DB      761  YLEWPMDEAOREGFWNLRAAI 782
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Search completed: March 12, 2005, 20:27:48
Job time : 76.2496 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-2

Perfect score: 4355
Sequence: 1 MMSASRIAGTLIPAMAFISC.....SMNPGVTGTCGNQGEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	15.2	661	2	RP105 - mouse
2	474	10.9	786	2	Toll protein-like
3	454	10.4	1097	2	Toll protein precu
4	433	9.9	1389	2	gene wheeler prote
5	421	9.7	1385	2	tlr protein - fru
6	396	9.1	1066	2	hypothetical prote
7	333.5	7.7	1134	1	chaptin precursor
8	316	7.3	605	2	insulin-like growt
9	305	7.0	853	2	insulin-like growt
10	303	7.0	605	2	disease resistance
11	299.5	6.9	662	2	insulin-like growt
12	299.5	6.9	1531	2	garp precursor - h
13	296.5	6.8	994	2	slit-1 protein hom
14	296	6.8	603	2	probable disease r
15	295	6.8	907	2	insulin-like growt
16	292.5	6.7	845	2	G protein-coupled
17	292.5	6.7	603	2	Hcr-0 protein - l
18	292.5	6.7	907	2	hypothetical prote
19	290	6.7	603	2	orphan G protein-c
20	290	6.7	855	2	insulin-like growt
21	289.5	6.6	1112	2	cf-4a protein - to
22	289	6.6	855	2	disease resistance
23	284.5	6.5	1134	2	disease resistance
24	281.5	6.5	622	2	hypothetical prote
25	280	6.4	890	2	synleutin - human
26	279	6.4	1027	2	disease resistance
27	278.5	6.4	1019	2	receptor protein k
28	278	6.4	1091	2	probable disease r
29	276.5	6.3	768	2	glial cell membran
					disease resistance

30	276	6.3	983	2	G84524	probable disease r
31	275	6.3	1523	2	T13953	MEG5 protein - ra
32	272	6.2	1469	2	B36665	slit protein - 2 pre
33	272	6.2	1480	2	A36665	slit protein 1 pre
34	270	6.2	1143	2	T10636	hypothetical prote
35	268	6.2	910	2	G84648	probable disease r
36	267	6.1	766	2	T01817	hypothetical prote
37	267	6.1	1784	2	C96615	hypothetical prote
38	266	6.1	863	2	A55173	cf-9 protein precu
39	263.5	6.1	967	2	T48210	hypothetical prote
40	262.5	6.0	1109	2	T18536	receptor-like prot
41	261.5	6.0	1051	2	T13174	gpi50 protein - fr
42	260	6.0	1064	2	B86465	probable protein k
43	259	5.9	1029	2	T00712	protein kinase hom
44	257.5	5.9	738	2	T19938	hypothetical prote
45	256	5.9	771	2	T02565	disease resistance

ALIGNMENTS

RESULT 1

RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56258
R.Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: I56258; MUID:95204928; PMID:7897216
A/Accession: I56258
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:062192; GB:D37797; NID:g761711; PIDD:BA07043.1; PID:g761712

Query Match

Best Local Similarity 28.7%; Score 663; DB 2; Length 661;

Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY	14	MAAFISC-VRESPWPCVAVVNTTYOCMEINLFYKIPDNLPTSTKMLDSEFPLHLSGY	72
DB	12	ALFLASCRAATSSDDCKIEKVNKTCENGLINIPGLTLPNSTCLEFSFVNLPTIQNT	71
QY	73	SFFSPRELQVLDLRSCIEIQTIEDGAYOSLSHSTLILGNPIQSLALGAFSGLSHOKLV	132
DB	72	TFSRLINLTFEDLTCQIYWIHEDTFQSOHRIDTVLTPNPLIFMAETRLSGPKALKLF	131
QY	133	AVETMLASLENPFGHILTKLKELVANHLIOSFKLPEYFSNLNLNEDLSSNKIQSIYC	192
DB	132	FQGTGISIDFIPLNQNTLSLYGSNHSIKLPKGPPT-EKLVKIDFQNALHYLSK	190
QY	193	TDRLVHQMPLINLSLSPNMFIOGAFKEIRLHKLTLLNNPDSLVNMTKTCIOGLAG	252
DB	191	EDMSSLQO--ATNLISLNLNGNDIAGIERGAFSAVFOSP---NNGGTQNLVLVIFGLGN	244
QY	253	LEVHLVIGEFENENLEFKSALGECNLTIEERPLAYLDYDDIIDLFNCLTNVSS	312
DB	245	STTQSLMIGTFEDMD-D-BDISPAVEGSCMSVESINL-QKHYFNNISNTHTCS----	298
QY	313	FSLVSVTTERVADPSYFNFGMQLHELVNCKFGQPTT-LTKLSIKRLTFTSNKGN--AFS	368
DB	299	-----GLQGLDLTATHTSLPSGLVGLSTLTKLVASANKFENLCQS	340
QY	369	EVDLPSLEF-----LDLSRNGLSFKCCSQSPGTTSLKY	403
DB	341	ASNPFSLTILSIGKNTKRLTGLTGLLENLRELDLSHDDTETSDDCCNLQRNLSHLSK	400
QY	404	LDLSFGVITWSSN-FLGLELHLDLPOHNLKQMSBSVFLSLNRLYLIDISHTTRVA	462
DB	401	LDLSYNEPLSTKTEAPKPCQDLDDLAFTRLKVKDAQSPFONHLKLVNLSHSLDIS	460

Db 573 IQLVGVHVKPOYSRQFKLRTDLVCSQNPVLEGTPEVROI EPQTLLCPDLFSDDERKCP 632
 QY 388 KGC-CSQSDFGTSLKYLDLSPNGVITWSSNPLGLEQELHDFQHSNKKOMSEFSVFTSL 446
 Db 633 RGCNCHVATYD---KALVINCH-----SGNLTHTVPRLPNL---HKNNQME-----LHL 675
 QY 447 RNLVLDISHHTTRVAFNGIFNGSLSLVLYKMGANSFOENFLPDI FTBLRLITFLDLSQC 506
 Db 676 ENNTLRLPSANT-----PGYESVTSIHLAAG-----NLTSIDVQDL 712
 QY 507 QLEQLSPFAFNSLSLQVLNMSHNNPFSLDTPPYKCLNSLOVLDYSLNHTMSKQELQH 566
 Db 713 -----PT-----NLTH-----LDISMNHL-----QMLN- 730
 QY 567 FPSLAFLN-----LTQNDFACTCEHSGFLOMICKDQROLVVERMECATPSDKQ 617
 Db 731 -ATVGFNLRMTKMSVLSLGNPMWCCTAKFLFLFTQDNFERIGDRHEMCKVNAEMR 789
 QY 618 MPVLSLNTTQMNKTI-IGVSV---LSVLVSVVAVALYKF-----YFHLMLLAGCI 665
 Db 790 MVELSTNDICPAKGVFTALAVIALTGLAGFTAAIYKFTQETIKIMLYAHNLL----- 845
 QY 666 KYGGENI-----YAFPIYSSQDEDDWRANLEYKLESGVPPFQCLAHYRPIPVATA 720
 Db 846 WFTVEEDIDKDKKFDAPFISYSHKQDSFTEDYLVPLQLEHGPOKFOLCVHERMVLVGHIP 905
 QY 721 NIHEGFKSRKVIYVSOHFIOSRMCIFEYELACTWQOFLSRAGIIFIV---LQKVEKT 777
 Db 906 NIM-RSVADSRKTTIVLSONFIKSEMARLEFPAARSALNBSKRSIIYIISDIDGVEK- 963
 QY 778 LRLQOVELYRLSRNTYLEMEDSVLGRHI FWRRLKALLDGKSNPEGTGTG 830
 Db 964 -LDELKAY-LKMTYLYKMGDP-----WFMDKLAFALPHRR---PVGNGIG 1005

RESULT 4

T13852
 gene wheelier protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13852
 R.Eidson, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
 Development 120, 885-899, 1994
 A.Title: The Drosophila 18 wheelier is required for morphogenesis and has striking simila
 A.Reference number: Z17796; MUID:95524375; PMID:7600965
 A.Accession: T13852
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1389 <EID>
 C.Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:9415682; PID:g1019104; PIDN:AAA7920
 C.Genetics:
 A.Gene: wheelier
 A.Cross-references: FlyBase:FBgn0004364

Query Match 9.9%; Score 433; DB 2; Length 1389;

Best Local Similarity 24.4%; Pred. No. 7.2e-19;

Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

QY 59 LDLSNPPLRHGYSFSPPELOVDLSRCIEQITEDGAYQSLSHLSTLITLGNPIQSLA 118
 Db 338 LNLNNALTRIGSKTFKELYFLQIIDMRNNSIGHIEGAFPLVNLHTLNLTAENRLHTLD 397
 QY 119 LGAFSGLSLOKLVAVENTLALST-ENFPIGHLKTKELVANLNLQSFPLPEYFNLNTL 177
 Db 398 NRIFNGLYVLYTL-TLNNLVSVESQAFRNCSDKELDLSN--QLEVEPAVODLSKL 454
 QY 178 EHLDSNKKQISYCTDLRLVHLQMPDLNT-----SLDISNPMNF 217
 Db 455 KTLDDGENQIDSEFKNTTPNNLQGLRLIDNRIGNITVGMFODLPRLSVNLAKNRIGS 514
 QY 218 IOPGAF-KEIRLHLKTLRNNPDSLVNMTCCIOGLAGLEVHRLVGEFRNE----- 266
 Db 515 IERGAFTKTEIARLDKNF-----LTDINGIPATLALMLNLSEHNLVWPFYAFIP 568

QY 267 GNLEKFD--KSAELGCLNL--TIEFRLAYLDYLDIIDLFNCLTNVSSFSVSVTIER 322
 Db 569 SNLKMLDHNGYIALGNYVYKLOEIRVTLTDASHNRITETI-GAMSVNSIELLEFINNI 627
 QY 323 VKDPSYN--FGMHLVYNCKFGQFPPLKLSKRLFTSK-----GNAPS----- 368
 Db 628 IGQIQANTFVDKTRILARVDYANVLSKISNALRVAVPASAKPVPEFYLGDPEDCSM 687
 QY 369 -----EVDLPSEFL-----DLRNGLSERK-----GC 390
 Db 688 EWLQRLNLTTRQHPHYVDLNLIECLMPHSAPLRPLASASADPVCKTSHCPTGHC 747
 QY 391 CSQSDFGTSLKYLDLSPNGVITWSSNPL--GLBQLEHDFQHSNKKOMSEFSVFTSLRN 448
 Db 748 CEYEGCECEVLCFNGSCCFHDATWATNIVDCGRDLAAL-----PNRIPOVSDYLDGN 803
 QY 449 LIYDISHHTTRVAFNGIFNGSLSLVLYKMGANSFOENFLPDI FTBLRLITFLDLSQC 508
 Db 804 MPELEVGHLTGRMLRALYLNASNLMTLQNS-----LAQVLNLEVLHLENNKL 852
 QY 509 EQLSPTAFNSLSLOVLNMSHNNPFSLDTPPYKCLNSLOVLDYSLNHTMSKQELQHP 568
 Db 853 TALSGTEFRSLGLIRELYLHNNMLTHISNATFEPLVSLVRLDNNRSLSPHLOYR-- 910
 QY 569 SSLAFLNLTQNDFACTCEH--OSFLOMICKDQROLVVERMECATPSDKQMPVL----- 621
 Db 911 -SLQGLTGRNAMSQCQQLBELAQFVSDNMMVVRADHDIYCLDAGIRBELIGNLANG 969
 QY 622 -----SLNTTQMNKTI-IG-----VSVLSVLVSVVAVALYKFYFHLMLLAGC 664
 Db 970 PDCSDLLDASASNTSSQDLGAIGCPMPAVLVILFVLVLIIVFVRESVRMLFA-- 1027
 QY 665 IKYG-----RGEN---YDAFVYSSODEDDWRANLEYKLESGVPPFQCLAHYRPIPV 715
 Db 1028 -HYGRVCEPRFEDGKLYDAIILHSEKDYFVCNIAELHGRPPRLCIGQRD-LPP 1085
 QY 716 VAIANILHEGFKSRKVIYVSOHFIOSRMCIFEYELACTWQOFLSRAGIIFIVLQK-- 773
 Db 1086 QASHQLV-EGARBSRKIIIVLTRLNLATENNRLEFRNA-----FHSRLGL---AQTLV 1136
 QY 774 -VEKTLRQOVELYRLSRNTYLEMEDSVLGRHI-----FWRRLKRL 815
 Db 1137 IIEETSVAEAEVDAELS--PYLK---SVPSNRLLTCDRYEMEXKLRYAI 1180

RESULT 5

T13887
 tlr protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13887
 R.Chang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A.Title: Expression of a novel Toll-like gene spans the parasite boundary and contrib
 A.Reference number: Z17805; MUID:95151581; PMID:7848870
 A.Accession: T13887
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1385 <CHI>
 C.Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:9913247; PID:g913248; PIDN:AAB33383
 C.Genetics:
 A.Note: tlr
 A.Cross-references: FlyBase:FBgn0004364

Query Match 9.7%; Score 421; DB 2; Length 1385;

Best Local Similarity 24.0%; Pred. No. 4e-18;

Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

QY 59 LDLSNPPLRHGYSFSPPELOVDLSRCIEQITEDGAYQSLSHLSTLITLGNPIQSLA 118
 Db 338 LNLNNALTRIGSKTFKELYFLQIIDMRNNSIGHIEGAFPLVNLHTLNLTAENRLHTLD 397


```

Oy 119 LGAFSGLSLQKLVAVENINLASL-ENFPIGHLKTLKEINVAHNLQSFELPEYSENLTNL 177
Db 398 NRIFFGLVYLTL-FLNNLVSVIVESQAFRNCSIDKEIDLSNN--QLTEVEPAADLSML 454
Oy 178 EHLDSNNKIOSICTDRLVHQMPLNL-----SLDISLNPNMF 217
Db 455 KTLDSGEMQISEFKNTRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVNLAKNRQIS 514
Oy 218 IQPGAF-KEIRLHLKTLRNNPDSLNVMTKCIQGLAGLEVHVLGEFRNE-----266
Db 515 IERGFNDKNTLEIARLDKFF-----LTDINGIPATLASILMLNLSNHLVMPDYATIP 568
Oy 267 GNLEKFD--KSALEGLCNL--TIEEPRLAYLDYLDIIDLFNCLTNVSSGLSVTTER 322
Db 569 SNLKMULDHGVYIEALGVYKLOEBIRVTLTDASHNRITEI-GAMSVNSIELFLINNNI 627
Oy 323 VKDFSYN--FGMQLHELVNCKRGQFPPLKLSIKLTFSTNK-----GGNAPS-----368
Db 628 IGOIQANTFVDKTRLARVDLVANVLSKISLNLARVAPVSAEKVPEFYLGNGPFECDSM 687
Oy 369 -----EVDLPSEPL-----DLNRNGLSEK-----GC 390
Db 688 EMLGRINNLTRQHPHVVDLGNIECLMPHSRSLPLASLSASDFVCKYSHCPGTCGC 747
Oy 391 CSQDGFCTSLKYLDLSFNGVITMSSNFL--GLEOLEHLDFOHSLKOMSEFVFLSRN 448
Db 748 CEYECSECEVIPCNGSCFHDATWATNIVDCGRQDLAL--PRIRPDVSDYLDLGN 803
Oy 449 LIYDISHHTTRVAFNGIFNGLSLEVLKMGNSQENFLPDIFTELNLFLDLSQQL 508
Db 804 MPELEVGHLTGRRLRALYLNASNLMTLQNS-----LAQLVNLVHLHNNKL 852
Oy 509 EQLSPTAENSLSLQVLNMSHNPFLDTPPYKCLNSLQVLDYSLNHMTSKKOLEQHP 568
Db 853 TALCECTERSGLRELVELHNNMLTHISNATPEPLVSLVLRDNRRSLPLHQYRR-- 910
Oy 569 SSLAFNLNTQDFACTCH--QSFLQWITQDQROLVEVERMECATPSDQGMPTL-----621
Db 911 -SLOGLTIGRNAWSCRCCQOLRELAQFVSDNMAVVDADHIYCLDAGIRBELIGNLANG 969
Oy 622 -----SLNTTCQNN-----KITIGSVLSVAVSVAVLYKFFPHMLLAGC 664
Db 970 PDCGDLDAASNSISSODLAGCYRLPLAAVLVILFDVLLITFVRESVRMLLF-- 1027
Oy 665 IKYG-----RGEN---IYDAFVIYSQDEBDVNRNELKNEBGPVPLCLHYEDFPI 715
Db 1028 -HYGRVCEPRFEDAGKLYDAIILHSEKDYEFVCNIAAELEHGRPPRLCIGQRD-LRP 1085
Oy 716 VAIANITHEGPHKSRKIVVVSQHFIQSRWCIFEYELAQTWQPLSPAGIIFVYLQK- 773
Db 1086 QASHLOLV-EGARASRKIILVLRLLATEWNRLEFRNA---FHESIRGL---AQLV 1136
Oy 774 -VEKTLIRQOVELRLSRNTYLEMEDSVLGRHI-----FMRRLKAL 815
Db 1137 IIEETSVSAEADVAELS--PYLK---SVPSNRLLTCRYMEKLRVAT 1180

```

RESULT 6

11564
 hypochemical protein C56R6.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15864
 R:Pulten, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans coemid C56R6.
 A:Reference number: S69019
 A:Accession: T15864
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1066 <FULL>
 A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
 C:Genetics:

A:Gene: C56R6.6
 A:introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9
 Query Match 9.1%; Score 396; DB 2; Length 1066;
 Best Local Similarity 26.9%; Pred. No. 1e-16;
 Matches 156; Conservative 100; Mismatches 227; Indels 98; Gaps 24;

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Oy 35 NITYQMEINPFYKIPDNLFFSTKNLDSFNLRLHSGSFSPFPELOVLDLRCEIOTE 94
Db 131 NITH-LMDTNVTETSEMKVILNR-----NKVRLDHGSFSPFKIRELDISTNOIQVE 184
Oy 95 DGAYQSLSHSTLILITGNPIQSLALGAPSGLSLQKLVAVETNLASLENPIGHLKTYE 154
Db 185 DSSEFVGHMQSILDSYRIAYLRG-----MKNF-----AKTLKT 221
Oy 155 LVNAHNLISQFKLPEYSENLTNLEHLDLSNKKIOSI-----YCTDLRVHQMPLNLSTL 208
Db 222 LKLAENNIHA--TPEALRDLRLNLNLNGKRLNRIGDYVKGCTDTLV-----EL 270
Oy 209 DLSLNPNFIQPGAFKEIRLHLKTLRNNPDSLNVMTKCIQGLAGLEVHVLGEFRNEGN 268
Db 271 FIANNYLEHPIHGVLSGKK-----QLEHLDISKKKIMSL-----KKPTS 309
Oy 269 LEKFDKALBGLCNLTIEEPRLAYLDYLDIIDLFNCLTNVSSGLSVTTERVYDPS 327
Db 310 LLSITKEETSTVRRLNLAGRNIMMSDYL--IFEHMBLTYVVDVSFVRIRPISPRVEKL 367
Oy 328 YNFGMQLHELVNCKRGQFPPLKLSIKLTFSTN--KGNAPSEVDLPSEFLDLSRN 383
Db 368 KNL--ESLFLQNNQLANPFLPRLDKRLHMLDNNQIOKIDN-PSLADLPQLQSLAGN 424
Oy 384 GLSPKCCSQSDFGTTSS--LKYLDLSFNGVITMS--NFLGLEOLEHLDFOHSLKOMSE 439
Db 425 QLDI---ITENMFSSSSSELKSLNLANKKHISNSSFSLDMLQQLRSHNNIRTTTS 481
Oy 440 FSVFLSRNLIIYDISHHTTRVAFNGIFNGLSLEVLKMGNSQENFLPDIFELRNL 499
Db 482 MT-PSNLRNRYLDLSHRRIKILPSALYQLPALDVHLDHNNINLE-IDRDAFSPSFDLQ 539
Oy 500 FLDSQQLBOLSTANNSLSLQVLNMSHNPFLDTPPYKCL-NSLQVLDVSLNHMT 558
Db 540 SLKLSHNAFRFRSCEPFGISQVHQDLSSQVNEIDIF---CARGIRKLISLANSVEK 596
Oy 559 SKQELQHPSPSLAFNLITQN-----DPACTCEHSPFLQ 592
Db 597 INRKLQD-ATELTSIDISHNGIIVDSDAFCBCKRKSHTK 636

```

RESULT 7

A29944
 chaoptin precursor - fruit fly (Drosophila melanogaster)
 N:Alternate names: photoreceptor cell-specific membrane protein
 C:Species: Drosophila melanogaster
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell]
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012;
 R:Zipursky, S.L.; Venkatesh, T.R.; Teplov, D.B.; Benzer, S.
 Cell 36, 15-26, 1984
 A:Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecule]
 A:Reference number: A21123; MUID:84106810; PMID:6420071
 A:Molecule type: protein
 A:Residues: 31-43, 'HX', 46-49, 'H' <ZIP>
 C:Genetics:
 A:Gene: FlyBase:chp
 A:Cross-references: FlyBase:FBgn0000313

A: Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
 C: Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
 C: Key words: cell adhesion; glycoprotein; membrane protein
 F: 1-29/Domain: signal sequence #status predicted <Sig>
 F: 30-1134/Product: chaoptin #status predicted <MAT>
 F: 80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F: 103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F: 128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F: 152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F: 177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F: 201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F: 226-248/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F: 250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F: 279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F: 303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F: 326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F: 351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F: 375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F: 401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F: 428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F: 453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F: 477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F: 502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F: 527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 F: 551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F: 577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F: 601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F: 625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
 F: 649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
 F: 673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
 F: 700-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
 F: 733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
 F: 757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
 F: 781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
 F: 805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F: 828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F: 854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F: 879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F: 903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F: 928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F: 949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F: 973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F: 996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F: 1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F: 1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.7%; Score 333.5; DB 1; Length 1134;
 Best Local Similarity 23.0%; Pred. No. 8.4e-13;
 Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

50 DNLPSTKSLDLPNPLRHLSYSPFSPPELQV-----L 83
 346 DSLVNSLQTLDSGNRLTGLHKLNNPVLAVISMKDKIKIQRTETFNVAHYTLKL 405
 84 DLS-----RCEIQTIEDGA---YOSLS-----HLSTLILTGPNIQ 115
 406 DLSGRNDPTNLQTLRNMTRKMNKSLSTISRLGSSVGPEDPKDGVLELDQITRASLS 465
 116 SLALGAFGLSLQGLVAVETVLASLEN---FPIGHKLTKLKEINVAHNLIOGFKLPEYRS 172
 466 GIOSHAFKRVKGLKRLDSENGISSTIENDAFHEIGH--SLISLKMHSVGSGALPAEPLR 523
 173 NLTNLEHLDLSNKKIOSICTDLRVLHOMPLNLISLISLNPNNFIOPGAFK---EIRHL 229
 524 HTLSIQELDFSNHHSMSMDTSFHLKLNRL-----LELHDKRIEQVLKCTFGGDHSKLE 579
 230 KLTLENN-----PSSLNVMKTCIQGLAGLEVHRLVLSGFNREGNLEKFDKSLALBS- 279
 580 EISLSEFNHLSISQHTFFDLALRK-----LHLDNKKIDIKIRRAFMNDELLEYLSIRGN 634
 280 -LCNLTIEBF-----FLAYDYLDLDI-----IDLNCLTNVSSFSLSVYTIIEVDPKFSYNF 330
 635 KINNLADESFQNLPKLEIILDMAFNQLPNFNFDYFDQVGTLSNIN--VNVSHNOIRQLMTNS 693

331 GWOHLELVNCKRGQPTLIKLSKRLTFTSNKGNVAFSEVDLPSEFLDLSNGLSF--K 388
 694 SW-----SGRNEHGMWYNSIKIKIDLSHNNSIILHP 724
 369 GCCSGSDSGTT-----SLKYLDSFNGVYTMSSN--FLGSEQLH 426
 725 GFYPAEALSTLHLGLGYNLSMNTTRDVGNNPHLOMLDSYWHLELDFDAKNTKQLOL 784
 427 LDFOHNSIKOMSEFVPSLRNLVLYLDSHTTTR--VAFNGIFNG-----469
 765 VFFGNVYLSLDPQ--DIFPVQGLRVVDSHNLKRLPNLPLFNGMEKLDVSHMMKTP 843
 470 ---LSLEVLKMAGNSFOENFLP-----DIFTELRLNLFLLDSQCQLBQLSPTAFNSLSS 521
 844 SSSLSLSLAALTCELHLNNFSTISHMDLSNKFPSRLAYLDSYVYLLRIDAVATMPK 903
 522 LOYLVMSHN-----NPF-----SLDTPPYKCLNSLOYLVDSLHIMTS 559
 904 LAVLDLSNRDLKVKDKSFMGLNSLILKLGLENVLSLTPVETRLTYLEFRGLGYNE-LPS 962
 560 KKOELQHPSSLAPLNTQNDPACTCEHQSFLOWIKDQRLVVEVERECATPSDKQ---616
 963 IPQELAHMNSNLRKMLDSNND-----LTNPVLTQALPHRLML 1002
 617 -GMPVLSNITTCOMNKTIIGSV--LSVLVSVVAVLVYKFFHMLLAGCI 665
 1003 SGNPITSLN-----NSPFDGVNDELMIDISNFRLHYREV-----GCL 1040

RESULT 8
 JCS239
 Insulin-like growth factor acid-labile chain - baboon
 C: Species: Papio sp. (baboon)
 C: Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C: Accession: JCS239
 R: Delnathy, P.; Baxter, R.C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A: Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
 A: Reference number: JCS239; MUID:97040714; PMID:886027
 A: Contents: liver
 A: Accession: JCS239
 A: Molecule type: mRNA
 A: Residues: 1-605 <DE>
 C: Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.3%; Score 316; DB 2; Length 605;
 Best Local Similarity 24.4%; Pred. No. 4.5e-12;
 Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

33 VNTIYQGMELNFIYKIPNNLPFSTGNLDSFNPLRHLSYSPFSPPELQVLDLSRCEIQ 92
 53 VNELSVFSSRRULTRLPDGIPEGTQALWDNSNLSIPPAFRNLISLAFNLQGGQLS 112
 93 IEDGAYOSLSHLSTLILTGPNIOSIATGAFS-----GLASL 128
 129 QKTVAVETNLASLENFPIGHKLTKLKEINVAHNLIOSFLKPEFSNLTULEHLDLSNKKIQ 188
 173 WDLNIGMSLAVLPDPAFRGGLGRLVLAIGRL--AYIQPALFSGLAELRELDLSRNALR 231
 189 STYCTDLVNLHOMPLNLISLISLNPNNFIOPGAFKTR-LHKLTLRNNFDSLNTMKTCT 247
 232 AI---KANVPQQLPRLQ--KYLYDRLLIAAVAPRGLGKALRMLDSLN--RAAGLEEDTF 286
 248 QGLAGLEVHRLVLSGFNREGNLEKFDKSLALBSLNLCTIEBRRLAYLDYLDIIDLFNCL 307
 287 PGLGLRLVRL-----SHNAIASLRPTFEDL-----HFILEL-----319
 308 TNVSSFSLSVYTIIEVDPKFSYNFQWOHLELVNCKRGQPTLIKLSKRLTFTS--NKGN 365
 320 -----QGHNRIRQLAERSFS--GIGQLEVLTLDHNOQVYKVGAFGLGTLNVAVNNLSGN 372

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OY 366 AFSEVDLSLEBIDLSR--NGLSFKGCC-----SOSDEPCTSLAKYIDLSPFYITMSSNPL 419
Db 373 CLR--NLBEQVFRGKGKJHSLBLEGSCIGRIAPHFPAJSGIRLEFLKDNQGVGIEEOSTL 430
OY 420 -GLEQLEHLDPQHSNIKOMSEFSVPLSLRNLIYLDISHTHTRVAQNGIENGSLSHVAKM 478
Db 431 WGIALLLEIDLTSSNQ-----THLP--HQGFQIGKLEYLL 465
OY 479 AGNSEQENFLP-DITETLRNLFTLDLSOCQLEQLSPYAFNSLSSIQVLMGHNHNFSLDT 537
Db 466 SHNRILAE--LEPDALGPLORAFWLDVSHNRILREALPGSLIASIGRIRYINLNN--SLRT 520
OY 538 PPYKICINSIQVLDVSYLNHIMTSKKOELQHPSSIAFLMLITONDFACTCEHOS----- 589
Db 521 FTPQ-----PPGLERLWLBGNPWCSCPLRALNDPQALON 554
OY 590 -----FLQWT---KQQRQLVVEVRMECAIPSDKQKQFVTSL 623
Db 555 PSAVPRFVOAICBGDDCQPPVYTYNNITICASBPPEVAGJLDL 597

```

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RESULT 9
T17461
disease resistance protein D - tomato
C|Species: Lycopersicon esculentum (tomato)
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C|Accession: T17461
R|Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A|Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resistance gene
A|Reference number: Z18801; MUID:99254130; PMID:10318973
A|Accession: T17461
A|Status: Preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-853 <PAR>
A|Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:G4335640; PID:G4235641; PIDN:AADI
C|Genetics:
C|Gene: NLOD

```

[illegible]

```

Db 454 ALLSHNNISGHISSAICULKTFILINLESMNIBGTIPQOLGEMSEILOY-----LD 504
QY 454 ISHTHRAVAFNGIPLNGLSLEVLKMAAGSFOENFLPDIPTELRNLFPLDLSQOQLEBLS 513
Db 505 USNNSLSGMTMTTFSIGNPLHIITKLDWNLQCKVPSLI-NCKKLELLDINNELNDTFP 563
QY 514 TAFNLSLSLOVLMGSHN-----NFSLDJFFPYKCLNSLOVL-- 548
Db 564 KMLGDLPLNLOVINPFSNKLYGPIRTNNLEFAKIRVUDLSNGRSGD-LPVSFFENFEAMKI 622
QY 550 -----DYSLNHMTSKK---OELQHPSSLAFNLNTONDFACTCEH-QS 589
Db 623 NGENNNGTRYVADLYSDYKAVLYITTKLDQELSRVLTQIILDSKXFE---GHIPN 679
QY 590 FLQWIKDQROLIVEVERNECATPSDKQGNVL-----SLNITCQNNKTIIGVSVLSVLV 643
Db 680 IIGDLIGLRTNLNSHNVLEGHIIPASPNQNSVLESIDLSSNKISGAIPOQLASLTPLFVLN 739
QY 644 VSVAVLVYKFFPHMLLAGCIKYGGENITYAFVYISSQDEBDMVNLVKNLEGVPPF 703
Db 740 LS-----HNHLV--GCIPKQKQ---FDSFENSYLGNDGLR-----GUPPS 775
QY 704 QLC 706
Db 776 RDC 778

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RESULT 10
 A41915
 Insulin-like growth factor-binding complex acid-labile chain precursor - human
 N:Alternate names: Acid-Labile Subunit (ALS)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A41915
 R:leong, S.R., Baxter, R.C., Camerato, T., Dai, J., Wood, W.I.
 M:Endocrinol. 6, 870-876, 1992
 A>Title: Structure and functional expression of the acid-labile subunit of the insulin-1
 A:Reference number: A41915; MUID:92357025; PMID:1379671
 A:Accession: A41915
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-605 <LEO>
 A:Cross-references: UNIPROT:P35858; GB:M86826; NID:G184807; PIDN:AAA56047.1; PID:G184808
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIP:110171)
 F:59-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F:530-553/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 Query Match 7.0%; Score 303; DB 2; Length 605;
 Best Local Similarity 24.4%; Pred. No. 2.9e-11;
 Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

RESULT 12
T42218
alt-1 protein homolog - rat
N:Alternate names: MEGP4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z4126; MUID:98560089; PMID:9693030
A:Accession: T42218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NA>
A:Cross-references: UNIPROT:088279; EMBL:AB011530; NID:g3449289; PDB:BAJ2460.1; PID:g3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGP4
C:Superfamily: fruit fly alt protein; EGF homology; leucine-rich alpha-2-glycoprotein
Query Match 6.9%; Score 299.5; DB 2; Length 1531;
Best Local Similarity 22.1%; Pred. No. 1,66-10;
Matches 167; Conservative 95; Mismatches 260; Indels 233; Gaps 27;
OY 4 ASRLAGTLIPAMAPLSCVRPESWPCVAVPNITVQCMEINFYKIPDNLPSTKNLDSF 63
DB 274 ACTLSSGSCPMNC-SC-----SNGIVDCRGKGLTALPALTPEMTIEIRLEL 318
OY 64 NPLRLSGSPSPPELOVLDSRCETOTIEDGAVQSLSHSTLTITGNPIQSLAGAPS 123
DB 319 NGIKSIIPGAAPSPYKRLRIDLSNNQIAEIPDAFOGLRSINSLVLYGNKITTIDPRGVFG 378
OY 124 GLSSLOXVAVETNLSLENPIGHLKTLKELNVANHLIQSPKJPEVSESNLTNHEHLLS 183
DB 379 GLYTIQLL-----LNA--NKINCIR-PDAQODIQNSLSLFLY 413
OY 184 SNKIQSI---YCTDLRVLHOMPLNLSDLSINPNFIQPGAFKEIRLKLTLRNPNDSL 240
DB 414 DNKIQSLAKGFTTSRAIQ-----TLHAGNP--FICDNLKMLA-----DFIART 456
OY 241 NVMTCTICGLAGLEVHRLV--LGEFRNEGNLEKDKSALBGLCNLTIEFRLAYLDYLL 297
DB 457 NPIET--TGACASPRRLANKRIGQIKS---KKRCSAKE-----QYFIPGEDHLL 503
OY 298 D-----DIIDFNCITNVSSFSVLVETIEBVKDFYNGWQHLVWCKF-----GQFP 346
DB 504 NSECTSDVACPRKCKCEASVVECSGLKSKIPR-RIPQSTTELRNNEISILEATGLPK 562
OY 347 TLKLSLRRLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCCQSDFGTTSLKYLDL 406
DB 563 --KLSHLKLKINLSNKK-----VSEIEDGTFE-----GATISSEHL 596
OY 407 SPNGYITMSSN-FLGLEQLHLDFOHSLKOMSEFSVLRLIYLDISHTTRVAVNG 465
DB 597 TANQESVRSQWFRGLDGLRTLMRNRRISCIHND-S-FTGLRNVLISLYNHIITTSIPG 655
OY 466 IFNGLSLEVLKMAINSFOENP----- 487
DB 656 AFDITQLSTLNLANPFCNCQLAMLDWLRKRTIYGNPRCQPDRLRQIPLODVAPR 715
OY 488 -----LPIDITTEL----- 495
DB 716 DFRCEGGEVGVCLPRQPOECACLDITVVRCSNGLQALPKGIPKXVTELYLDQNGFTL 775
OY 496 -----RNLTFLLDSQCQLEQLSPYAFNSLSIQVINMGHNHNFSLDTPPYKCLNSIQ 547
DB 776 VPGQLSTFKYQLQVLDLSNNKISSLSNSSFTTMSQLTTTILSYNAQCIPLAFQGLRSLR 835
OY 548 VLIDYSLNIMTSSKQELQHPSSSLAFNLTLQNDPACTEHOSSFLOWINDQQLVVEVRM 607
DB 836 LLISHGNDVSTLQSGIFADV--TSLSHLAIGANPLYCDCHLRWLSWVTKYK--EPGIA 891

OY 608 ECA-----TPSDK---QGMPLSLNITNC 627
DB 892 RCAGPPEMEGKLLTTPAKKPECCGPPSLAVQAKC 926
RESULT 13
H96510
probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96510
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huiztar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzilli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-994 <STO>
A:Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PDB:AAJ34245.1; GSPDB:GT
C:Genetics:
A:Gene: F2G19.6
A:Map position: 1
Query Match 6.8%; Score 296.5; DB 2; Length 994;
Best Local Similarity 23.0%; Pred. No. 1,46-10;
Matches 161; Conservative 102; Mismatches 271; Indels 167; Gaps 31;
OY 2 MSASRLAGTLIPAMAPLSCVRPESWPC-----VEVVPNTVQCMEINFYKIPDNL 52
DB 213 MSSVDISAPPIPEFSYMSRSRLTKGCNLLGRPPNSVLIDIPNESISLDHNL-----NL 267
OY 53 PFSTKNLDSFNPRLHGSY-----SPSPPELOVLDSRCETOTIEDGAVQSL 102
DB 268 EGSIPNP-LRNNSLKLKSIYNTSFGTIPNSISLKLHLSKLOQSAFSGRIPESSLS 326
OY 103 HLSTLITGNPIQSLAGAPSGLSLQKLVAVETNLSLENFP--IGHLTKLKELVANHN 160
DB 327 HLSLVLVSENNPVEIPESSVSNLQQLLPVSDNNLNG--NPSLSLNLNQLRVIDICSN 384
OY 161 LIQSFKLPEFSNLTNHEHLDLSNKKIQSYCTDRLVHQMP--LNLSS---LDSLNP 214
DB 385 HFTGF-LPPTISQLSNLEFSSACDNPFG-----SIPSLFNISLITLGLSYNQ 433
OY 215 MNFQPAFKEIRLKLTLRNPNDSLNVMTCTICGLAGLEVHRLVLDGEFRNEGLBEKFDK 274
DB 434 LN-----DTNVI-----KNTSLHNLQR 451
OY 275 SALEGLCNLTIEFRLAYLDYLDIIDLFCNCLTNVSSFSLVSY--TIERVKDPSYNGF 331
DB 452 LLIDN-----NNKKAQVD-----LDVFLSLKRLVSLALSGPLSTTNTISDSERSSH 499
OY 332 WQHLVYNVCKGQPTTKLSLKLRTFTSNKGNAPSEVD---LPSEFLDLSRGL- 385
DB 500 LEVLELSCGNIEEPF-IRNRQLSISIDLSNNNIKQVNPWMLRLELSTVDLSNNSLI 558
OY 386 SFRKCCQSDFGTTSLKYLDLSFNGVITWSSN-----FLGBQLEHLDFOHSLKOMSE 439
DB 559 GFNG-----SLKALSGSKIVMLDLSNAPQGLFMPRPRTIYFLSYNNFTGYIP 608
OY 440 FSVLSLRNLIYLDISHTTRVAFNGIFNGI-----SSLEVLKMAINSFOENPLPD 490
DB 609 PSI-CGLANPLIIDLSS-----NNNLHGLIPRCLEAQSSLSLVNLRNNSL--DGLPLN 656
OY 491 IFTELRNLTPLDLSQCQLEQLSPYAFNSLSLQVLNMSHNNPFSLDTPPY--KCLNSLQV 548

Db 659 IFMAKAVLSLSDVSNHTLEGKLPASLAGCSALEITLIVSNNT--NDTPFWMINSIPKIQV 716
QY 549 IDYSLNHTMTSKKQELQH-----FPSSIAFLINTQNDPACTCEHQSFLQWIKDQRQLL 601
Db 717 LVLRBNNF-----KGLHNVNDGVWFGFP--LLRITDVSHNDPVGTLTSDYIMNTALSKS-- 769
QY 602 VEEVERMECATPSD---KQMPVLSLNTTCQMNKTTIGVSVL 639
Db 770 -ETELQYIGDPEDYGYTSLVLMNKGVSMEMQRIITKYTVI 809

RESULT 14

JC1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI282
R:Dat, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A:Reference number: JCI282; MUID:93038676; PMID:1384485
A:Accession: JCI282
A:Molecule type: mRNA
A:Residues: 1-603 <DAI>
A:Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A:Experimental source: liver
A>Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.8%; Score 296; DB 2; Length 603;

Best Local Similarity 24.1%; Pred. No. 7, 8e-11;

Matches 155; Conservative 84; Mismatches 243; Indels 162; Gaps 24;

QY 40 CMEINLPYKIPDNLPESTKNLIDSLFNPRLHLSYSPFPPELQVLDLSRCEIQTIEDGAYQ 99
Db 60 CSSKNL/THLPDIPVSTRALMLDGNLISIPSAFQNLSSLDPLNLQSGWLSLEPQLL 119
QY 100 SLISHLSTLITLNPFIQSLALGAFSGLSIQKLVAVETNLASLENPIGHLKTLKELNVA- 158
Db 120 GLQNLVYLHLERNLRNLAVGLFTHPTSLASLSSNLLGRLEBGLFQGLSHMLDNLGM 179
QY 159 -----NHLI-----QSFKLPEYFSNLTNLEHLDSKSKIOSICTDLR 196
Db 180 NSLVVLPDTPVPGGLGNHLEVLVAGKLTLYLPALPCGGLGELRELDLSRAKLSV--KAN 236
QY 197 VLAHQPLNLISLDSLNPMNFIQPGAFAKEIR-LHKLTLRNPDSLNVMKTCIQGLAGLEV 255
Db 227 VVVLHPLRQ-KLYLDRNLITAVAPGAFGLGMKALRMLDLSHN-RVAGLMEDETFPGLLGLHV 294
QY 226 HRLV-----LGEPR-NEGNIKEKPKSALBGLCNLTTEBFPLAYLDYVL 297
Db 295 IRLANNAIASLRPRTPFKDLHLEELQLGHNRIROLGEERFEEGLQLEV---LTLNDNQI 350
QY 298 DDI-IDLPNCLTNVSSFLSVSTI---ERV---KDFSYNFGMQLHELVNCKFGQPTLX 349
Db 351 TEVRVAGSGLPNAVVMNLGNCLNSLPKRVFQGLDKLSLHLESCLGHVLAHTF--AG 408
QY 350 LKSLKRLTFTSNKGNAPSEVD-----LPSLEFLDSRNGLSPKCCSQSDPGTTSLYK 403
Db 409 LSGRLRLFLRD-----NSISIEQSLAGSELLELDITNRLTH--LPRQLFOGIGHLEY 462
QY 404 LDSLNGVITMSSNPLGLEOLEHLDPOHSNKKQMSSEFVLSLRNLIYDISHHTTRVAF 463
Db 463 LLLSTNOLTTLSAEVLG-----PLQRAFWLIDISHNHLIELTA 498
QY 464 NCIFNGLSLEVLKMAKNGSFOENPLPDIPTELRNLTFLDLSQCLEQSLPFAFNSLSLQ 523
Db 499 EQLFSSLSGKVRYLIRNNSLQ--TFSP-----QGLERL----- 530
QY 524 VLMNSHNPFSLDTPPYKCLNSLOVL-DYSLNHTMTSKKQELQHPSSIAFLINTQNDPA 582

Db 531 -----WIDANPMQSCPEPLKALRDPALQN-----PGVAPRFVQ----- 563
QY 563 CTCHEQSFLQWIKDQRQLLVEVERMECATPSDKQMPVLSLNT 626
Db 564 -VCE-----GDDCQGVYTYNNITTCAGPANVSGLDRDYSY 598

RESULT 15

JG0193

G protein-coupled receptor FEX - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C:Accession: JG0193

R:Herney, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.

Biochem. Biophys. Res. Commun. 254, 273-279, 1999

A:Title: Identification of a novel seven-transmembrane receptor with homology to glycopr

A:Reference number: JG0193; MUID:99121227; PMID:9920770

A:Accession: JG0193

A:Molecule type: mRNA

A:Residues: 1-907 <HER>

Query Match 6.8%; Score 295; DB 2; Length 907;

Best Local Similarity 23.0%; Pred. No. 1, 5e-10;

Matches 167; Conservative 110; Mismatches 243; Indels 206; Gaps 32;

QY 11 LIPNAAPLSCVREMECEVAVP-----ITYQCEMLNFYKIPNLPSP 55
Db 9 LLSLALQLQVLAAGS-SGPPDAPRGCPSHCHCELDGMRLRVDCSDGLSPLNSLVF 67
QY 56 TKNDLSFNPRLHLSYSPFPPELQVLDLSRCEIQTIEDGAYQSLSH---LSTLITLG 111
Db 68 TSYLDLSMNNISQDPA-----SLHRLCTLEELRLAG 99
QY 112 NPIQSLAIGAFSGLSLQKLVAVETNLASLENPIGHLKTLKELNVAHNLIOSFCLPEYF 171
Db 100 NALTHIPKGAFTGLSLVLVLMQNNQKRVBEALQNRISQSLRLDANH-I-SYVPPGCF 158
QY 172 SNLTNLEHLDSNNTQISITCTDRLVLAHQPLNLISLDSLNPMNFIQPGAFAKEI-RLHX 230
Db 159 SGLSHRLHMLDNNLTDVPOAFRSLALO---AMTLALKHINHIDYAGNLSLV 214
QY 231 LTLRNN-FDSLNVMKTCIQGLAGLEVHRLVLEGFENEGNLEKFDKSALEGLCNLTIEBER 289
Db 215 LHLHNNRHSIG--KKCPDGLHSLETLD-----NYNNLDEF-PTALKTISN----- 258
QY 290 LAIYDYLDIIDL---FNCLTNVSSFLSVSTI--ERVKDFSYNFGMQLHELVNCKFGQ 344
Db 259 LKEIGFHSNNIRSIPERAF-----VGNPSLITIHFYDNPQIFGVSAFOHLP-----E 306
QY 345 PPTLKLKSLKLTFTSNKGNAPSEVDPSLEFLDSRNGLSPKCCSQSDPGTTSIX 402
Db 307 LRTLTNGASHITRPHLTGTA-----TLESILTAKISSLPQAVCDQ---LPLNQ 355
QY 403 YLDSFNGVITMSSNPLGLEOLEHLDPOHSNKKQMSSEFVLSLRNLIYDISHHTTRVA 462
Db 356 VLDSYNLELDLP--LSGCQKLOKIDLHN----- 384
QY 463 FNGIFNGLSLEVLKMAKNGSFOENPLPDIPTELRNLTFLDLSQCLEQSLPFAFNSLSL 522
Db 385 -----EIVIKSTFQQLF-----NLRSLNLAHMKIATIHPPAFSTLPSL 424
QY 523 QVLMNSHNPFSLDTPPYKCLNSLOVLDYSLNHTMTSKKQELQ-----HPSSIAFLINT 576
Db 425 IKLDLSN--LSSFPVTLG-----HGLTHLKLVTNRALQSLIPANFP-ELKTIEM 473
QY 577 TQNDPACT---CE--HQSFLQWIKDQRQLLVEVERMECA--TPSDKQMPVLSLNTQCM 629
Db 474 PSAYCCAFGCGCENYKISNQMKDDGNSVDYDHHKXQAGLCQVQDERLELDLEEDL 533
QY 630 NK-----TIIGVSLSVLVVS---VVAVLVK---FYFILM 659

Db	534	NAHSHVQCSPRGPFKEHLEFGSWLIRIGVTTAVLITSCNALVALTVPRTPLYISSIK	593
Oy	660	LIAGCI	665
Db	594	LLIGVI	599

Search completed: March 12, 2005, 19:56:52
Job time : 30.6477 sec8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 21.9643 Seconds

(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-4

Perfect score: 4141
Sequence: 1 MELNFKYKIPDNLPRSTKNDL.....SWNEGTGTCNNQGEATSI 799

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4141	100.0	844	US-09-949-016-9438	Sequence 9438, App1
2	599.5	14.5	784	US-09-982-308B-23	Sequence 23, App1
3	590	14.2	661	US-08-514-014-4	Sequence 4, App1
4	590	14.2	661	US-08-833-823-4	Sequence 4, App1
5	539	13.0	775	US-09-949-016-8799	Sequence 8799, App1
6	309	7.5	605	US-09-063-950-5	Sequence 5, App1
7	297	7.2	605	US-08-190-802A-49	Sequence 49, App1
8	297	7.2	605	US-08-477-346-49	Sequence 49, App1
9	297	7.2	605	US-08-473-089-49	Sequence 49, App1
10	297	7.2	605	US-08-487-072A-49	Sequence 49, App1
11	297	7.2	605	US-09-538-092-1087	Sequence 1087, App1
12	297	7.2	623	US-09-949-016-10995	Sequence 10995, App1
13	290	7.0	603	US-08-190-802A-50	Sequence 50, App1
14	290	7.0	603	US-08-477-346-50	Sequence 50, App1
15	290	7.0	603	US-08-473-089-50	Sequence 50, App1
16	290	7.0	603	US-08-487-072A-50	Sequence 50, App1
17	289.5	7.0	1112	US-09-353-585-3	Sequence 3, App1
18	287.5	6.9	662	US-09-538-092-1325	Sequence 1325, App1
19	287.5	6.9	662	US-09-949-016-6619	Sequence 6619, App1
20	287.5	6.9	665	US-09-949-016-10710	Sequence 10710, App1
21	286.5	6.9	1525	US-09-191-647-2	Sequence 2, App1
22	286.5	6.9	1525	US-09-540-245A-2	Sequence 2, App1
23	286.5	6.9	1525	US-09-540-153-2	Sequence 2, App1
24	286	6.9	1112	US-09-353-585-2	Sequence 2, App1
25	284.5	6.9	907	US-09-170-496D-264	Sequence 264, App1
26	284.5	6.9	907	US-09-170-496D-278	Sequence 278, App1
27	283.5	6.8	1166	US-10-101-464A-900	Sequence 900, App1

28	279.5	6.7	1529	4	US-09-312-283C-396	Sequence 396, App1
29	277.5	6.7	1523	3	US-09-182-024A-2	Sequence 2, App1
30	273	6.6	620	4	US-09-907-794A-73	Sequence 73, App1
31	273	6.6	620	4	US-09-905-125A-73	Sequence 73, App1
32	273	6.6	620	4	US-09-902-775A-73	Sequence 73, App1
33	273	6.6	620	4	US-09-906-700-73	Sequence 73, App1
34	273	6.6	620	4	US-09-903-603A-73	Sequence 73, App1
35	273	6.6	620	4	US-09-904-920A-73	Sequence 73, App1
36	273	6.6	620	4	US-09-909-064-73	Sequence 73, App1
37	273	6.6	620	4	US-09-905-381A-73	Sequence 73, App1
38	273	6.6	620	4	US-09-906-618-73	Sequence 73, App1
39	270	6.5	1101	3	US-08-986-485-2	Sequence 2, App1
40	266.5	6.4	1091	3	US-08-986-485-5	Sequence 5, App1
41	265.5	6.4	863	2	US-08-666-271-2	Sequence 2, App1
42	265.5	6.4	1874	4	US-09-331-403-2	Sequence 2, App1
43	264	6.4	1480	3	US-09-191-647-7	Sequence 7, App1
44	264	6.4	1480	3	US-09-540-245A-7	Sequence 7, App1
45	264	6.4	1480	3	US-09-540-153-7	Sequence 7, App1

ALIGNMENTS

```
RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match      100.0%; Score 4141; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MELNFKYKIPDNLPRSTKNDLSFNPRLHLSGYSFFSPELOVLDLSREIQTIENGAQVS 60
|||||
61 LSHSTLILGNPISIALGAFSGLSYQKVAVEYNLASLENPFIQHTLKELVNVAHN 120
|||||
106 LSHSTLILGNPISIALGAFSGLSYQKVAVEYNLASLENPFIQHTLKELVNVAHN 165
|||||
121 LIQSFKLPEYPSNLTNLEHLDLSNNKIQSIYCTDLRVLHQPMLNLSIDLSPNNFTOP 180
|||||
166 LIQSFKLPEYPSNLTNLEHLDLSNNKIQSIYCTDLRVLHQPMLNLSIDLSPNNFTOP 225
|||||
181 GAFKPIRLHKTLLNNPISIALGAFSGLSYQKVAVEYNLASLENPFIQHTLKELVNVAHN 240
|||||
226 GAFKPIRLHKTLLNNPISIALGAFSGLSYQKVAVEYNLASLENPFIQHTLKELVNVAHN 285
|||||
241 CNLTIEERFLAYLDYDDIIDLFNCLTNVSSFSVLSTIRVXDFSNFGMOHLELVNC 300
|||||
286 CNLTIEERFLAYLDYDDIIDLFNCLTNVSSFSVLSTIRVXDFSNFGMOHLELVNC 345
|||||
301 KFGFPILTKLSLRKLTFTSNKGNAPSEVDLPSELEFLDLSRNGLSPFKGCCQSDFTTS 360
```

Db 346 KFGPFTLKSLKSLKLTFTSNKGNAGFSEVLPSELEFDLSNGLSFGCCSQSPFGTTS 405
Qy 361 LKYLDLSFNGVITMSNSFLGJELEHLDFOHSNLKQMSFVLSRLNLYLDLSHTTR 420
Db 406 LKYLDLSFNGVITMSNSFLGJELEHLDFOHSNLKQMSFVLSRLNLYLDLSHTTR 465
Qy 421 VAFNGIFNGLSLEVLKAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSPPTAFNSLS 480
Db 466 VAFNGIFNGLSLEVLKAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSPPTAFNSLS 525
Qy 481 SLOVLMNSHNNPFSIDTPPYKCLNSLOVLDVSLNHTMSKQEOLOHPSSSLAFLNLTND 540
Db 526 SLOVLMNSHNNPFSIDTPPYKCLNSLOVLDVSLNHTMSKQEOLOHPSSSLAFLNLTND 585
Qy 541 FACCEHOSFLOMTIDORQLLVEVERMECAPSDKQGPVLSLNTTCOMNTIIGVSVLS 600
Db 586 FACCEHOSFLOMTIDORQLLVEVERMECAPSDKQGPVLSLNTTCOMNTIIGVSVLS 645
Qy 601 VLVSVAVLVYKFFHMLMLAGCIKYRGENIYDAFIYSSODEDWVRLNLYKLEBGV 660
Db 646 VLVSVAVLVYKFFHMLMLAGCIKYRGENIYDAFIYSSODEDWVRLNLYKLEBGV 705
Qy 661 PPQOLCHYRPPFPAVAIAANIIEGFKSRKVIVVSQHTIQRWCIFEYELIAQTWQFL 720
Db 706 PPQOLCHYRPPFPAVAIAANIIEGFKSRKVIVVSQHTIQRWCIFEYELIAQTWQFL 765
Qy 721 SSRAGIIFIVOKVEKTLRQOVELYRLNSRTYLEMDSVLRHIFMRRLKALLDGS 780
Db 766 SSRAGIIFIVOKVEKTLRQOVELYRLNSRTYLEMDSVLRHIFMRRLKALLDGS 825
Qy 781 WNPBGTVGTGCMQDEATSI 799
Db 826 WNPBGTVGTGCMQDEATSI 844

RESULT 2
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tam, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: J80601QC
; CURRENT APPLICATION NUMBER: US/09/982,308B
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 14.5%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.5e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

Qy 8 IPDNLPSTKMLDSFNLRLHGSYFSPPELOVLDLSRCEIQTEGAGVQSHSTL 67
Db 46 IPGSLTEAVKSLDLSNNRITITYSNDLORCVNLQALVLTSGINTIEEDSPSSLSLEHL 105

Qy 68 ILTGNPIQSIALGAFSGLSLQKL-----VAETNLASLENPIGLHKT----- 111
Db 106 DLSYNYLSNLSSSWFKLSSLTFLNLGNPKYKLTGETSLFSLTKQLRLRGVNDTFTKI 165
Qy 112 -----LKEANVAHNLQSFKLPEYPSNLTNLEHLDLSNK-----IQSI 150
Db 166 QKDPFAGVTFLEBELEIDASDQSYE-PKSLKSIQNVSHLILMHQHILLEIFVDVTSV 224
Qy 151 YCTDLRVLHQPPLNLTSLDSLNPMPN--IQGAFKEIRLHKLTNRN--NFDGL-NYMK 204
Db 225 ECLER-----DIDLDFFHSLSSTGTSNL-IKKFPRVVKITDESLPQYMK 271
Qy 205 TC--IQGLAGLEVRLV--GEFRNEGULEKFPKALBGLCNLTIEFRLA--YLDYYL 257
Db 272 LNLQISGLELEFDDCTINGVGNFRASDNDNRVIDPKAYE--TLTIRLHLPFYLEY-- 326
Qy 258 DDIIDFNCLTNVSSFVSVTYTIRVYDFSNFQWQHELYNCKFGQPTLKLSKRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKV-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVLPSELEFDLSRN-----GLSFKCCSQSDPGTTSKLYLDLSFNGVI 372
Db 358 -----HLKLELYDLSENLMVEYLKNSAC-----EDAWESLQTLIRQN--- 397
Qy 373 TMSNPLGLQLEHLDFOHSNLKQMSFVFLSLRNLTYLDLSHTTRVAFNGIFNGLS 432
Db 398 -----HL-----ASLEKTEG--TLTLKNTLNIDISK----- 422
Qy 433 LEVLMKAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEOLS---PTANSLSSLOVLMNSH 489
Db 423 -----NSFHS--MBETQWPEKMKYLNLSSTRHSVGCIP-----KTEILIVSN 466
Qy 490 N--NFSLD-----TFP--YKCLNSLOVLDVSLNHTMSKQEOLOHPSSSL 531
Db 467 NNLNLPFLSLNPOLKELYISRNKMTLPDASLPLMLVLVKKISRNAITTFSEKQDLSF--HTL 525
Qy 532 AFLNLTQNDPACCEHOSFLOMTIDORQLLVEV-----ERMECAPSDKQGPVLSLNT 586
Db 526 KTEBAGNNFICSEFLSTQ---EQALAKVLIDWPANYLCPSPHVGQOQOVRLS 581
Qy 587 -----QNMKTIIGVSVLVVSVAVLVYKFF--FHLMLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRIALVSGMCALFILLTGLVCHRHGIMYKMMWAMQARPKRADSRNICY 641
Qy 635 DAFIYSSODEDWVRLNLYKLEBGVPPFOLCHYRPPFPAVAIAANIIEGFKSRKV 694
Db 642 DAFIYSERDAYWENLMQELBNPFPKCLHAKRFIOGKIIDNII-DSIKSHKIV 700
Qy 695 VVSQHTIQRWCIFEYELIAQTWQFLSSRAGIIFIVLOKVEKTLRQO-VELYRLSRNT 753
Db 701 FVLSSENVKSEWCYELDFSHFRLFDENNDAAILILLEPIEKKAIPORFCKLRKIMTKT 760
Qy 754 YLEWEDSVLRHIFMRRLKAL 775
Db 761 YLEWPMDEAQREGFWNLRAAI 782

RESULT 3
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-014-4

Query Match 14.2%; Score 590; DB 1; Length 661;

Best Local Similarity 29.3%; Pred. No. 1.4e-45;

Matches 191; Conservative 107; Mismatches 266; Indels 88; Gaps 23;

3 LNFYKIPNDLPSTKNDLSFNPLRHLSYSPFSPPELOVLDLSRCEIQTEDGAYQSL 62
42 LGLSIPPTLNTBTFLEFSFNPLPTINRTRSLMNTFLDLTRCQINWHEDEFGHH 101
63 HLSTLLTGNPIQSLALGAFSGLSLOQLVAVENTNLASLENPICHTLKEINVAHNL 122
102 QLSLTVLGNPLFMALTSINGPKSLKHLFLIQGISNLEFPVANHLESLVYGSNHI 161
123 QSFKLPEYFNSMLNLEHDLSSNKIOSIYCTDLRVLHQMPLNLSLDSLNPMNFIOGA 182
162 SSIKPKPFP-ARNLKVLDPQNNALHYISREDMSLEQ-AINLSLNNGNNAKIEIGA 218
183 FKEIRLHLKLTIRNPFDSINVMKTCIOGLAGLEVHVLGEEFRNEGNLEKFKSALEGICN 242
219 FDSIVFGQL----NGGTPNLSVIFNGLQNSTQSLWIGTFEDIDD-EDISSAMKIGCE 273
243 LTIEFRLAYDYLDIID-LFNCLTNVSSFSIVSVTIERVKDFSYNGQHLELVN-- 299
274 MSVESLNLQ-EHRSDISSTTFQCFQLOQLDLTATHLKGLPS-----GKGLNLKKL 326
300 -----CKF--GQFPTL-----KLKSLKLTFTSNKGNAFSEVLDPSLEFDL 340
327 VLSVNHFDOLCOISANPPSLTHLYIRGVKKLHLGVGCELEKLN-----LQTLDL 377
341 SRNGLSFGCCSQDPFGTTSLLKYLDSFNGVITMSSN-FLGLEQLEHDFQ---HSNLK 395
378 SHNDLEASDDCSLOLKNLSHDLTINLSHNEPGLSQAFKCEPQLELDLATRHLINAP 437
396 QMSEFS--VFLSLRNLII--LDISHTTRVAFNGIFNGLSLEVLRKMAANSFOENFL--P 449
438 Q-SFQNLHFLQVNLGTCFLDTSNQH-----LLAGLPVLRHNLKNGHFDQDTITKT 489
450 DIFTELRLUTFLDLSQCOLEQSLPFAFNSLSLOLVNMSHNF--SLDTPFY----- 500
490 NLLQTVGLEVLVLISSCGLLSIDQAFHSLGMSHVDSHNSLTCDSIDSLSHLKIYLN 549
501 KCLNSLOLVDSYLNIMTSSKQELQHPFSLAFNLNTONDPACTGCEHSGFIOMIKORQL 560
550 LAANSINIISPLLLIL-----SQGSTINLSHNPDLCTSNHFLTWYKENLAK 598
561 LVEVERMECATPSDKQMPVLSLNTTCQNNKTIIGSVLSVLVSVAVLVY 612

DB 599 LEGSEETTCANPPSLRGVKSVDKLSGCI--TAIGIFLYVELL-LLAIIILF 647

RESULT 4
US-08-833-823-4

Sequence 4, Application US/08833823
Patent No. 5969093

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKenough

TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,823

FILING DATE: 10-APR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/514,014

FILING DATE: 11-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G16000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 661 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-823-4

Query Match 14.2%; Score 590; DB 2; Length 661;

Best Local Similarity 29.3%; Pred. No. 1.4e-45;

Matches 191; Conservative 107; Mismatches 266; Indels 88; Gaps 23;

3 LNFYKIPNDLPSTKNDLSFNPLRHLSYSPFSPPELOVLDLSRCEIQTEDGAYQSL 62
42 LGLSIPPTLNTBTFLEFSFNPLPTINRTRSLMNTFLDLTRCQINWHEDEFGHH 101
63 HLSTLLTGNPIQSLALGAFSGLSLOQLVAVENTNLASLENPICHTLKEINVAHNL 122
102 QLSLTVLGNPLFMALTSINGPKSLKHLFLIQGISNLEFPVANHLESLVYGSNHI 161
123 QSFKLPEYFNSMLNLEHDLSSNKIOSIYCTDLRVLHQMPLNLSLDSLNPMNFIOGA 182
162 SSIKPKPFP-ARNLKVLDPQNNALHYISREDMSLEQ-AINLSLNNGNNAKIEIGA 218
183 FKEIRLHLKLTIRNPFDSINVMKTCIOGLAGLEVHVLGEEFRNEGNLEKFKSALEGICN 242
219 FDSIVFGQL----NGGTPNLSVIFNGLQNSTQSLWIGTFEDIDD-EDISSAMKIGCE 273
243 LTIEFRLAYDYLDIID-LFNCLTNVSSFSIVSVTIERVKDFSYNGQHLELVN-- 299
274 MSVESLNLQ-EHRSDISSTTFQCFQLOQLDLTATHLKGLPS-----GKGLNLKKL 326

QY 300 -----CKF--GQFPTL-----KLSKRLFTSNKGNASEVDLPSELFLDL 340
DB 327 VLSVNHFDQLCOIAANPSPSLTHLYIRGNVKKLHGVCLEKLGK-----LQTLIDL 377
QY 341 SRNLSPFGCCSQSDPFGTSLKYLDSLSPNGVITMSN-FLGLBELEHDPQ-----HSLTK 395
DB 378 SHNDIEASDCCSLQKLNLSHLOTLNLSHNEBPLQLOSAFKCECPQLELDLAFTRLIHIAAP 437
QY 396 QMSFSS--VPLSLNRLIY--LDISHTHTRVAFNGIFNGISLSEVLKMAKNSFOENFL--P 449
DB 438 Q-SFQONHFLQVANTLYCFDITSNQH-----LLABLPLYRLHNLKGNHFOGOTITKT 489
QY 450 DIFTELNRNLTLDSLQCOLEQSPFAPSNSLSLOYLNHNNFF--SLDTFPY-----500
DB 490 NLQTVGSLLEVTLISSCGLSIDQAFHSLGKMSHVDLSHNSLTCDSIDSLSHKGIYLN 549
QY 501 KCLNSLOVLDYSLNHNIMSKKQELQHPSSSLAFNLTONDPACFCEHOSFIQWKDQROL 560
DB 550 LAANSINISPRLLPIL-----SQOSTINLSHNPDLCTCSNHLFTWKENLHK 598
QY 561 LVEVERECATPSDKQMPVLSLNTITCOMKTIIGVSLVSVVAVVAVLY 612
DB 599 LESEBETTCANPSPSLRGVKSVDKLSGCI--TAIGIFLYFL-LALILFL 647

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-8799

Query Match 13.0%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 9.9e-41;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;
QY 8 IPDNLPTSTKNLDSFNPRLHLSYSFFSPPELOVLDISRCETIOTIEDGAYQSLSHLSTL 67
DB 81 IPGSLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSGINTIIEBDSFSSLSLEHL 140
QY 68 ILTGNPIQSIALGAFSGSLQKL-----VAVENNLASLENFPIGHLKT-----111
DB 141 DLSYVLSNLSNNKPLSLTFLNLGNPKYTLGETSLFPHLYLQLILRVGNMDTPYTKI 200
QY 112 -----LKEINVAHNLIQSFCLPEYFSNLTNLEHLDLSNNK-----10S1 150
DB 201 QKQFAGLTFLBELEIDASDQSYE-PRSLKSLQNVSHLILHMKQHILLEIPVDVYSSV 259
QY 151 YCTDLRVLHQPLANLNLSDLSLNPWF--IOPGAFKEIRLHKLTIRN--NFDL-NVWK 204
DB 260 ECLER-----DTLDLTFHFSELSTGETNSL-IKKFTFRNKYITDESIFQYMK 306
QY 205 TC--IOGLAGLEVHRLV--GEPRNEGNLEKPKMSALEGCONITIEFRLLA--YLDVYL 257
DB 307 LNLQISGLLELPDDCTLVGNFRPASDNRVIDPGKVE--TLTIRRLHLPFYLFY--361

QY 258 DDIIDLFNCLTNVSSFSLSVETTERVDFSYNGMOMLELVNCKFGQPTLKLKSLRLT 317
DB 362 -DLSTVSLTERVK-----RITVENSXVF-----LVPCLLSQ-----392
QY 318 FTSNKGNAASEVDLPSELFLDSRN-----GLSFKCCSQSDPFGTSLKYLDSLSPNGVI 372
DB 393 -----HLKSLLEVLDISENLMBEYKNSAC-----EDAWPSLQTLILRON---432
QY 373 TWSNFLGLBQLEHLDPOHSLNLMKMSSESVFLSLRNLYDLSHTHTRVAFNGIFNGIASS 432
DB 433 -----HL-----ASLEKTB- -TLTILKLNLTNIDISK-----457
QY 433 LEVLKMAKNSFOENFLPDIPTTELNRNLTLDSLQCOLEQLS---PTAFNSLSLQVLMNSH 489
DB 458 -----NSFHS--METQWPEKMKYLNLSRHSVIGCIP-----KTEILDVSN 501
QY 490 N--NFSGLD-----TFP-YCLNSLOVLDYSLNHNIMSKKQELQHPSSSL 531
DB 502 NNLNLPFLANLPOLKELYISRNKMLTLPDASILPMLVLKLSRNAITTFSEKOLDSP-HTL 560
QY 532 AFLNLTONDPACFCEHOSFIQWKDQROLVEV-----ERMECATPSDKQMPVLSLNT 586
DB 561 KTELAGGNFTCSCEPLSFQ-----EQALAKVLDMPANYLDCSPSHRGQOVQVRLS 616
QY 587 ---COMKTIIGVSLVSVVAVVAVLYKRY--FILMLAGCIXGR-----GENI-Y 634
DB 617 VSECHRALVSGMCCALFILLITLGVLCRPHGLMWKMMAMVLAQRKRKAPSRNICY 676
QY 635 DAFVYSSQEDWRYNELVKNLEBGVPPFOLCHYRPFITGVAIANIIEGFKSKRYI 694
DB 677 DAFVYSERAYWYENMLVQLEFNPNPFLCLHKRDPFGKMWIDNI-DSEIKSHKV 735
QY 695 VVWSQFIQSRMCIFEYELAQWQFLSSRAGIFIVYQKV 734
DB 736 FVLSNFVKSCKYELDFSHFRLFDENNAIILILEPT 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRF
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.5%; Score 309; DB 3; Length 605;
Best Local Similarity 24.5%; Pred. No. 1.4e-19;
Matches 155; Conservative 92; Mismatches 225; Indels 150; Gaps 23;
QY 4 NFYKIPDNLPTSTKNLDSFNPRLHLSYSFFSPPELOVLDISRCETIOTIEDGAYQSLSH 63
DB 64 NLTRLPDGIQGTALWLDNSNNISIPPAFRNLSSLAFLNLQCGQGSLEPQALGLEN 123
QY 64 LSTIILTNPIQSIALGAFS-----GLSSLOKVAVENTRLA 99
DB 124 LCHLHLEERNQRLSLAVGTFAYPALALLGLSNNRSLSELDEGLPEGGLNLDMLNGMSLA 183
QY 100 SLENFPIGHLKTEINVAHNLIQSFCLPEYFSNLTNLEHLDLSNNKIQSYCTDLRVHL 159
DB 184 VLPDAAFRGIGGLRELVLAGNRL-AYLQPALFGLAELRELDLSRNALRAI--KANVFA 239

```

QY 160 QMPLNLSTLSDINPMNFIOGAFKEIR-LHKLTIRNPFDSLNVKTKCIOGLAGIEVRL 218
D 240 QLPRLQ-KLYIDRNLIAAVGAFGLKALRWLDSHN-RVAGLEDETFPGILGRVRL 297
QY 219 VLGEFRNEGNLEKPEKSALEGLCNLTIEFRFLAYDYLDIIDLFCNLTWVSFSLVS 278
D 298 -----SHNAIASLRPTFEDL-----HLEEL-----QLGHN 324
QY 279 TIEVKDFSYNFGMOHLELVNCKFGQPPYLKLSKRLTFTS--NKGNAFSEVDLPSEL 336
D 325 RIRQLAERSFE-GIGQLEVLTLDNQLOEVKAGFLGTLNVAVMNLSCNCLR--NLPRQV 381
QY 337 FLDSL-R-NGLSFKGCC-----SQSDFGTSLKYLDLSNGVITMSSNFL-GLBQLEHIDF 389
D 382 FRGKJLSHLBESSCLGRIRPHFTGSGRRFLKONGVGLIEQSLMGIAELIEIDL 441
QY 390 QHNLKQMSSEFSVLSLNLTYLDISHHTTRVAFNGIFNGLSLEVLMAQNSFOENLFP 449
D 442 TSNQL-----THLP-----HQLFQGLKLEYLLSHRLAE--LP 474
QY 450 -DIFTELRLTLFDLSQCOLEQLSPTAFNSLSLQVLNMSHNFPSLDTPEYKCLNSIQV 508
D 475 ADALGPQRAFWLVDVSHNRLEALPESLSLASIGRLRYNLRRN---SLRTFTPQ----- 524
QY 509 LDYSLNHTMSKKQELQHPFSSLAFLNLTQNDFACTCEHQS-----FLQWI 554
D 525 -----PPGLERLWLEGNPMDCSCLKALRDFALQNPASVPRFOAI 565
QY 555 ---KDORQLVVERMECATPSDKQMPVLSL 583
D 566 CEGDDCQPPVTTYNNITCASPEVAVGLDRL 597

```

RESULT 7

```

US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519803
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

```

```

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

```

```

Query Match 7.2%; Score 297; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```

```

QY 4 NPYKIPDNLSTPNLSDINPMNFIOGAFKEIR-LHKLTIRNPFDSLNVKTKCIOGLAGIEVRL 63
D 64 NLTRLPQGVPGTQALWLDGNLSSVPPAQNLSLGLFNLQGGQSLSPFQALLGLEN 123
QY 64 LSTLLGNPIQSIALGAFS-----GLSLLOKLVAVETNIA 99
D 124 LCHLHERNQRSALATGFPATTPALASIGLSNNRSLREDSGLFEGLSLMDNLGMSLA 183
QY 100 SLENPIGHLKTYLELVANHLIQSFKLPEYFSNLTNLEHLDLSNKKIQSIYCTDLRYLH 159
D 184 VLPPAARFGISLRELVLAGNRL--AYLOPALFSGIAELREBIDLSRNALRAI---KANFV 239
QY 160 QMPLNLSTLSDINPMNFIOGAFKEIR-LHKLTIRNPFDSLNVKTKCIOGLAGIEVRL 218
D 240 QLPRLQ-KLYIDRNLIAAVGAFGLKALRWLDSHN-RVAGLEDETFPGILGRVRL 297
QY 219 VLGEFRNEGNLEKPEKSALEGLCNLTIEFRFLAYDYLDIIDLFCNLTWVSFSLVS 278
D 298 -----SHNAIASLRPTFEDL-----HLEEL-----QLGHN 324
QY 279 TIEVKDFSYNFGMOHLELVNCKFGQPPYLKLSKRLTFTS--NKGNAFSEVDLPSEL 336
D 325 RIRQLAERSFE-GIGQLEVLTLDNQLOEVKAGFLGTLNVAVMNLSCNCLR--NLPRQV 381
QY 337 FLDSL-R-NGLSFKGCC-----SQSDFGTSLKYLDLSNGVITMSSNFL-GLBQLEHIDF 389
D 382 FRGKJLSHLBESSCLGRIRPHFTGSGRRFLKONGVGLIEQSLMGIAELIEIDL 441
QY 390 QHNLKQMSSEFSVLSLNLTYLDISHHTTRVAFNGIFNGLSLEVLMAQNSFOENLFP 449
D 442 TSNQL-----THLP-----HRLFQGLKLEYLLSHRLAE--LP 474
QY 450 -DIFTELRLTLFDLSQCOLEQLSPTAFNSLSLQVLNMSHNFPSLDTPEYKCLNSIQV 508
D 475 ADALGPQRAFWLVDVSHNRLEALPESLSLASIGRLRYNLRRN---SLRTFTPQ----- 524
QY 509 LDYSLNHTMSKKQELQHPFSSLAFLNLTQNDFACTCEHQSFLQWID-----QRQ 559
D 525 -----PPGLERLWLEGNPMDCP---LXALRDFALQNPASVPRF 561
QY 560 LIVERMECATPSDKQMPVLSLNTCCOMNKTIIIGSV 598
D 562 VQALCEGDDCQPPAYTYN-----NITCASPEVAVGLD 594

```

RESULT 8

```

US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:

```

```
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,346
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/487,072
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 2550-0025.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 605 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor binding
/ protein complex, Fig. 32
/ US-08-477-346-49
```

Query Match 7.2%; Score 297; DB 3; Length 605;

Best Local Similarity 24.4%; Pred. No. 1.8e-18;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```
QY 4 NFKYIPNLPSTKNDLSFNPRLHLSYSFSPPELQVLDLSRCEIQTEDGAYQSLSH 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 NLRLPGVGGGTQALWLDGNNLSVPPAFAONLSSIGFNLQGGQSGSLPPQALLGLEN 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 LSTLILGNPIOSIALGAFS-----GLSLQKLVAVETNLA 99
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 LCHHLERNGRLSLALGTFAHTPALASLGNNRLSRLEDGLFEGLSLMDLNGMNSLA 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 SLENFPIGHLKTLKELNVANHLIOSFKLPEYFSNLTNLEHLDLSNNKIOSIYCTDLRYLH 159
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VLPDAFRGSGSLRELIVAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KAVVFV 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 QMPILNLSLDSLNPNMFIOGAFKEIR-LHKLTLRNPFSLNVMKTCIGLAGLEVHRL 218
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 QLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGGLGLRVLR 297
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 VLGFNRNEGNLEKFDKSLBGLCNLTIEEFLAYLDYLDIIDLFNCLTVNVSFSIVSV 278
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 298 -----SHNAISLRPRTRKDL-----HFLBEL-----QLGHN 324
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 TIERVKDPSYNGQHDELVNCCKFGQPPYLKLSKELTPTS--NKGNMFSVLDPSLB 336
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 325 RIRQLARSTF-GLQGLEVLTLDHNOQEVKAGFLGTVAVMNLGSCNCR--NLDEOV 381
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 FLIDLSR-NGLSFKCC-----SQSDFGTSIKYIDLSFNGVYTMSSNFL-GLLEULHDF 389
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 382 FRIGKLSHSLHESSCGIRIRPHTFTGSGRLRLFLKONGLVGIEOSLWGLAELEIDL 441
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 QHSLKQMSFSEVSLRNLIYLDISHTRTVAENGIFNGLSLSEVLKMGANSQENFLP 449
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 442 TSNOL-----THLP--HRLFGGKLEVLILSLNRILAE--LP 474
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 450 -DIFTELRLNLTFLDLSOCOLEQSLPTAFNSLSLQVLMNSHNPFSDTFPYKCLNSIQV 508
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 475 ADALGPIQRAFWLDVSHNRLEALPNSLLAPLGRRLRYISLRNN---SLRTFTPQ----- 524
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 LDYSLNHNIMTSKQELQHPSSSLAFLNLTQNDPACTEHSQFLQWIID-----ORQ 559
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 525 -----PPGLERLWLBGNPMDCCP-----LKALRDFAQNPSAVRPF 561
QY 560 LILVERMECATPSDKQGMVLSLNTICQNNKTIIGSV 598
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 562 VQALCEGDDCOPAYTYN-----NITCASPPPEVVGIDL 594
```

RESULT 9

US-08-473-089-49

Sequence 49, Application US/08473089

Patent No. 6342368

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 605 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Insulin-like growth factor binding

protein complex, Fig. 32

INDIVIDUAL ISOLATE: Insulin-like growth factor binding

protein complex, Fig. 32

US-08-473-089-49

Query Match 7.2%; Score 297; DB 3; Length 605;

Best Local Similarity 24.4%; Pred. No. 1.8e-18;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```
QY 4 NFKYIPNLPSTKNDLSFNPRLHLSYSFSPPELQVLDLSRCEIQTEDGAYQSLSH 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 NLRLPGVGGGTQALWLDGNNLSVPPAFAONLSSIGFNLQGGQSGSLPPQALLGLEN 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 LSTLILGNPIOSIALGAFS-----GLSLQKLVAVETNLA 99
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 LCHHLERNGRLSLALGTFAHTPALASLGNNRLSRLEDGLFEGLSLMDLNGMNSLA 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 SLENFPIGHLKTLKELNVANHLIOSFKLPEYFSNLTNLEHLDLSNNKIOSIYCTDLRYLH 159
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VLPDAFRGSGSLRELIVAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KAVVFV 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 QMPILNLSLDSLNPNMFIOGAFKEIR-LHKLTLRNPFSLNVMKTCIGLAGLEVHRL 218
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 QLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGGLGLRVLR 297
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

QY 219 VLGERRNEGNEKPDKSALEGLCNLTIEERFLAYIDYLDIIDLFNCLTNVSSFLYSV 278
Db 298 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 324
QY 279 TIERKDFSYNFGMCHLELVNCKFGQFPPLKLSIKRLTFTS--NKGNAFSEVDLPSE 336
Db 325 RIRQLAERSFE-GLGQLEVLTLIDHNOLOEVKAGAFGLGTVNAVMNLSCNCR--NLPEQV 381
QY 337 FLIDLSR-NGLSFKGCC-----SQSDFGTTSLSKYLDLSFNGVITWSSNFL-GLBQLEHLDF 389
Db 382 FRGKGLKLSHLBEGSCCLIRIPHTFTGLSGRLRLKONGLVGIEQGLMGLAELELDL 441
QY 390 QHSNLIKQMSERSVFLSLRNLYLDISHHTTVANFNGISGLEVLKMAGNSFOENFLP 449
Db 442 TSNQL-----THLP-----HRLFOGKLELYLLSRRLAE--LP 474
QY 450 -DIFTELRLTFLDLSQCOLBOLSPAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOV 508
Db 475 ADALGPLOARAWLDVSHNRLEALPNSLLAPLGRRLYLSLRNN--SLRTFTPO-----524
QY 509 LDYSLNHTMSKQELQHPSPSLAFNLTONDFACTCEHOSFLQWIKD-----ORQ 559
Db 525 -----PGLERLWLEGNPMDGCP-----LKALRDPALONPSAVPRF 561
QY 560 LLEVERNECATPSDKQGMPLSLNITQOMKXTIIGVSU 598
Db 562 VQAICEGDDCQPAYTYN-----NITCASPEVVGDL 594

RESULT 10
US-08-487-072A-49
Sequence 49, Application US/08487072A
Patent No. 6423684

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theorof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32

US-08-487-072A-49
Query/Match 7.2%; Score 297; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

QY 4 NFYKIPDNLPPSTYKNDLSFNPPLRLGYSFSPPELOVLDLSREIOTIEDGAYQASH 63
Db 64 NLTRLPDVPQGTALWMDGNLSSVPPARQNLISLQFLNLQGGQLSLPEQALIGEN 123
QY 64 LSTLITLNGNPIQSIALGAFS-----GLSLQKLVAVETNYA 99
Db 124 LCHLHLERNQRLSLALGTFATTPALASIGLNNRLSRLEDGLFEGLSLMDLNGWSIA 183
QY 100 SIENPPIGLKTLKELVANAHLIOSFKLPEYFSNLTNLEHLDSNNKIQSIYCTDLRYLH 159
Db 184 VLPPDAFRGLSLNELVLAGRL--AYLOPALFSGLAELRELDLSNNALRAI--KANFV 239
QY 160 QPPLNLSLDLSLNPANFIQGAKEIR-LHKLTLRNNPDSLNWKTICQGLAGLEVRL 218
Db 240 QLPRLQ-KLYIDRLMLAAVAGAFGLKALRWLDLSHN-RVAGLLEDTPFGILGRVRL 297
QY 219 VLGERRNEGNEKPDKSALEGLCNLTIEERFLAYIDYLDIIDLFNCLTNVSSFLYSV 278
Db 298 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 324
QY 279 TIERKDFSYNFGMCHLELVNCKFGQFPPLKLSIKRLTFTS--NKGNAFSEVDLPSE 336
Db 325 RIRQLAERSFE-GLGQLEVLTLIDHNOLOEVKAGAFGLGTVNAVMNLSCNCR--NLPEQV 381
QY 337 FLIDLSR-NGLSFKGCC-----SQSDFGTTSLSKYLDLSFNGVITWSSNFL-GLBQLEHLDF 389
Db 382 FRGKGLKLSHLBEGSCCLIRIPHTFTGLSGRLRLKONGLVGIEQGLMGLAELELDL 441
QY 390 QHSNLIKQMSERSVFLSLRNLYLDISHHTTVANFNGISGLEVLKMAGNSFOENFLP 449
Db 442 TSNQL-----THLP-----HRLFOGKLELYLLSRRLAE--LP 474
QY 450 -DIFTELRLTFLDLSQCOLBOLSPAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOV 508
Db 475 ADALGPLOARAWLDVSHNRLEALPNSLLAPLGRRLYLSLRNN--SLRTFTPO-----524
QY 509 LDYSLNHTMSKQELQHPSPSLAFNLTONDFACTCEHOSFLQWIKD-----ORQ 559
Db 525 -----PGLERLWLEGNPMDGCP-----LKALRDPALONPSAVPRF 561
QY 560 LLEVERNECATPSDKQGMPLSLNITQOMKXTIIGVSU 598
Db 562 VQAICEGDDCQPAYTYN-----NITCASPEVVGDL 594

RESULT 11
US-09-538-092-1087
Sequence 1087, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Manefield, Traci A.
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:


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; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

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Query Match 7.28; Score 297; DB 4; Length 605;

QY	4	ANFYKIPDNIPESTKNUIDLSFNPRLRHGISYSPFSBPFLQYUIDLSRCETQITEDGAYOSLSH	63
Db	64	NITRLPDEGVGGTQALMTMDGNMLSSVPPAAFONLSSIGELINTQGGOLGSELPALLGLENN	123
QY	64	LSLLITGCGPISGLAIGAFS-----GSSLOKIVAVETNLA	99
Db	124	LCHLTLERNQRLSLALGTTAHTPALASLGSNNRSLRLEDGLFEGIGSLMDLWGMWSLA	183
QY	100	SLENFPICHLKTLKELNVANHNLIOSEKLPDEYSNLTNLEHLDLSSNKIOSIYCTDLRYLH	159
Db	184	VLPDAAFRGIGSLREIYVLNAGRLLAVLOPALSFGIALELRELDLSRUALRAI---KANFV	239
QY	160	OMPLNLNLSJDSLMPNPFIOQAPAFKEIR-LHKLTLKNPDSLVNMTCTIOGLAGLEVHR	218
Db	240	QUPRLQ-KLYUDRNLIAAVPAPAFGLKALRWUIDLSHN-RVAGLLEDTPEGLLGLRVLRL	297
QY	219	VLGEFRNMGNTLEKFPKSALEGCNLTIEEFRLAYLVDIIDLFPNCCLTNVSSFSVLVS	278
Db	298	-----SHNAIASLRPRITFOL-----HPLBEL-----QLGHN	324
QY	279	TIERKVDPSYNGMCHLELVNCKFCQGFPLTKLSKLRLFTPS--NKGNAFSEVDLPDLSE	336
Db	325	RIRQIAERSFE-GLQGLEVLTLIDHNQLOEVKGAFLGTLNVAAVMNLISGCLR--NLPEOV	381
QY	337	FLDLSR-NGLSERKGC-----SQSDPGTSLKLYDLSFNGVITMSSNPL-GLEOLEHDP	389
Db	382	FRGLGKHSIMHEGSCLEGRIRPHPTFGLSGKLRLPLKONGVIGIEBQSLMGLAELELDL	441
QY	390	OHSNIKQWSESVFLSLRNLIVLIDISHHTRVAFNGIENGLSLEVLKMAGNSFOENFLP	449
Db	442	TSNOL-----THLP-----HRLFOGLKLEVLILSRRLAE--LP	474
QY	450	-DIFELRNLFTFLDLSQOOLEQSLPTAFNSSLQYLVNMSHNNFSLDTPPYKCLNSLOY	508
Db	475	ADALGPLPRAPFLVDVSHNRLLEPNLSLAPLRRLRLISLRN--SLRTFTPO-----	524
QY	509	LDYSLNHTMSKKQELOHPPSSLAFLNLQONDFACTCEHOSFLOWIKD-----ORO	559
Db	525	-----PGLERLMEGNPMWDCCP-----LKALRDALQNPASVPRF	561
QY	560	LLVERBERECATPSDKQGMFVLSLNTICQAKNTIIGSV	598
Db	562	VOALCEGDDCCOPPAYTN-----NITASPREVGLD	594

RESULT 12
US-09-949-016-10995

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; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

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Query Match	7.2%;	Score 297;	DB 4;	Length 623;
Best Local Similarity	24.4%;	Pred. No. 1.9e-18;		
Matches 156;	Conservative 91;	Mismatches 240;	Indels 152;	Gaps 24

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01 4 MFYKIPDMLPSTYKXLDLSFNPRLRHGVSFSPFPELVYLDLSRCEIQTIEDGAVYSLGH 63
02  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
03 82 NUTRIPDVGPGGTQALWMDGNLSSVPPAFAFNLSSLGFLNLQGGQGLSELPQALGLLEN 141
04  LSTLLTGNPIQSLMALGAFS-----GLSSJOKLVAVETNLA 99
05  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
06 142 LCHLHLEBNQRLSLATGTFHAPRLPALASLGLSNNRSLRELDGLPEFGIGSLMDNLGNNSLA 201
07  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
08 100 SLENFPIHLKTKELNVAHNLIQSFKLPEYFSNLTNIEHDLDSNKGISQSYCTDLRVLA 159
09  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
10 202 VLPDAFPFGLSIRELVLAGNRL-AYLPALFSGLAELRELDLSRNALRAI---KANVAV 257
11  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
12 160 QMPLNLNLSDLSINMNFLOPGAFAFEIR-IHKLTLRNNDLSLNNKTCIQGLAGLEVHLL 218
13  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
14 258 QUPRLQ-KLYDRNLIAAIPAFAFGGLKALRWLDLSHN-RVAGLJEDTTPGLJGLRVRL 315
15  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
16 219 VLGEPFRNGNEKFPKDSALBGLCNLTIEBFRLAYLDYLDITDFNCULTNVSSFSLSV 278
17  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
18 316 -----SHNAIASLRPTFYDL-----HFLEEL-----QLGHN 342
19  219 TIERKYDPSYNGMHWLNLVNCBEOQFPLKLKSLKLLFTFS--NKGNAFSEVLDPSLE 336
20  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
21 343 RIRQIAESSF-B-GIGQLEVLTLHDNQLOEVKAGAPLGLTNVAVMNLISGCLR--MLPEOV 399
22  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
23 337 FLDLISR-RGLSPFKGCC-----SQSDPGTTSKLKYLDFSPNGVITWSSNPL-GLEOLEHDLF 389
24  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
25 400 FRGLGKLHSLHBGSCCLGIRPHRTTGSLGRRLTLXONGLVGIEBQSLMGALHELLELD 459
26  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
27 390 QHSNLKQMSSESVFLSLRNLIVLDISHTTRVAENGIFNGLSLEVLKXAGNSFOENPLP 449
28  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
29 460 TSNQL-----THLP-----HRLFQGLKLEYLLLSRRRLAE--LP 492
30  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
31 450 -DIFELRNLFLDLSQOLEQASPTANSLSSLOVLMMSHNNFSLDTPFKCLNSLOY 508
32  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
33 493 ADALGPIORAFWLDVSHNRLELPNSLIAPGRLEFYLISLRNN--SLRTFTPO----- 542
34  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
35 509 LDYSLNHTMSKQELQHFPSLSAFLNLTONDFACTCEHQSFLOWIKD-----ORO 559
36  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
37 543 -----PGLERLWLEGNPMWDCGP-----LKLALRDPAQLGNPAVPRF 579
38  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
39 560 LLYVERMECATPSDKQGMVLSLNLITQANKTIIIGVAV 598
40  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
41 580 VOALICEGDCCQPPAYTN-----NITCASPEVVGDL 612

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RESULT 13 0802A-50
US-08-190-802A-50
Sequence 50 Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WO-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P. O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-190-802A-50

Query Match 7.0%; Score 290; DB 1; Length 603;
Best Local Similarity 24.1%; Pred. No. 7.8e-18;

Matches 154; Conservative 84; Mismatches 240; Indels 162; Gaps 24;

QY 4 NPYKIPDLPESTKNDLSFNPRLHGSYFSPPELQVLDLSRCEIOTIEBGAYQSLSH 63
DB 64 NUTHPDIPVSTRALWMDGNLSSIPSAFQNLSSLDPLNQGSLWLSLEQALLGLON 123
QY 64 LSTLLITGNPIQSIALGAFSGLSLOKLVAVENTLASLENPPIGHLKTLKEINVA----- 118
DB 124 LYUHLERRRLNLA VGLFTHTPLASLSLSNLLGRLEBGLFQGLSHLMDLNLGMNSLV 183
QY 119 -----NHLI-----QSFKLPEYPSNLTNLEHLDLSNKKIQSIYCTDLRYLHQ 160
DB 184 VLPDTPFOGLNLHLEVLVAGNKLTYLOPALFCGLGELELRELDLSRAALRSV--KANVFVH 240
QY 161 MPLLNLSDLSLNPNNFIOPGAFKEIR-LHKLTLRNPFDSLNVMTKCIQGLAGLEVHRLV 219
DB 241 LPRLO-KLYLDRNLITVAVPGAFGLKALRWLDLSHN-RVAGIMEDTTPGLIGLHVLRLLA 298
QY 220 -----LGEFR-NEGNTLEKFPDKSALBGLCNLTIEFRILAVLYLDYLDI- 260
DB 239 HNAIASLRRTFKDLHLEELQGNHRIQDGERTFEGQLQEV---LTLDNDQITEVR 354
QY 261 IDLENCILNVSSFSLSVSTI---ERV--KDPSTNFGQHLLELYNCKFGQPTLKLKSL 313
DB 355 VGAFSGLFVAVMNLISGNCISRLSPERVFOGLDKLSLHSHSCIGLHVLRHTF--AGLSGL 412
QY 314 KRLTTSKNGCAFEVD-----LPSLEFLDLSNNGSFKKCCSQSDPTSLKYLIDS 367
DB 413 KRLFLRD---NSISIEEQSLAGSELLELDLITRLTH--LPROLFGGLHLELTLIS 466
QY 368 FNGVITMSNPLGLQLEHLDFOHSNLKOMSEFVSFLSLRNLIYLDISHTRVAFNGIF 427
DB 467 YNQLTTLGAEVLG-----PIQRAFWLDISHNHLLETLAEGIF 502
QY 428 NGISLEVLTKAGNSFOENFLPDITTELRLNLTFLDISQCEQLSPTAANSLSLQVLYNM 487
DB 503 SSLGRVRLISLNNISIQ-TFSP-----QPLERL----- 530
QY 488 SHNPFSLDTPPYKCLNSLOVL-DVSLNHTMSKKOELQHPSSLAFLNLTONDFACTCE 546
DB 531 -----WLDANWDCSPLKALRDLALQ-----PGVPRFVQT-----VCE 566
QY 547 HOSFLOWIKOROLLVEVERMECATPPSDKQMPVLSLNT 586

DB 567 -----GDDCQPYTYNNITCAGPANVSGLDLRDVSSET 598

RESULT 14

US-08-477-346-50

Sequence 50, Application US/08477346

Patent No. 6262023

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: MD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESS: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,072

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINL SOURCE:

INDIVIDUAL ISOLATE: Insulin-like growth factor bind.

INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33

US-08-477-346-50

Query Match 7.0%; Score 290; DB 3; Length 603;
Best Local Similarity 24.1%; Pred. No. 7.8e-18;

Matches 154; Conservative 84; Mismatches 240; Indels 162; Gaps 24;

QY 4 NPYKIPDLPESTKNDLSFNPRLHGSYFSPPELQVLDLSRCEIOTIEBGAYQSLSH 63
DB 64 NUTHPDIPVSTRALWMDGNLSSIPSAFQNLSSLDPLNQGSLWLSLEQALLGLON 123
QY 64 LSTLLITGNPIQSIALGAFSGLSLOKLVAVENTLASLENPPIGHLKTLKEINVA----- 118
DB 124 LYUHLERRRLNLA VGLFTHTPLASLSLSNLLGRLEBGLFQGLSHLMDLNLGMNSLV 183
QY 119 -----NHLI-----QSFKLPEYPSNLTNLEHLDLSNKKIQSIYCTDLRYLHQ 160
DB 184 VLPDTPFOGLNLHLEVLVAGNKLTYLOPALFCGLGELELRELDLSRAALRSV--KANVFVH 240
QY 161 MPLLNLSDLSLNPNNFIOPGAFKEIR-LHKLTLRNPFDSLNVMTKCIQGLAGLEVHRLV 219
DB 241 LPRLO-KLYLDRNLITVAVPGAFGLKALRWLDLSHN-RVAGIMEDTTPGLIGLHVLRLLA 298

QY 220 -----LGER-NEGULEKPKKALBGLCNLTIEPRLAYDYLDI- 260
Db 299 HNAIASLRPTFKDLHFLBELLQGHNRIRQGERTEFGQLQEV---LTINDQITEVR 354
QY 261 IDLFNCLTNVSSFSLVSTI---ERV---KDFSYNFGMOHLEIVNCKEFGPPTLKLSL 313
Db 355 VGAFSGLFNVAVMNLGNCISLPRPRVFGQDKHSHLHSCIGHVRLHTF--AGLSGL 412
QY 314 KRLFTSNKGNAGSEVD-----LPSLEFLDLSHNGLSFKGCCSQSDFGTTSIKYLDLS 367
Db 413 RRLFLRD---NSISIEQSLAGSELLELDLTNNRLTH--LPRQLFGQIGHLEYLLS 466
QY 368 FNGVITMSSNPLGLEQLHLDPOHNSLKQMSFVSFLSLRNLIYDISHHTRAVFNIGF 427
Db 467 YNQLTTLSAEVLG-----PLQRAFWLDSHNLHLETLAEGLF 502
QY 428 NGLSLEVLKMGAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSPFAPNSLSLQVLNM 487
Db 503 SSLGRVYLSLRNNSLQ--TFSP-----QPLERL----- 530
QY 488 SHNFFSLDTPPYKCLNSLOVL--DYSLNHMTSKQELQHPSSLAFLNLTQNDFACTCE 546
Db 531 -----WLDANPMDSCPLKALRDFALQ-----PGVPRFVQT-----VCE 566
QY 547 HQSFLQWIKDQROLVVERMECATPSDKQGMVLSLNTIT 586
Db 567 -----GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598

RESULT 15

US-08-473-089-50
Sequence 50, Application US/08473089

Patent No. 6342368
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theroef

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids
TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: protein

HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.

INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33

US-08-473-089-50

Query Match 7.0%; Score 290; DB 3; Length 603;
Best Local Similarity 24.1%; Pred. No. 7.8e-18;

Matches 154; Conservative 84; Mismatches 240; Indels 162; Gaps 24;

QY 4 NFYYIPDNLPSTYKNDLSFNPLRLHLSYSFSPPELQVLDLSCEIQTIEDGAYQSLH 63
Db 64 NLTHLPDIPVSTRALWDGNNLSISPAAFOQNSLSDPFLNLOQSWRLSEPPQALLGION 123
QY 64 LSTLIILGNPISALAFSGLSLQKLVAVENTLASLENPIGHLTKIELNVA----- 118
Db 124 LYTHLERNRILRNLAVALFTTPSLASLSLSSNLLGRLEBGLFGCLSHLMDNLGMNSLV 183
QY 119 -----HNL-----QSFKLPEYFSNLTNLEHLDLSNKKIQSIYCTDLRYLHQ 160
Db 184 VLPRVFGQGNLHLEVLNAGKXLYLQPALFCGELRELDLSNMLRSV---KANNFVH 240
QY 161 MFLNLSLDSLNPWNFIQCAFEIR-LHKLTIRNPFSLNVMKTCIQIAGLEVHRLV 219
Db 241 LPRLO-KLYIDRLNLTAVAGAFGMKALRWLDLSH--RVAGLMEDTFPGILGHLVRLA 298
QY 220 -----LGER-NEGULEKPKKALBGLCNLTIEPRLAYDYLDI- 260
Db 299 HNAIASLRPTFKDLHFLBELLQGHNRIRQGERTEFGQLQEV---LTINDQITEVR 354
QY 261 IDLFNCLTNVSSFSLVSTI---ERV---KDFSYNFGMOHLEIVNCKEFGPPTLKLSL 313
Db 355 VGAFSGLFNVAVMNLGNCISLPRPRVFGQDKHSHLHSCIGHVRLHTF--AGLSGL 412
QY 314 KRLFTSNKGNAGSEVD-----LPSLEFLDLSHNGLSFKGCCSQSDFGTTSIKYLDLS 367
Db 413 RRLFLRD---NSISIEQSLAGSELLELDLTNNRLTH--LPRQLFGQIGHLEYLLS 466
QY 368 FNGVITMSSNPLGLEQLHLDPOHNSLKQMSFVSFLSLRNLIYDISHHTRAVFNIGF 427
Db 467 YNQLTTLSAEVLG-----PLQRAFWLDSHNLHLETLAEGLF 502
QY 428 NGLSLEVLKMGAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSPFAPNSLSLQVLNM 487
Db 503 SSLGRVYLSLRNNSLQ--TFSP-----QPLERL----- 530
QY 488 SHNFFSLDTPPYKCLNSLOVL--DYSLNHMTSKQELQHPSSLAFLNLTQNDFACTCE 546
Db 531 -----WLDANPMDSCPLKALRDFALQ-----PGVPRFVQT-----VCE 566
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Db 567 -----GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598

Search completed: March 12, 2005, 19:58:59
Job time : 32.9643 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 70.7097 Seconds

(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985b-4

Perfect score: 4141

Sequence: 1 MEINFYKIPDNLPTSTKND.....SMNPEGTGVTGCMQEATSI 799

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4141	100.0	799	10	US-09-950-041-8
2	4141	100.0	799	14	US-10-128-166-7
3	4141	100.0	799	16	US-10-732-563-8
4	4141	100.0	799	16	US-10-732-796A-8
5	4141	100.0	837	10	US-09-950-041-26
6	625.5	15.1	661	15	US-10-038-854-135
7	625.5	15.1	661	15	US-10-037-417-107
8	603.5	14.6	784	10	US-09-950-041-4
9	603.5	14.6	784	15	US-10-456-947-46
10	602.5	14.5	784	14	US-10-095-627-12
11	602.5	14.5	784	16	US-10-732-563-4
12	602.5	14.5	784	16	US-10-732-796A-4
13	602.5	14.5	784	17	US-10-741-600-1390

14	602.5	14.5	784	17	US-10-741-600-1391	Sequence 1391, Ap
15	599.5	14.5	784	13	US-10-145-014-23	Sequence 22, Appl
16	590	14.2	661	13	US-10-114-893-10	Sequence 10, Appl
17	590	14.2	661	15	US-10-038-854-134	Sequence 134, Ap
18	573	13.8	1032	10	US-09-954-987B-192	Sequence 12, Ap
19	573	13.8	1032	14	US-10-272-502A-31	Sequence 31, Appl
20	573	13.8	1032	15	US-10-407-952-32	Sequence 32, Appl
21	567	13.7	1050	10	US-09-954-987B-175	Sequence 175, Ap
22	567	13.7	1050	14	US-10-272-502A-22	Sequence 22, Appl
23	567	13.7	1050	15	US-10-407-952-26	Sequence 26, Appl
24	531.5	12.8	1032	10	US-09-950-041-37	Sequence 37, Appl
25	531.5	12.8	1040	9	US-09-864-761-38325	Sequence 38325, A
26	531.5	12.8	1041	10	US-09-954-987B-184	Sequence 184, Ap
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28	531.5	12.8	1041	14	US-10-272-502A-26	Sequence 26, Appl
29	531.5	12.8	1041	15	US-10-407-952-28	Sequence 28, Appl
30	531.5	12.8	1041	16	US-10-732-563-16	Sequence 16, Appl
31	531.5	12.8	1041	16	US-10-732-796A-16	Sequence 16, Appl
32	530.5	12.8	1041	9	US-09-168-978-3	Sequence 3, Appl
33	530.5	12.8	1041	9	US-09-978-295A-498	Sequence 498, Ap
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ALIGNMENTS

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RESULT 1
US-09-950-041-8
Sequence 8, Application US/09/950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kaszelen, Robert A.
APPLICANT: Ho, Stephen W.K.
APPLICANT: Liu, Yong-Jun
TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-8
Query Match 100.0%, Score 4141, DB 10, Length 799;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US2003007279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAUAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDMAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Query Match 100.0%; Score 4141; DB 14; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1

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; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 581830003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-563-8

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 KEGQFPTLKLSLRKLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFPGCCSQSDFGTTS 360
Db 301 KEGQFPTLKLSLRKLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFPGCCSQSDFGTTS 360

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Db 721 SSRAGIIFIVLQKYEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFRRRLKALLDOKS 780

Qy 781 WNPBGCTVGTGNCWQEAITSI 799
Db 781 WNPBGCTVGTGNCWQEAITSI 799
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Db 781 WNPBGCTVGTGNCWQEAITSI 799

RESULT 4
US-10-732-796a-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-796a-8

Query Match      100.0%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELNFKYKIPDNLPSFTKNLIDLSFNPLRHLSYSFFSPFPELOVLDLSRCEIQTIEDGAYOS 60
Db 1 MELNFKYKIPDNLPSFTKNLIDLSFNPLRHLSYSFFSPFPELOVLDLSRCEIQTIEDGAYOS 60

Qy 61 LSHSTLILITGNPIQSIALGAFSGLSLQKVAVETNLASLENPFIGHLKTILKEINVAHN 120
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Qy 181 GAFKEIRLHKLTLRNNPDSLNVMTCTIOGLAGLEVHRVLGEPFNEGULEKFDKLSALBGL 240
Db 181 GAFKEIRLHKLTLRNNPDSLNVMTCTIOGLAGLEVHRVLGEPFNEGULEKFDKLSALBGL 240

Qy 241 CNLTIEERFLAYLDYDDIIDLFNCLTNVSSFSLSVVTIERVKDFSYNFGMOHLELVNC 300
Db 241 CNLTIEERFLAYLDYDDIIDLFNCLTNVSSFSLSVVTIERVKDFSYNFGMOHLELVNC 300

Qy 301 KEGQFPTLKLSLRKLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFPGCCSQSDFGTTS 360
Db 301 KEGQFPTLKLSLRKLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFPGCCSQSDFGTTS 360

Qy 361 LKYLDLSFNGVYITMSSNFIAGLEQLEHLDFOHSNLIKQMSSEFVFLSLRNLILYLDISHTTTR 420
Db 361 LKYLDLSFNGVYITMSSNFIAGLEQLEHLDFOHSNLIKQMSSEFVFLSLRNLILYLDISHTTTR 420

Qy 421 VAFNGIFNGLSLSEVLKMAAGNSFOENFLPDIFTELRNLTFLDLSQCOLEQSPRAFNSLS 480
Db 421 VAFNGIFNGLSLSEVLKMAAGNSFOENFLPDIFTELRNLTFLDLSQCOLEQSPRAFNSLS 480

Qy 481 SLOVLNHNHNFPSLDTFPPYKCLNSLOVLDVSLNHNMTSKQEOLOHPFSSLAFLNLTOND 540
Db 481 SLOVLNHNHNFPSLDTFPPYKCLNSLOVLDVSLNHNMTSKQEOLOHPFSSLAFLNLTOND 540

Qy 541 FACTCEHOSFLOMKDQROLVVEVERMECAPPSDQKQMPVLSLNTTCQMNKTTIIGSVYLS 600
Db 541 FACTCEHOSFLOMKDQROLVVEVERMECAPPSDQKQMPVLSLNTTCQMNKTTIIGSVYLS 600

Qy 601 VLNVSVAVLVYKRYFPHMLLAGCIKYGRGENITYDAFIYSSQDEBWRNELVKNLEBGV 660
Db 601 VLNVSVAVLVYKRYFPHMLLAGCIKYGRGENITYDAFIYSSQDEBWRNELVKNLEBGV 660

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Db 661 PPOLCLHYRDFIPGVAIAANIHEGFKSRKVIIVVSOHFIQSWCIFEYIAQTWOFL 720
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Qy 781 WNPBGTVGTGCMWQEATSI 799
Db 781 WNPBGTVGTGCMWQEATSI 799

RESULT 5
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaestlein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-26

Query Match 100.0%; Score 4141; DB 10; Length 837;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 GAFKEIRLHKLTLLNNFDSLNVMTKCIQGLAGLEVHRLVLGEFNNEGNLKFKDLSALEGL 240
Db 219 GAFKEIRLHKLTLLNNFDSLNVMTKCIQGLAGLEVHRLVLGEFNNEGNLKFKDLSALEGL 278
Qy 241 CNLTIEBRRLAYLDYLDIIDLFNCLTNVSSFSVLVYTLERKXDFSYNFGMQLHLEIVNC 300
Db 279 CNLTIEBRRLAYLDYLDIIDLFNCLTNVSSFSVLVYTLERKXDFSYNFGMQLHLEIVNC 338
Qy 301 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELFLDLSRNLSLSPKCCSOSDFGTS 360
Db 301 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELFLDLSRNLSLSPKCCSOSDFGTS 360
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Db 339 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELFLDLSRNLSLSPKCCSOSDFGTS 398
Qy 361 LKYLDSLSPNGVITWSSNFIQLEQLEHLPQHSNKLKMSSEFVFLSLRNLITLIDLSHTTR 420
Db 399 LKYLDSLSPNGVITWSSNFIQLEQLEHLPQHSNKLKMSSEFVFLSLRNLITLIDLSHTTR 458
Qy 421 VAFNGIFNGLSLLEVLKMGNSFOENFLPDI FTFLRNLITFLDLSQCLEQSLPTAFNSLS 480
Db 459 VAFNGIFNGLSLLEVLKMGNSFOENFLPDI FTFLRNLITFLDLSQCLEQSLPTAFNSLS 518
Qy 481 SLOVLNMSHNNFSLDTPPYKCLNSLOVLXSLNHTSKQELQHPSSLAFLNLOND 540
Db 519 SLOVLNMSHNNFSLDTPPYKCLNSLOVLXSLNHTSKQELQHPSSLAFLNLOND 578
Qy 541 FACTCEHOSFLOWIKDOROLLVEVERMECATPSDKQMPVLSLNTCCMMNTIIGVSVLS 600
Db 579 FACTCEHOSFLOWIKDOROLLVEVERMECATPSDKQMPVLSLNTCCMMNTIIGVSVLS 638
Qy 601 VLVSVAVALVYKPYFHLMLLAGCIKYGRGENIYDAFVIYSSODEDWVRNELVNLBEGV 660
Db 639 VLVSVAVALVYKPYFHLMLLAGCIKYGRGENIYDAFVIYSSODEDWVRNELVNLBEGV 698
Qy 661 PPOLCLHYRDPFIPGVAIAANIIHEGFHKSRRVIVVVSQHFIQSRWCIFEEYIAQTWQFL 720
Db 699 PPOLCLHYRDPFIPGVAIAANIIHEGFHKSRRVIVVVSQHFIQSRWCIFEEYIAQTWQFL 758
Qy 721 SSRAGIIFIVLQVKEKTLRQOVVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 780
Db 759 SSRAGIIFIVLQVKEKTLRQOVVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 818
Qy 781 WNPBGTVGTGCMWQEATSI 799
Db 819 WNPBGTVGTGCMWQEATSI 837

RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernel, Corine
; APPLICANT: Eileen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchiernev, Velizar
; APPLICANT: Spaderma, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimiro Y
; APPLICANT: Gangoli, Baha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
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PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-038-854-135

Query Match 15.1%; Score 625.5; DB 15; Length 661;
Best Local Similarity 28.5%; Pred. No. 2.6e-41;

Matches 186; Conservative 113; Mismatches 273; Indels 81; Gaps 15;

3 INFYKIPNDLPSTKNLDLSEFNPRLHLSYSPFSPPELQVLDLSRCETQIEDGAYOSLS 62
42 LGANIEPGLPNTSECLSEFSPVLPNTQNTFSRLINLTFDLTRCOIYWHEDTFQSOH 101
63 HLTSLITLGNPQSLALGAFSGLSLOKVAVENTNLASLENFPIGHLTKLKELVANHLI 122
102 RLDTLVLTANPLIFMAETALSGPKALKLFIQTQISSIDFPIHNOXTLESLYIGSMHI 161
123 OSFKLPEYFNSLNTNENHLDLSNKLQSIYCTDLRVLHQMPNLNLSLDSINPMNFIOGA 182
162 SSIKLPKPGPT-EKLKLVDPQNNALHYLSKEWSSLOQ-ATNLNLNLNGNDIAGIEPGA 218
183 FKEIRLHLKTLRNPNDSINVMKTCIQGLAGLEVHRLVGEFENEGNEKFKDSALEGLCN 242
219 FDSAVFQSL---NGGTONLVIRFKLKNSTIQSLWIGTFEDMD-EDISAVREGICE 273
243 LTIEFRLAYLDYLDIIDLFCNLTNVSSFSVLTIERVKOFSTYNGWHLBVNCKF 302
274 MSVESINL-OKHYFENISSNTFHCPS-----GLQELDLTAVHL 310
303 GQFPT--LKLKSLKLTFTSNKGN--AFSEVDLPSEF----- 337
311 SELPSGLVGLSTLTKLVLSANKFENLCOI SASNPSTLTHLSIKGNTKLELGTGLENL 370
318 ----LDSRNGVSPFKCCSOSDPFTTSLKYLDLSFNGVITWSSN-FLGLEQLEHDPQHS 392
371 NLRELDLHDDIETSDCCNLQDRNLSHLQSLNLSNEPRLSKTEAFKCPQLELDLAF 430
393 NLKQMSFVSPLSLNLIYLDISHTTRVAFNGIENGSLSEVLKMAQNSFOENFL--PD 450
431 RLKVDASQFQNLHLKLVNLNLSHSLDISSEQLFDGRLAQHLNLQGNHFFKGIQKTN 490
451 IFTELRNLTFLDSCOCLEQSLPTAFNLSLSLOVNLMSHNNFSLDTPFYKLNLSQ--V 508
491 SLQGTGRLEILVLSLSCDSSIDQHAFTSLKMMNHVDSLHNR--LTSSIEHLSLKGIY 547
509 LDYSLNHMTSKKQELQHFPSLAFL-----NLTONDFACTCEHQSFLQWIKDQROLIV 562
548 LNLASNHISII-----LPSLLPILSQOQRTINLQNPDLDCSNITFLEWKKEMQKLE 600
563 EVERNECAITPSKQMPVLASLNTIQQANKTIIGVSVLSVLVSVAVLVYKFY 615

DB 601 DTEDTLCEPNPLNGVRISDVTLSCSMAAVGIFPLIVLVAIILITAVKYF 653

US-10-037-417-107

Sequence 107, Application US/10037417
Publication No. US20040052806A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh
APPLICANT: Alsebrook II, John P
APPLICANT: Tcherenev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verneet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Sureeh G
APPLICANT: Anderson, David M
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eileen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Query Match 15.1%; Score 625.5; DB 15; Length 661;
Best Local Similarity 28.5%; Pred. No. 2.6e-41;

Matches 186; Conservative 113; Mismatches 273; Indels 81; Gaps 15;

3 INFYKIPNDLPSTKNLDLSEFNPRLHLSYSPFSPPELQVLDLSRCETQIEDGAYOSLS 62
42 LGANIEPGLPNTSECLSEFSPVLPNTQNTFSRLINLTFDLTRCOIYWHEDTFQSOH 101
63 HLTSLITLGNPQSLALGAFSGLSLOKVAVENTNLASLENFPIGHLTKLKELVANHLI 122

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Db 102 RLDVTIYANPLIFMAETALSGPKALKHLPFIQTGISIDFLPHNOKTESLYGSNHI 161
Qy 123 OSFKLPEYFNSLNTLEHLDSNKNISQISYCTDLRYLHQWPLNLTSLDLSLNMNFIOPGA 182
Db 162 SSIKPKKPPF-EKAKVLDFOQNAIHYLSKEMMSLQO--ATNLNLANGNDIADIEFGA 218
Qy 183 FKEIRLHKLTJLRNPNFDSINWKTCTGAGLAGEVHRLVIGEFRNEGNEKFPKSALEGICN 242
Db 219 FDSAVFQSL---NFGCTQNLIVIFKGLKNSTIQSLMTGTFEDMD-EDISPAVEGICE 273
Qy 243 LTIEFRLAYLDYVDDIIDLFCNLTNVSFSLVTEIRVVDPSYNGMQLLEVNCXF 302
Db 274 MSVESINL-QKHYPFNISNTPHCS-----GLQELDITATHL 310
Qy 303 GQFPF-LKLSIKLFTFSNKGK--AFSEVDLPSEF----- 337
Db 311 SELPGLVGLSTLKLVLASANKFELCOISANFPSLTHLSIKGNTKLELGTCLENDL 370
Qy 338 ---LDSRNGISFKGCCSQSDFGTTSKLYLDLSFNGVITWSSN-FLGLEQLHLDPQHS 392
Db 371 NLRELDLHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTEAFKCPQLELLDAFT 430
Qy 393 NLKQSEFSVLSLENLVYLDISHTHTVAFNGIFNGLSLEVLKQAGNSQENFL--PD 450
Db 431 RLKVAQSPQNLHLVLNLSHSLDISSEQLPDLQHLNLTQNHFPKGNIOKTN 490
Qy 451 IFTELRNLTFDLDSQCOLEOLSPFAFNSLSLQVLNHNPNFSDTFPPYKCLNSLO--V 508
Db 491 SLQIGRLIELVLSTFCDLSIDQAFSLKMNHVDLSHR---LTSSIELSLHKIY 547
Qy 509 LDVSLNHIMTSKQELQHPSSLAPL-----NLTONDPACTCEHQSLQWIKDQROLV 562
Db 548 LNLASNHSII-----LPSLLPILSQORTNLRLQNPDLCTCSNIYFLEWKEMQKLE 600
Qy 563 EVERNECATPSDKQMPVLSLNTQNMKTIIGVSVLSVVAVLVYKPY 615
Db 601 DTEDTLCPNPLLRGVRLSDVTLSCSMAVGIFFLIVELVAIILLPAVXVF 653

RESULT 8
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaetelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-950-041-4
Query Match 14.6%; Score 603.5; DB 10; Length 784;
Best Local Similarity 27.0%; Pred. No. 1.9e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

Qy 8 IPDNLPSSTKNLDSFNPRLRHGYSFPSPFELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
Db 46 IPSGLTEAVKSLDSNNRIRITYISNSDLQRCVNLQALVLTSGINTIEBDSFSSLSLEHL 105
Qy 68 ILTGNPIQSLALGAFSGSLSLQK-----VAVENLASLENFPGHKT----- 111
Db 106 DLSYNYLSNLSSSWFKPLSLTFPLNLGNPKYLTGETSLFSHLTKQLIRVGNMDTFKI 165
Qy 112 ---LKEINVAHNLISQFKLPEYFNSLNTLEHLDSNKN-----IQSI 150
Db 166 QKRPAGITPELELEIDASDQSTE-PKSLKSIGNVSHLILMHQHLLEIPVDYVSSV 224
Qy 151 YCTDLRYLHQWPLNLTSLDLSLNMNFI--IQPGAKEIRLHKLTJLRN--NFDL-NVMK 204
Db 225 ECLERL-----DTDLDTFHSELSGTETNSL-IKKFTRNVKTI DESLFGVMK 271
Qy 205 TC--IQGLAGEVHRLV---GEFRNEGNEKFPKSALEGICNTIEFRLA--YLDVYL 257
Db 272 LNLQISGLLELEFPDCTLNGVNFRASDNDRVIDPGKVE--TLTIRLHI PRFYLKY-- 326
Qy 258 DDIIDLFCNLTNVSFSLVTEIRVVDPSYNGMQLLEVNCXKFGQFPYLKLSKRLT 317
Db 327 -DLSTLYSLTRVK-----RTVENSKYF-----LVPCLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSELEFLDSRN-----GLSFKCCSQSDFGTTSKLYLDLSFNGVI 372
Db 358 ---HLKSLLEYLDISENLMEVEYLLKNSAC---EDAPMSLQTLILRON--- 397
Qy 373 TMSNPLFLGLELELDQHSNLKQMSFVSFLSLRNLYLDISHTHTVAFNGIFNGLS 432
Db 398 ---HL---ASLEKTKG--TLTILKNTLNIDISK----- 422
Qy 433 LEVLKMGANSFOENFLPDIFTELRNLTFDLDSQCOLEOLS---PTAFNSLSLQVLNMSH 489
Db 423 -----NSFHS--METCOMPEKMKYLNLSRTHSVGCTP-----KTLEILDVSN 466
Qy 490 N--NPSISL-----TFP-YKCLNSLQVLDVSLNHIMTSKQELQHPSSL 531
Db 467 NNLNLFSLNLPQLKELYSRKMLTLPDASILPWLVLKISRNALITFSPKQLOSF-HTL 525
Qy 532 AFLNLQNDPACTCEHQSLQWIKDQROLVAV-----ERNECATPSDKQMPVLSLNT 586
Db 526 KTLFAGGNFTCSCEFLSFTQ---EQALAKVLIDMPANYLCPSPHVGQVQVDVRLS 581
Qy 587 ---QNMKTIIGVSVLSVVAVLVYKPY--FHMLLAGCIIKGR-----GENI-Y 634
Db 582 VSECHRALVSGMCCALFLLILTLGVCHRFGHLMYKMMAMWQAGRKPKASRNICY 641
Qy 635 DAFVITYSSQDEWDVNRNVLVKNLEBGPVFPOLCLHYRDPFGVALIANIIEGHFKSRKYI 694
Db 642 DAFVYSERDAYWVENIMQELFNPNPFKCLHKRDPFGKWIIDNII-DSIKSHKTV 700
Qy 695 VVVSQHFIQSRWCLFEVEIAQWTFPLSSRAGIIFIVQAKVEKTLIRQO--VELYLLSRNT 753
Db 701 FVLSSENFVKSBCRYELDFSHFLFEENNDAIILILEPEKKAIIPQFCKLRKIMNXT 760
Qy 754 YLEWEDSVLGRHIFWRRLKAL 775
Db 761 YLEWPMDEAQRGFWVNLRAAI 782

RESULT 9
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US2004005841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
```


Db 106 DLSYNYLNLSSWFKPLSLTLFLNLGNPKYKTLGETSLFSLHTLQTLRVGNMDFTFKI 165
Qy 112 -----LKEINVAHNLIQSFKLPEYPSNLTNLEHLDSNNK-----IQSI 150
Db 166 ORKDFAGLTLELEIDASDQSYE-PKSLKSIQVSHLILMKQHILLEIFVDVTSV 224
Qy 151 YCTDLRVLHQMPLNLSDLSLNPMPN--IQGAFKEIRLHKLTLRN--NFDL-NVMK 204
Db 225 ECLER-----DTDLDTFHFSLSLSTGETNSL-IKKFTFRNVKITYDESIFQYMK 271
Qy 205 TC--IQGLAGLEVHRLVLT--GEFRNGNLEKFDKSALEGICNLITIEFRLA--YLDYVL 257
Db 272 LLNQISGLLEBFDCTLNGVGNFRASDNDRYIDGKVE--TLTIRRLHPRFLYF-- 326
Qy 258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGMQLHELVNCKFGQFPTLKLKSLRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSOSDFTTSLKYLDLSFNGVI 372
Db 358 -----HLKSLLEYDLSENLMVEEYLKNSAC--EDAMPSTLQTLILRN-- 397
Qy 373 TMSNPLGLBQLLEHDFHNSNLKOMSEFSVFLSLRNLYLDISHHTHTVAFNGIFNGISS 432
Db 398 -----HL-----ASLEKTEG--TLTILKLNLTNIDISK----- 422
Qy 433 LEVLKMGNSFOENFLPDIPTELRNLTFLDLSOCCOLEBS--PTAFNSSLQVLNMSH 489
Db 423 -----NSFHS--METCOWPEKMKYLNLSSTRHISVTCIP-----KTLIEDVSN 466
Qy 490 N--NPFSLD-----TFP--YKCLNSLOVLDYSLNHTMTSKQELCHPSSL 531
Db 467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVLIKISRNALITFSKQOLDSF-HTL 525
Qy 532 AFLNLTQNDPACTCEHOSFLOMIKQROLVENV-----ERMECATPSDKOGMPVLSLNT 586
Db 526 KTLGAGNNFICSCFSLFTQ-----EQALAKVLIDMPANYLSDSPSHVHQOVQDVRLS 581
Qy 587 ---COMNKTIIGVSVLSLVVSVAVLVYKFY--FHMLLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRTALVSGMCALFLILTLTGVLCHRFHGLMWMWMMAMLAQARKPRKAPSRLICY 641
Qy 635 DAFVYSSQDEBWRNELVKNLEBGPVFPOLCLHTRDIPGVAYIAANIHHGFKSKRYI 694
Db 642 DAFVYSERDAYWVENLMVOELENFNPFKLCHKRDPDPGKWIIDNII-DSIEKSHKTV 700
Qy 695 VVVSQHFIQSRWCIFEYEIAQTWQFLSRAGIIFIVLOKVEKTLRQO-VELVRLSRNT 753
Db 701 FVLSNFVKSCKEYELDFSHRFLFDENNDAIILILEPIEKALPQRFCKLRKIMNTKT 760
Qy 754 YLEWEDSVLGRHIFWRRLRKAL 775
Db 761 YLEWPMDEAQRGEGFWNLRAAI 782
RESULT 11
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732,563
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-732-563-4
Query Match 14.5%, Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 2,36-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;
Qy 8 IPDNLPTSTKNLDSFNPRLHLSYSPFPELOVLDSRCEIOTIEDGAYQSLSHSTL 67
Db 46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVYTSNGINTIEEDSPSSGSLHL 105
Qy 68 ILTGNPISQALGAFSGLSLQK-----VAVENNLSLENFPGLHKT----- 111
Db 106 DLSYNYLNLSSWFKPLSLTLFLNLGNPKYKTLGETSLFSLHTLQTLRVGNMDFTFKI 165
Qy 112 -----LKEINVAHNLIQSFKLPEYPSNLTNLEHLDSNNK-----IQSI 150
Db 166 ORKDFAGLTLELEIDASDQSYE-PKSLKSIQVSHLILMKQHILLEIFVDVTSV 224
Qy 151 YCTDLRVLHQMPLNLSDLSLNPMPN--IQGAFKEIRLHKLTLRN--NFDL-NVMK 204
Db 225 ECLER-----DTDLDTFHFSLSLSTGETNSL-IKKFTFRNVKITYDESIFQYMK 271
Qy 205 TC--IQGLAGLEVHRLVLT--GEFRNGNLEKFPKSALEGICNLITIEFRLA--YLDYVL 257
Db 272 LLNQISGLLEBFDCTLNGVGNFRASDNDRYIDGKVE--TLTIRRLHPRFLYF-- 326
Qy 258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGMQLHELVNCKFGQFPTLKLKSLRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSOSDFTTSLKYLDLSFNGVI 372
Db 358 -----HLKSLLEYDLSENLMVEEYLKNSAC--EDAMPSTLQTLILRN-- 397
Qy 373 TMSNPLGLBQLLEHDFHNSNLKOMSEFSVFLSLRNLYLDISHHTHTVAFNGIFNGISS 432
Db 398 -----HL-----ASLEKTEG--TLTILKLNLTNIDISK----- 422
Qy 433 LEVLKMGNSFOENFLPDIPTELRNLTFLDLSOCCOLEBS--PTAFNSSLQVLNMSH 489
Db 423 -----NSFHS--METCOWPEKMKYLNLSSTRHISVTCIP-----KTLIEDVSN 466
Qy 490 N--NPFSLD-----TFP--YKCLNSLOVLDYSLNHTMTSKQELCHPSSL 531
Db 467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVLIKISRNALITFSKQOLDSF-HTL 525
Qy 532 AFLNLTQNDPACTCEHOSFLOMIKQROLVENV-----ERMECATPSDKOGMPVLSLNT 586
Db 526 KTLGAGNNFICSCFSLFTQ-----EQALAKVLIDMPANYLSDSPSHVHQOVQDVRLS 581
Qy 587 ---COMNKTIIGVSVLSLVVSVAVLVYKFY--FHMLLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRTALVSGMCALFLILTLTGVLCHRFHGLMWMWMMAMLAQARKPRKAPSRLICY 641
Qy 635 DAFVYSSQDEBWRNELVKNLEBGPVFPOLCLHTRDIPGVAYIAANIHHGFKSKRYI 694
Db 642 DAFVYSERDAYWVENLMVOELENFNPFKLCHKRDPDPGKWIIDNII-DSIEKSHKTV 700
Qy 695 VVVSQHFIQSRWCIFEYEIAQTWQFLSRAGIIFIVLOKVEKTLRQO-VELVRLSRNT 753
Db 701 FVLSNFVKSCKEYELDFSHRFLFDENNDAIILILEPIEKALPQRFCKLRKIMNTKT 760
Qy 754 YLEWEDSVLGRHIFWRRLRKAL 775
Db 761 YLEWPMDEAQRGEGFWNLRAAI 782
RESULT 12
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.

APPLICANT: Ghosh, Tarnu K.
APPLICANT: Fink, Jason R.
TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
FILE REFERENCE: 58182US004
CURRENT APPLICATION NUMBER: US/10/732,796A
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent version 3.2
SEQ ID NO 4
LENGTH: 784
TYPE: prt
ORGANISM: Homo sapiens
US-10-732-796A-4

Query Match 14.5%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.3e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

8 IPDNLPESTKNDLSPNRLHLSYSPFPELQVLDLSRCEIQTEGAYQSLSHLSTL 67
46 IPSGLTEAVKSIDLSNNRITYISNSDLQRCVNLQALVLTSGINTIEBDSFSSLSLEHL 105
68 ILTGPIQSLALGAFSGLSLQKL-----VAETNLASLENPIGHLKT----- 111
106 DLSYVLSNLSWPKPLSSLFLNLGNPKYTLGETSLFSHLTKQLRLRVGNMDTFKI 165
112 -----LKELVANHLIQSPFLPEFSNLTNLEHLDSNK-----IOGI 150
166 QKDRAGLTFLEBELIDASDLOSYE-PKSLKSIQVSHLILHMKGHILLLEIFVDVTSSV 224
151 YCTDLRVLHQPMLNLSDLSLPMNF--IQGAFKEIRLHKLTLRN--NPSL-NVWK 204
225 ECLER-----DTDLTFHSELSTGETNSL-IKKFPRNVKITDESIFQVWK 271
205 TC--IQGLAGLEVHRLV---GEFRNBEGLKFDKSALEGLCNLTIEERLA--YLDYYL 257
272 LMQISGLLELEFDDCTLNGVGNFRASDNDVDPGKVE--TLTIRLHLPREFLYF-- 326
258 DDIIDLFNCLTNVSSFSLSVTVIERKDFSYNFGMHLELVNCKRGQFPYLKLSKRLT 317
327 -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLSQ----- 357
318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSPKCCSOSDFTTSLKYLDLSPNGVI 372
358 -----HLKSLLEYLDSENLWVEYLKNSAC--EDAMPSLQTLILQN-- 397
373 TMSNFFLGLEQLEHLDFOHSNLKQWSEFVSFLSNLILYLDISHHTVAENGINGLSS 432
398 -----HL--ASLEKTEG--TLTLTKLTLNIDISK----- 422
433 LEVLKMGNSFOENFLPDIFTELRLNLFPLDSOCOLEOLS--PTAFNLSLSLQVLYNMGS 489
423 -----NSFHS--MPETCQMPKMKYLNLSSTRHSVTGCI P-----KTLLEILDVSN 466
490 N--NFFSLD-----TFP--YKCLNSLQVLDYLSNHTIMTSKQELQHPFSSL 531
467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVKISRNLITPFSKQDLDSF--HTL 525
532 AFLNLTQNDPACTGCHOSFLQWIKQROLVAV-----ERMBCATPSDKQGPVLSLNT 586
526 KTLBEGANNFISCEFLSFTQ-----EQQALAKVLIDWPANYLSDSPSHRGOQVODVRUS 581
587 -----CQMKNTIIGSVLSVLSVAIVLVYKFP--FHMLLAGCIKGR-----GENI-Y 634
582 VSECHRTALVSGMCCALLILILITGVLCRFHGLMTKMMAMWLAKKRPKAPSRNLCT 641
635 DAFVLYSSQDEDMVRENELVKNLEEGVPPOLCLAYEDFI PGVAIAANIIEGFRKSRXY 694
642 DAFVYSERDAYWENLWVQELLENFNPFPKLCIHKRDPFGKWLIDNII--DSIKSHKIV 700
695 VVVSQHFTOSRWCIFETAYLAQTWQFLSSRAGIIFVYLQVVEKTLRQO--VELYRLISRT 753
701 FVLSENFVKSWECKYELDPSHFLPDENNDAIILILEPIEKKALPQRCKLRKIMNTXT 760

QY 754 YLEMEDSVLGHIFWRRLKAL 775
DB 761 YLEMPMEADQREGFVNLRAAI 782

RESULT 13
US-10-741-600-1390
Sequence 1390, Application US/10741600
Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1390

LENGTH: 784

TYPE: prt

ORGANISM: Homo sapiens

US-10-741-600-1390

Query Match 14.5%; Score 602.5; DB 17; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.3e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

8 IPDNLPESTKNDLSPNRLHLSYSPFPELQVLDLSRCEIQTEGAYQSLSHLSTL 67
46 IPSGLTEAVKSIDLSNNRITYISNSDLQRCVNLQALVLTSGINTIEBDSFSSLSLEHL 105
68 ILTGPIQSLALGAFSGLSLQKL-----VAETNLASLENPIGHLKT----- 111
106 DLSYVLSNLSWPKPLSSLFLNLGNPKYTLGETSLFSHLTKQLRLRVGNMDTFKI 165
112 -----LKELVANHLIQSPFLPEFSNLTNLEHLDSNK-----IOGI 150
166 QKDRAGLTFLEBELIDASDLOSYE-PKSLKSIQVSHLILHMKGHILLLEIFVDVTSSV 224
151 YCTDLRVLHQPMLNLSDLSLPMNF--IQGAFKEIRLHKLTLRN--NPSL-NVWK 204
225 ECLER-----DTDLTFHSELSTGETNSL-IKKFPRNVKITDESIFQVWK 271
205 TC--IQGLAGLEVHRLV---GEFRNBEGLKFDKSALEGLCNLTIEERLA--YLDYYL 257
272 LMQISGLLELEFDDCTLNGVGNFRASDNDVDPGKVE--TLTIRLHLPREFLYF-- 326
258 DDIIDLFNCLTNVSSFSLSVTVIERKDFSYNFGMHLELVNCKRGQFPYLKLSKRLT 317
327 -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLSQ----- 357
318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSPKCCSOSDFTTSLKYLDLSPNGVI 372
358 -----HLKSLLEYLDSENLWVEYLKNSAC--EDAMPSLQTLILQN-- 397
373 TMSNFFLGLEQLEHLDFOHSNLKQWSEFVSFLSNLILYLDISHHTVAENGINGLSS 432
398 -----HL--ASLEKTEG--TLTLTKLTLNIDISK----- 422
433 LEVLKMGNSFOENFLPDIFTELRLNLFPLDSOCOLEOLS--PTAFNLSLSLQVLYNMGS 489
423 -----NSFHS--MPETCQMPKMKYLNLSSTRHSVTGCI P-----KTLLEILDVSN 466
490 N--NFFSLD-----TFP--YKCLNSLQVLDYLSNHTIMTSKQELQHPFSSL 531
467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVKISRNLITPFSKQDLDSF--HTL 525
532 AFLNLTQNDPACTGCHOSFLQWIKQROLVAV-----ERMBCATPSDKQGPVLSLNT 586
526 KTLBEGANNFISCEFLSFTQ-----EQQALAKVLIDWPANYLSDSPSHRGOQVODVRUS 581

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QY 587 ---COMKTIIGVSVLSVSVAVLVYKPY--FHLMLAGCIYGR-----GENI-Y 634
DB 582 VSECHRTALVSGMCCALFLLILLTGVLCHRPHGLMYKMMWAMWAOAKRPRKAPSRLICY 641
QY 635 DAFVYSQDEDDWVNEVLKQNEBQVPPOLCLHYRDPFGVALAANIHEGFHRSRYI 694
DB 642 DAFVYSERDAYWVENLWQLENNPPFKLCHKRDPFGKMIIDNII-DSIEKSHKTV 700
QY 695 VVVSQHFIOSRWCIFEYEIAQTMQFLSRAGIIFIVLQKVEKTLRQO-VELYRLLSRNT 753
DB 701 FVLSNFVKSSEWCXYELDFSHFRLPDENNDAAIILILEPIEKKAIPQRFCKLRKIMTKT 760
QY 754 YLEWEDSVLGRHITWRRLRKAL 775
DB 761 YLEWPMDEAQREGFWVNLRAAI 782

RESULT 14
US-10-741-600-1391
; Sequence 1391, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1391
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1391

```

```

Query Match 14.5%; Score 602.5; DB 17; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.3e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

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```

QY 8 IPDNLFPSTKNLDSFNPRLHLSYSPFSPPELOVLDSRCCEIOTIEDGAVQSLSHTL 67
DB 46 IPSGLTEAVKSLDLSNNRITITYSNSDLQRCVNLQALVLTSGNITIEEDSPSSLSLEHL 105
QY 68 ILTGNPIQSIALGAFSGLSLOKL-----VAVENTLASLENFPIGHLKT----- 111
DB 106 DLSVNYLSNLSWSFKPLSLTFNLGNPYKTLGETSLFSHLTKQLLRVGNMDFTKI 165
QY 112 -----LKELVANHLIOSFKLPYFYSNLTLNLEHLDSNKK-----IQSI 150
DB 166 QKDFAGLTFLELEIDASDLSYE-FKSLKSIQVNSHLIHKQHILILEIFVDVTSV 224
QY 151 YCTDLRVLHQPMLNLDSLNSPNMF--IQGAKKEIRLHKLTLRN--NPDSL-NYMK 204
DB 225 ECLERK-----DTDLDTFHFSBLSTGETNSL-IKKEFYRNVKIDTESLFQVWK 271
QY 205 TC--IOGLAGLEVRLVL--GEFNNENLEKFKDSALEGICNLITIEEFRLA--YLDTYL 257
DB 272 LLNQSGLELEFDDCTINGCNFPAANDRVIDGKYE--TLTIRLHLHPRFTLYF-- 326
QY 268 DDIDLFNCLTNVSSFSVSVTIEVKOPSYNFGQHLVELVCKFGQFPPTLKLSLKRLT 317
DB 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCLLSQ----- 357
QY 318 FTSNKGNAFSEVDLPSLEFLDSRN-----GLSPKGCOSQDFCTTSKXLYLDSFNQVI 372
DB 358 -----HKSLEYLDLSNLWVEYLKNSAC--EDAMPSLQTLILRQN-- 397
QY 373 TMSNFIQLIEQLEHLDPOHSNLSKQMSFVSFLSLNLTYLDSISHTHTVAENGIFNGLS 432
DB 398 -----HL-----ASLEKTEG--TLTTLTKNLINIDSK----- 422
QY 433 LEVLMAGNSFOENLPDIPTLELRNLTPLDLSQCLBOLS--PTAFNSLSLQVLANMSH 489

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DB 423 -----NSFHS--MPETCQMPKMKYLNLSSTRHSVTCIP-----KTLBILDSN 466
QY 490 N--NPFSLD-----TFP-YKCLNSLOVLDVSLNHMTSKQELQHPSSL 531
DB 467 NNILFSLNLPQLKELYISRNKMTLTPDASLLPMLVLKTSRRAITTFSSQOLDSF-HTL 525
QY 532 AFLNLTQDFACTGSEHOSFLOWIDORQLVEV-----ERMECATPSDKQMPVLSNIT 586
DB 526 KTLKAGGNF:CSCEPISFTQ-----EQALAKVLIDMPANVLCOSPSHVRQOYQDVRLS 581
QY 587 ---COMKTIIGVSVLSVSVAVLVYKPY--FHLMLAGCIYGR-----GENI-Y 634
DB 582 VSECHRTALVSGMCCALFLLILLTGVLCHRPHGLMYKMMWAMWAOAKRPRKAPSRLICY 641
QY 635 DAFVYSQDEDDWVNEVLKQNEBQVPPOLCLHYRDPFGVALAANIHEGFHRSRYI 694
DB 642 DAFVYSERDAYWVENLWQLENNPPFKLCHKRDPFGKMIIDNII-DSIEKSHKTV 700
QY 695 VVVSQHFIOSRWCIFEYEIAQTMQFLSRAGIIFIVLQKVEKTLRQO-VELYRLLSRNT 753
DB 701 FVLSNFVKSSEWCXYELDFSHFRLPDENNDAAIILILEPIEKKAIPQRFCKLRKIMTKT 760
QY 754 YLEWEDSVLGRHITWRRLRKAL 775
DB 761 YLEWPMDEAQREGFWVNLRAAI 782

```

```

RESULT 15
US-10-145-014-23
; Sequence 23, Application US/10145014
; Publication No. US20020168755A1
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: J806010D
; CURRENT APPLICATION NUMBER: US/10/145,014
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/982,308
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-014-23

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Query Match 14.5%; Score 599.5; DB 13; Length 784;
Best Local Similarity 27.0%; Pred. No. 4e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

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```

QY 8 IPDNLFPSTKNLDSFNPRLHLSYSPFSPPELOVLDSRCCEIOTIEDGAVQSLSHTL 67
DB 46 IPSGLTEAVKSLDLSNNRITITYSNSDLQRCVNLQALVLTSGNITIEEDSPSSLSLEHL 105
QY 68 ILTGNPIQSIALGAFSGLSLOKL-----VAVENTLASLENFPIGHLKT----- 111
DB 106 DLSVNYLSNLSWSFKPLSLTFNLGNPYKTLGETSLFSHLTKQLLRVGNMDFTKI 165
QY 112 -----LKELVANHLIOSFKLPYFYSNLTLNLEHLDSNKK-----IQSI 150

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Db 166 QKDPAGLTPEELIEDSDLOSFE-PKSLKSIQUNVSHILHMKOHILLEIFVDVTSV 224
QY 151 YCTDLRVLHQBPLNLISDLISLPMNF--IQGAFKEIRLHKLTLRN---NPDSL-NVMK 204
Db 225 ECLBEIR-----DTRDITHEFSLSTGEITNSL-IRKFTFRNVKITDESILQVWK 271
QY 205 TC--IQGLAGLEVHRLVL--GEFNEGNLEKFKSALEGLCNLTIEEFRLA--YLDYYL 257
Db 272 ILNQISGLLELEFPDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIIPRYLFY-- 326
QY 258 DDIILFNCLTNVSSFSVSVTIERVKDSYVFGWQHLELVNCKFGQFPTLKLKSKRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKVE-----LVPCLLSQ----- 357
QY 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSQSDFGTTSKLYDLSEFNGVI 372
Db 358 -----HLKSLEYLDLSNLWEEYLNKSAC-----EDAMPSLQTLILRN--- 397
QY 373 TWSNPFLEGLEHLDFOHSNLKQMSSESVFLSNRLIYDISHTHTRYAENGIFNGLS 432
Db 398 -----HL-----ASLEKTGE--TLTLKNLTNIDISK----- 422
QY 433 LEVLAMAGNSFOENFLPOLFTELRNLTFLDLSQCLEQLS---PTAFNSLSLOVLNMSH 489
Db 423 -----NSFHS--MPEYQWPKWKYLNLSSTRHSVTGCI-----KLEILDVSN 466
QY 490 N--NPFSLD-----TFP--YKCLNSLOVLDYSLNHINTSKQELQHPSSL 531
Db 467 NNLNLPSLNLPOLKELYISRNKLTMLPDASLLPMLLVLKISRRAITTFESKQDLSF-HTL 525
QY 532 AFLNLTQNDFACTCEHQSFLOMIKQORQLLEV-----ERMECATPSDKQMPVLSLNT 586
Db 526 KTLBAGNNFICSCEPLSFTQ---EQALAKVLIWPNANYLCDSPSHVRGOQVDVRLS 581
QY 587 ---QOMNTIIGVSVLSVSVAVLVYKFY--FILMLACICKYR-----GENT-Y 634
Db 582 VSECHRIALVSGMCCALFLILLTGLCHRFGHLMYKMMWMLQAKRKPRAKPSRNICY 641
QY 635 DAFVIYSSODEDMVNRNELVKNLEEGVPPOLCLHYRDFIPGVAIANIIEGFFHKSRYI 694
Db 642 DAFVSYSEBDAYWERNLWQELFNRPFKLCIHKRDFIPGKIIDNII-DSIEKSHKTV 700
QY 695 VVVSCHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLOKVEKTLRQO--VELYRLLSRNT 753
Db 701 FVLSNPFVSEWCKYELDFSHPRLPDENNDAILILBPIEKKAIPQRFCKLRKIMNTKT 760
QY 754 YLEWEDSVLGRHIFWRRLKAL 775
Db 761 YLEWPEDEAQRGEGFWNLRAAI 782

Search completed: March 12, 2005, 20:27:52
Job time : 74.7097 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 20.6156 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-4

Sequence: 1 MELNFFYKIPDNLPTSTKLD.....SNPEGTGTCGNMQEATSI 799

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

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Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	625.5	15.1	661	2	I56258	RP105 - mouse
2	474	11.4	786	2	T08664	Toll protein-like
3	452	10.9	1097	2	A29943	Toll protein precu
4	421	10.5	1385	2	T13852	gene wheeler prote
5	433	10.2	1385	2	T13887	tlr protein - fruti
6	392	9.5	1066	2	T15664	hypothetical prote
7	333.5	8.1	1134	1	A29944	chaoptin precursor
8	309	7.5	605	2	UC5299	insulin-like growt
9	302	7.3	853	2	T17461	disease resistance
10	297	7.2	605	2	A41915	insulin-like growt
11	296	7.1	1531	2	T42218	slit-1 protein hom
12	292	7.1	994	2	H95510	probable disease r
13	291	7.0	845	2	T07039	Hcr9-0 protein - t
14	290	7.0	605	2	JC1282	insulin-like growt
15	290	7.0	855	2	T07015	Cf-4A protein - to
16	289.5	7.0	603	3	T24315	hypothetical prote
17	289.5	7.0	1112	2	T10504	disease resistance
18	289	6.9	855	2	T17460	disease resistance
19	287.5	6.9	662	2	S42799	garp precursor - h
20	284.5	6.9	907	2	JB016	orphan G protein-c
21	284	6.9	603	2	JC6128	insulin-like growt
22	284	6.9	907	2	UG0133	G protein-coupled
23	281.5	6.8	622	2	JC7973	syntleurn - human
24	281	6.8	1134	2	T04587	hypothetical prote
25	280	6.8	890	2	T00800	disease resistance
26	278.5	6.7	1019	2	C96519	probable disease r
27	276.5	6.7	768	2	T17462	disease resistance
28	276	6.7	983	2	G84524	probable disease r
29	276	6.7	1027	2	B85089	receptor protein K

30	270.5	6.5	1523	2	T10363	MEG5 protein - ra
31	270	6.5	1143	2	TL9635	hypothetical prote
32	266.5	6.4	1091	2	A58532	glial cell membran
33	266.5	6.4	1784	2	C96615	hypothetical prote
34	265.5	6.4	863	2	A55173	cf - 9 protein precu
35	265	6.4	910	2	G84648	probable disease r
36	264.5	6.4	766	2	T01817	hypothetical prote
37	264	6.4	1469	2	B36665	slit protein 2 pre
38	264	6.4	1480	2	A36660	slit protein 1 pre
39	262.5	6.3	967	2	T48210	hypothetical prote
40	261.5	6.3	1051	2	T13174	gpi50 protein - fr
41	260.5	6.3	1109	2	T18536	receptor-like prot
42	259	6.3	1029	2	T00712	protein kinase hom
43	257	6.2	738	2	T19938	hypothetical prote
44	254	6.1	771	2	T02565	disease resistance
45	253.5	6.1	991	2	T52400	receptor-like prot

· ALIGNMENTS

RESULT 1

RP105 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I56258
 R:Miyaake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
 J: Immunol. 154, 3333-3340, 1995
 A:Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a membrane protein.
 A:Reference number: I56258; MUID:95204928; PMID:7897216
 A:Accession: I56258
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-661 <RSS>
 A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:G761711; PIDN:BAA07043.1; PID:G761711

[illegible]

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QY 451 IFTLRNLTFLDLSGQCBQLSPFAPNSLSLQVLMNHNPFSLDTPPYKCLNSLQ--V 508
Db 491 SLQGTGRLEIVLWLSFCDLSSIDQAFSLKMNHNHDLSHNR---LTSSIEALSHKGIY 547
QY 509 LDVSLNHNMTSKKQGLQHPSSLAFL-----NLQNQPACTCEHOSFLOWKQDROLLV 562
Db 548 LNLASNHSII-----LPSLLPILSOQRTNLNQNPLDCTCSNYFLFMYKEMQKLE 600
QY 563 EVERMECATPSDKQMPVLSLNTIQNMKTTIIGVSVLSVLSVVAVLVYKRY 615
Db 601 DTEDTLCENPILRGVRLSDVTLSCSMAVGIFILVFLVAILLIFAVKXF 653

RESULT 2
T08664
Toll protein-like receptor DKFPZ54710610.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08664
R:Pousterka, A.; Klein, M.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16466
A:Accession: T08664
A:Molecule type: mRNA
A:Residues: 1-786 <PDB>
A:Cross-references: UNIPROT:Q15399; EMBL:AL050262
A:Experimental source: fetal brain; clone DKFPZ54710610
C:Genetics:
A>Note: DKFPZ54710610.1

Query Match 11.4%; Score 474; DB 2; Length 786;
Best Local Similarity 25.5%; Pred. No. 4.2e-22;
Matches 204; Conservative 130; Mismatches 303; Indels 162; Gaps 32;

QY 83 SGLSLQKLVAVETLNLASLENFPIGHLKT-----LKELVANVNLISQFLLPEYFENL 134
Db 34 NGLIIVPDDLSQKTIILNISQVYSELMTSDLSLSKIRILISNRLOYDISFKRN- 92
QY 135 TNLHLDLSSNKKIQSIYCTDLRLVHQMPPLNIS-LDLSLPMNFI-----QPGAFKEIRIAH 189
Db 93 QELVYLDLSDHNLVXISC-----HPTVNLKHLDFSNAPDALPICKERQNMQLKFL 144
QY 190 KLTILRNNDLSLNMVMTCTCQGLAGLEVHRLV-----GFRNKGULEKFDKSALEGLCNL 243
Db 145 GLS-----TTHLEKSVLPILAHNLISKVLVGLGETYGEKEDPGGLQDFNTESLHIVPT 198
QY 244 TIEERFLAVLDYLDIIDLFNCLTNVSSFSLVATIERVKDFSYNFGQHLVNCNFKG 303
Db 199 NKE-----HFHLDVSVKTYANIELSNIKCVLEDSKCSYFLSLIAKIQ 241
QY 304 QPPTLKLSLKRLLPFTSNK-----GNAFSEVDLP-SLEFLDLSRNGLSFKG 349
Db 242 TNPKLSSLLANNIETFTWNSFRIQLVHTTWYSSISNVKIQGLDPRDPYSTSLKA 301
QY 350 CCSQ---SD-----FGTTSLK-----YLDLSFNGVI-- 372
Db 302 LSIHQVSDVDFGFPQSYIYEIFSNMNIKNFTVSGTRVMYMLCPSKISPFLLHDFSNMLLT 361
QY 373 -TMSNFGLEBOLBHLDPQHSNLKOMSEFS-VFLSLRNLIYLDISHTRVAFN---GIF 427
Db 362 DTVEVNCCHLELELTLLIQMNQKLKSLAEMTTQMKSLQQLDIS-QNSVSYDEKKKDC 419
QY 428 NGLSLLEVLMKAGNSFOENF--LPDIFTELRLNFLDLSQOCOLBOLSPTAFNLSLSLQV 484
Db 420 SWTSLSLILMNSNSNLTDTIPRCLEP-----RIKVLDLHSKIKISI-PKQVVKLEALQ 472
QY 445 LNMSSNNFSLDTPF---YKCLNSLOVLDVSLNHNMTSKQELQHPSSLAFLNLTOND 540
Db 473 LNVAVN---SLTDLFGCGSFSLSVLIIDHNSVSHPSADPFQSCQKMS---IKAGNP 525
QY 541 FACTEHOSFLOWKQDROLLVEY-----ERMECATPSDKQ-----MPVLSLNTIQ 588
Db 526 FOCTELSEBF---VKNIQVSSSEVLEGMFDSYKCPSSYRGTLTLKDFHMSLSNITLL 582
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QY 589 MNKTIIGVSVLSVLSVVAVLVYKFFPHMLLAGCIKRYGENI-----YDAEV 638
Db 583 IVTIIVATMLVLAIVTSLICYLDLPYTLR--NVCOMTQTRRABRNPILEELQRLQFHAFI 641
QY 639 IYSSODEWYVWNEVLNKLLE-EGVPPFQCLHYRPFIVGVALAANIHEGFHKSRYVYV 697
Db 642 SYSGHDSFWVWNEILLPNIKEGGM--QICLERNFVPQKSIIVENII-TCLERSYKSLFVL 697
QY 698 SQHFPIOSRWCIPEYEIAQTMQFSLSRAGIIPYIVQKV-EKTLNQOVELYLLSRNTYLE 756
Db 698 SPNFVQSWCHYELYPFAHNLPHGGSNSLILILEPPIQYSIPSSYHKLKSLMARRTYLE 757
QY 757 WEDSVLGHIFWRRLKRL 775
Db 758 WPKESKRGGLFWANLRAAI 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C:Genetics:
A:Gene: FlyBase:T1
A:Cross-references: FlyBase:FBgn0003717
C:Keywords: transmembrane protein
P11-17/Domains: signal sequence #status predicted <SIG>
P18-1097/Product: Toll protein #status predicted <MAT>

Query Match 10.9%; Score 452; DB 2; Length 1097;
Best Local Similarity 24.1%; Pred. No. 1.6e-20;
Matches 224; Conservative 140; Mismatches 329; Indels 238; Gaps 42;

QY 8 IPDNLPSSTKN---LDLSPNLRHLGSYSPFPELOVLDSRCEIQTIEDGAYQSLSHL 64
Db 165 IPANILDTMRNLSHLELRAN-IEEMPSHLFDLLENLSIEFGSNKLRQMPPRGIFGKPKL 223
QY 65 STLLTNGPIOSLALGAFSGLSLQKLVAVETNLASLENFPIGHLKTLELVANHLIOS 124
Db 224 KQLNLMNSQNLNLTQKDFEGATSVLGIDIHNGIEQLPHDFAHLTVVTDINLSANLFRS 283
QY 125 FKLPE-YFSNLTNLEHDLSSNKKIQSIYCTDLRLVHQMPPLNISLSDLSLPMNFIQPGAF 183
Db 284 --LFGQLEFDHAKHLEVRALMNKRYPLATLPBRALRANQPELOIILRLAEQLQ---PDDL 337
QY 244 TIEERFLAVLDYLDIIDLFNCLTNVSS--FS---LVSTYIIR-----VDFPSINF 290
Db 393 T-----DLRLD-----NLTLGISGDIFFSNLGNLVTLVMSRNLRTIDSRFAFVSTN 438
QY 184 KEIRLKLTLNNDPSLNMVMTCTCQGLAGLEVHRLVGEFRNENGLKFDKSALEGLCNL 243
Db 338 FE---HSQTINISLIGNNLKTLPLATLEHQVNLSLDLSNN--RLTHLPDLSLFAHTTNL 392
QY 244 TIEERFLAVLDYLDIIDLFNCLTNVSS--FS---LVSTYIIR-----VDFPSINF 290
Db 393 T-----DLRLD-----NLTLGISGDIFFSNLGNLVTLVMSRNLRTIDSRFAFVSTN 438
QY 291 GMDHLEL-----VNCKRGQPP---TLKLSLKLTLFTSNKGNAFS 328
Db 439 GLRHLHLDHNDIDIQPLDIDMLQVINSPPGYVHGGLITLALRK-NSIIFYNDMKKTM 497
QY 329 EVDLPSEFLDLSRNGLSFKGCCSQSDFGTSLKYLPLSPNGVITWSSNFGLEBOLBHD 388
Db 498 Q-----LRELDLSYNNIS-----SLGYEDLAF-----LSQNR-----HVN 528
QY 389 FOHSNLKOMS-BFVSPLS--LRNLIIYLDISHHT-----TRVAPNGIFNGL----- 430
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Db      529 MTHANKIRIALPBDVHLEGVYNNLVHVDLNDNPLVDCCTIIMFQIVGVHKHPQYSROF 588
Qy      431 -----SSLEV 435
Db      589 KLRTRLVYCSQPNVLEGTFRQIEPTQLICPLDFSDPRERKCPRGCNCHVATYDQALVI 648
Qy      436 LKMAQNSFOENFLPDIFTELRLVTELDL-----SQOLEQLSPFAFNSLSLQVLMNSH 490
Db      649 NCHSGNLTFRPLPMLH---KMQMLMELHLENNTLRLPSANTPGVESVTS---LHLAGN 702
Qy      491 NEFSLDLTFPYKCLNSLOVLVYSLNHTMTSKKQELQHPSSLAFLN-----LTON 539
Db      703 NLTSLVDVQLP---TNLHLDISMNHL-----QMLN--ATVAGFLNRTMKRSVKLSGN 751
Qy      540 DFACTCEHOSFLOMICKDQRLVEVERMECATPSDKGMPVLSTNTCOMNKTII-IGVSV 598
Db      752 PAMCCTAKPLLLFQDNPERIGDRNEMCVAAEMPTRELVSTNDICAEKGVFIALLAV 811
Qy      599 ---LSLVVSVAVLVYKF-----YHMLLAGCIKYRGENT---YDAFVIYSS 642
Db      812 VIALTGLLAGFPAALYYKQTEIKIMLVANHL-----WFTBEDLDKDKKFDAFISYSH 867
Qy      643 QDEDMVRNELVKNLEEGVPPPOLCLAYRPFICGVAIAANIHEGFHKSRYVWVSQHPI 702
Db      868 KDQSFIEDLVLPOLHEGPKFQLCVHERDVLVGHIPENIM-RVADSRRTIIVISQNEI 926
Qy      703 OSRWCIPEYEIAQTOFQLSSRAIIFIV---LQVEKTLRQOVELYRLSHNTYLEMD 759
Db      927 KSEMARLEFRARHRAINLNGRSRIIVIIYSDIGDVK--LDEELKAY--LKNATYILKMD 982
Qy      760 SVLGRHIFWRRLKALLDQKSNMPEGTG 790
Db      983 P-----WEMDKLRFALPHRR---PVGINGNG 1005

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13852
R.Eldon, E.; Kooyer, S.; D'aveyln, D.; Duncan, M.; Lawinger, P.; Boctas, J.; Bellen, H.
Development 120, 885-899, 1994
A.Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A.Reference number: Z17796; MUID:95324375; PMID:7600965
A.Accession: T13852
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1189 <ELD>
A.Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:G415682; PID:G1019104; PIDN:AAA7920
C.Genetics:
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Query Match      10.5%; Score 433; DB 2; Length 1389;
Best Local Similarity 24.4%; Pred. No. 3.4e-19;
Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

Qy      19 LDSLNPPLRHGYSYFSPPELOVLDLSRCEIQTIEDGAYQSLSHSTLILGNPIQSLA 78
Db      338 LNLNNALTRISQKTFKELYFLQIIDMRNNSIGHIEGAFPLPYNLHTNLNENRLLHTID 397
Qy      79 LGAFSGLSLOKLVAVETMLASL-ENFPIGHLKTLKELVAHNLIOFPLPEYFSNLTVL 137
Db      398 NRIFGLYLVTKL-TLNNLVSVESQARNCSDLKEIDLSN--OLTEVPAVVDLSML 454
Qy      138 EHLDSLNRIGIYCTDLVTLQOMPLNT-----SLDLSINPMNF 177
Db      455 KTLIDGENDISPEKNTFRNLNQLTGLRIDNRIGNITVGMFODLPRLSVLNLAKRRIOS 514
Qy      178 IQPGAF-KEIRLHLKTLRNPFDSLNMKTCIOGLABEVRHLVGSFRN----- 226
Db      515 IERGAADKNTLEIARLDRKF-----LTDINGIFPTLASLMLNLSNHLVWFVDAFIP 568

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Qy      227 GNLEKFD--KSALGELCNL--TIEEFLAYLDYLDIIDLFPNCLTNVSSFSLSVTIER 282
Db      569 SNLKWLDIHGVYIEALGVYKLOEBIRVTLTDASHNRITEL-GAMSVPSISILLPINNNI 627
Qy      283 VQDFSYN--FGQHLELVNCKRGQPTLYKLKSLKTLFTSNK-----GNAPS----- 328
Db      628 IGOIQANTFVDKTRLARVDLVANVLSKLSLNALRAVPAVSAEPRVDEFYIGNPFCDGSM 687
Qy      329 -----EVDLPSELFL-----DLNRNGLSFK-----GC 350
Db      688 EWLQRIINLTTQRHNVVDLGNIECLMPHSRAPLPLASLSASDFVCYESHCPPTGC 747
Qy      351 CSQDFGFTSLKYLDLSFNGVITMSNPL--GLEOLEHLDFQHSNLKQNSFVSPLSN 408
Db      748 CEYQCECEVICPGNCSCHDATMTATNIYDCGRQDLAAL-----PRIPQDVADLYLDGN 803
Qy      409 LIYLDISHTHRAVANGIPNGLSLEVLKMAQNSQENFLPDIFTELRLVTLFDSQCL 468
Db      804 MPELEVGHVGRNRRLALYLNASNMTLQNS-----LAQVLNRLVHLNENKL 852
Qy      469 EQLSPFAFNSLSLOVLMNSHNPFLDTPPYKCLNSLOVLVSLNHTMTSKKQELQHP 528
Db      853 TALBGTERRSLGLLELYLHNMMLTHISNATREPLVSEVLRLDNRRSLPHLQYRH-- 910
Qy      529 SSLAFLNLTQNDFACTCEH-QSFLQWIKDQRLVEVERMECATPSDKGMPVL----- 581
Db      911 SLQGLTIGRANWSCRQQLRELQFVSDNMAVVDADHIYCLDAGIKRELEHIGLIANG 969
Qy      582 -----SLNTICQMKTI-ITG-----VSULVSVSVAVLVYKFYHMLMLAC 624
Db      970 PDCSDLLDASNISSQDLACIGPCMPALVILFVAVLIIYVFPEVSVMMLFA-- 1027
Qy      625 IKYG-----RGEN---IYDAFVIYSODEDMVRNELVKNLEEGVPPOLCLAYRDFIRG 675
Db      1028 -HYGVVCEPRFEDGKLYDAIILHSKQDEVVCNIALEHGRPPRLCTCQQRD-LFP 1085
Qy      676 VAAANIIEGFHKSRYVWVSQHFIOQRWCIFEYEIAQTOFQLSSRAIIFIVLQK-- 733
Db      1086 QASHQVLV-EGARBARXKIIILVTRMLATENRIFRMA-----FHSILGL-----AQKLV 1136
Qy      734 -VEKTLRQOVELYRLSHNTYLEMDVYLGRHT-----FWRRLKAL 775
Db      1137 IIEFTSVSAEADVALS--PYLK--SVPSNRLLTCDRYFEWELKRYAL 1180

RESULT 5
T13887
c1r protein - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13887
R.Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A.Title: Expression of a novel Toll-like gene spans the parasegment boundary and contri
A.Reference number: Z17805; MUID:95151581; PMID:7848870
A.Accession: T13887
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1385 <CHI>
A.Cross-references: UNIPROT:Q24591; EMBL:676155; NID:G913247; PID:G913248; PIDN:AAB3383
C.Genetics:
A:Note: c1r
A:Cross-references: FlyBase:FBgn0004364

Query Match      10.2%; Score 421; DB 2; Length 1385;
Best Local Similarity 24.0%; Pred. No. 1.9e-18;
Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

Qy      19 LDSLNPPLRHGYSYFSPPELOVLDLSRCEIQTIEDGAYQSLSHSTLILGNPIQSLA 78
Db      338 LNLNNALTRISQKTFKELYFLQIIDMRNNSIGHIEGAFPLPYNLHTNLNENRLLHTID 397

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OY 79 LGAFSGLSLQXVAVENTLASL--ENPFIHGLKLTKELVANHLIQSKLDEYSNLTNL 137
 Db 398 NRIFNGLYVLTCL-TLNNNLVSVESQAFRNCSDIKELDISSN--QLTVEEAAQDLSML 454
 OY 138 EHLDSNKKIOSIYCTDRLVHQMPLNL-----SDLSINPNPF 177
 Db 455 KTLDDGENQIISFPKNTFRNLNQLTGLRLIDNRIGNITVGMFOPLLRLSVLNLAKNRQS 514
 OY 178 IQPGAF-KEIRLHKLTLRNNFDSLNVKTCIQGLAGLEVHRLVIGEFENE----- 226
 Db 515 IERGAFFDKTEIEAIRLDKFF-----LTDINGIPATLASLIMLINSBNLWMPDYAFIP 568
 OY 227 GNLEKFD--KALBELCHL--TIEFRLAYDYDDIIDLFNCLITNVSISLYSVITER 282
 Db 569 SNLKMALDHGVYIEALGVYKQLQEEIRVTTLDASHNRITEL-GAMSVNSITELLFINNI 627
 OY 283 VKDFESYN--FGQHLVELVNCCKFGQPTLKLKSLKELFTSNK-----GGNAFS----- 328
 Db 628 IGOIQAMTFVDKTLRLARLDLYANVLSKISLALNRVAPVSAKPPPEFYLGANPECCDSM 687
 OY 329 -----EVDLPSEFL-----DLSRGLSEK-----GC 350
 Db 688 EMLGRINNLTRQHPHVVDLGNIECLMHSRSLAPRLASLSASDPVCYKESHCPPTCHC 747
 OY 351 CSQSPFGTSLKLYDLSPNGVITYMSNFL--GLEQLEHLDQHNLSKMSFSFVPLSLRN 408
 Db 748 CEYECQCEVEICPGNCSCFHDATWATNTIVDCGRDPLAL--PNRLPDVSDYLDGNN 803
 OY 409 LIYLDISHTHTRVAFNGIFENGSLSEVLKMGAGNSQENFLPDIPTIELNLTFLDLSQCL 468
 Db 804 MPELEVGHLTGRRLNRALYLVASNLMTLQNS-----LAQLVNLVYHLNENKCL 852
 OY 469 EQLSPTANSLSSQLVLMNSHNPFSLDTPPYKCLNSLOVLVDSLNHIMTSKKLOLHPF 528
 Db 853 TALBESTERSGLRELVLHNNMLTHISNATPEPVLVSLEVLRLDNNRSLSLPHLQYRN-- 910
 OY 529 SSIAFLNLTQNDFACTGEH--QSFLOMTQDQQLVEVERMECATPSDKQGMPLV----- 581
 Db 911 SLQGLTGLGRNVAWSCRCQQLRELQFVSDNMMVADADIDYCLDAGIKREBELIGNLANG 969
 OY 582 -----SLNTICQNN-----KTIISVSVSVSVSVVAVLVYKFFHMLLAGC 624
 Db 970 PDCSDILDASNSNISSODLAGGTRLPPLAALVLIPLDVLITVFPFRESVRMMLFA-- 1027
 OY 625 IKYG-----RGEN---LYDAFVIYSSQDEDMVNEVLKNLEEGVPPQLCLAHYDFIPG 675
 Db 1028 -HYGRVCEPFPEDAGKLYDAIILHSEKDYFVCNRLAALEHGRPPRLDIOGRD-LPP 1085
 OY 676 VALAANIIEGHFHKSRKVIYVVSQHFQISRMCIFEYELAQTWQPLSSPAGITFVLQK-- 733
 Db 1086 QASHLLQV-EGARASRKIIILVLTENRLATEWNRILEFNA---FHESIRGL-----AQLTV 1136
 OY 734 -VEKTLIAQVLELYRLSLRNTYLTLEMEDSVLGRHI-----FMRRLKRL 775
 Db 1137 IIEETSVSAEADVAELS--PYLK--SVPSNRLLTCDRYWEKRLRYAI 1180

RESULT 6
 T15864
 hypothetical protein C5686.6 - *Caenorhabditis elegans*
 CSpecies: *Caenorhabditis elegans*
 CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 CAccession: T15864
 R: Fulton, L.
 submitted to the EMBL data library, November 1995
 A: description: The sequence of C. elegans coemid C5686.
 A: reference number: S69019
 A: accession: T15864
 A: status: preliminary; translated from GB/EMBL/DBJ
 A: molecule type: DNA
 A: residues: 1-1066 <full>
 A: cross-references: UNIPROT: Q18902; EMBL: U39996; NID: g1055114; PID: g1055120; PIDN: AAA810

[illegible]

A,Intons: 1/3 80/3, 318/3, 377/2 422/2, 702/1 745/3, 831/2, 998/2
 C,Superfamily: chaperonin; leucine-rich alpha-2-glycoprotein repeat homology
 C,Keywords: cell adhesion; glycoprotein; membrane protein
 F,1-29/Domain: signal sequence #status predicted <SIG>
 F,30-1134/Product: chaoptin #status predicted <MAT>
 F,80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
 F,103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F,128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F,152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F,177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F,201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F,226-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F,250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F,279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F,303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F,326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F,351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F,375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F,401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F,428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F,453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F,477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F,502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F,527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 F,551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F,577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F,601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F,625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
 F,649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
 F,673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
 F,708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
 F,733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
 F,757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
 F,781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
 F,805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F,828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F,854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F,879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F,903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F,928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
 F,949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F,973-996/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F,996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
 F,1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F,1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 8.1%; Score 333.5; DB 1; Length 1134;
 Best Local Similarity 23.0%; Pred. No. 4.7e-13;
 Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

10 DNLPRSTKRLDSPNPLRLHLSVSFPSPFELGV-----L 43
 346 DSLVNSLQILDSSNNLTGLHKLRFNPFVLRVLYSMRDKIKIQKPTTFNVAHTLKL 405
 44 DLS-----RCEIQIETEDGA---YOSLS-----HLSTLILTNPIQ 75
 406 DLSGRNDPTNLQTLRNMTRKMNMSLISRLSSSVGPEDKDFCEVLELDQIRASLS 465
 76 SLALGAFSLSLQKLVAVETNLASLEN--PPIGLKTLKELNVAHNLIQSFKLPETYS 132
 466 GQSHAFKVRGKRLDFSENGISSTIENDAFHEIGL--SLISLKMSHGSGALPAEPRL 523
 133 NLTNLEHLDLSSNKIOSICTDLRLVHOMPLNLISLISLPMNFIOPGAFK--EIRHL 189
 524 HTLSIQEIDFSNNHSSMSWDSFPHKLNRL-----LELDNRLEQVLKTFPGGDHSKLE 579
 190 KLTLRNN-----FDSLNVKTCIQGLAGLEVRLVLFGEFNEGNLEKFDKSLAG- 239
 580 EISLRFNHLTISIQHTFFDLALRK-----LHLDKDKIKIRRAPMNDLELYSLRGN 634
 240 -LCNLTIEEF-----RLAYIDYLDL-----IDLNCLTNVSSFSLSVYTIERKDSYNF 290
 635 KINNLADESFQNLPKLEILDMAFNQLPNFNFYFDQVGLTSLNIN--VNVSHNOIRQLMYS 693

291 GMQHLELVNCKFGQFPTLKLSLRLRFTSNKGNANSEVDLPSELEFIDSRNGLSF--K 348
 694 SW-----SGRNEHGGWHSNKKIDLDLSHNNISILHP 724
 349 GCCSOSDRGT-----SLKYDLSNNGVITMSSN--FLGLEOLEH 386
 725 GYFRPAELSLTHLHLYNSLNMTRDYEGNMPHLOMDLSYMWIHELDQFADKNTKOQL 784
 387 LDFOHNSLKOMSESVFSLRLNLYLIDSHYTR--VAENGIFNG----- 429
 785 VFPGHNYSLDIPQ-DIFPVGQRLVDSHHNKLGPNNLYTNGMEKLDVSHNMMLKIP 843
 430 ---LSLEVLKMAQNSFOENFLP-----DIFTELRLTFDLISQCLFOLSPAFNSLS 481
 844 SSSLSLALMLCELHLSNNFSTHSDLSNKRFSRLAYLDISYVYLIRIDAVFATWPK 903
 482 LQVLMNSN-----NFF-----SLDFPKKCNLSLOVDLSLHNTS 519
 904 LAVIDLSHNRDLKWKDKSFMLENSLKLGLNVLSTVPEIRLKYLEFRLGYNE-LPS 962
 520 KKOELHPPSSLAFLNTRQNDFACTCEHQSFLOWIKDQROLVEVERMECATPSDKQ--- 576
 963 IPOELANMSLRLMLDSNND-----LTNVPLMTQALPHLRRLML 1002
 577 -GMPVLSNITTCOMNKTIIGSV--LSVLVSVVAVLVYKFFHMLLAGCI 625
 1003 SGNPITSLN-----NSFQVNEDEMLDISNFRLHYREY-----GCL 1040

RESULT 8
 J05239
 Insulin-like growth factor acid-labile chain - baboon
 C,Species: Papio sp. (baboon)
 C,Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C,Accession: J05239
 R,Delnany, P.; Baxter, R. C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A,Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
 A,Reference number: J05239; MUID:97040714; PMID:8886027
 A,Contents: liver
 A,Accession: J05239
 A,Molecule type: mRNA
 A,Residues: 1-605 <DE>
 C,Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.5%; Score 309; DB 2; Length 605;
 Best Local Similarity 24.5%; Pred. No. 7.2e-12;
 Matches 155; Conservative 92; Mismatches 235; Indels 150; Gaps 23;

4 NFYKIPDMLPSTKRLDSPNPLRLHLSVSFPSPFELQVLDLRCEIQIETEDGAYQSLSH 63
 64 NTRLPDGIPEGTOALMDSSNLSIPPAARNLSSIAFLNLDQGSLSLEFQALLGLEEN 123
 64 LSTLILTNPIQSLALGAFS-----GLSSIQKLVAVETNLA 99
 124 LCHLLEERNQRLSLAVGFAYTPALALGLSNRRLSLREDEGLFEGILGMLMDNLGNSTIA 183
 100 SIENPPIGLKTLKELNVAHNLIQSFKLPYFSNLTNLEHLDLSSNKIOSICTDLRLVHL 159
 184 VLPDAFRLGLRLVLAGNRL--AYLDLPALFSGIARELDLSRNALRAL--KANFA 239
 160 QMPPLNLSLDSISLPMNFIOPGAFKEIR-LHKLTLRNNFDSLNVKTCIQGLAGLEVRL 218
 240 QLPRLQ-KLYDRNLIAAVAFGLGKALMWLDLSH--RVAGLLEDFPGLGLGRVRL 297
 219 VLGEFRNEGNLEKFDKSLBGLCNLTIEFRLAYIDYLDLIDLNCLTNVSSFSLSV 278
 298 -----SHNLIASLRPTTFEDL-----HFLERD-----QLGHN 324
 279 TIERVKDSYNFGMHLELVNCKFGQFPTLKLSLRLRFTSN--NKGANSEVDLPSE 336
 325 RIRQLAERSFE-GIQQLVLTLDHNOLOEVKVGAFGLTNVAVMNLGNCIR--NLPEOV 381

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QY 337 LLDLSR-NGLSKGGC-----SQSDFGTSUKYLDLSNGVITMSNPL-GLEQLEHDF 389
Db 382 FRGLKCHSHLHBGSCLPRIKPHYPAJSGKLRLPLKONGVAVGBEBSGLWGLAELEHLD 441
QY 390 QHSNLKQMSSEFSVFLSNRLYYLDLSHTHTTRAVFNGIENGLSSLEVLTMAGNSFOENLP 449
Db 442 TSNQJ-----THLP---HQLFGQJGKJLEYLLSHNRLAE--LP 474
QY 450 -DIFELRNLPFLDSCQLEBOLPFAFNUSLSLOVLMASHNNFSLDTPFYKCLNSLOV 508
Db 475 ADALGCPRLAFPLDVSHNRLEALPGSLIASIGRLKYLMLRN--SLKTFPQ----- 524
QY 509 LDYSLNHTMSKKOELQHPSSLIAPLNTONDFACTCEHOS-----FLOWI 554
Db 525 -----PCLERLWLEGNPMWDCSCLKALRDPALQNPASVPRFYQAI 565
QY 555 ---KQQRQLLVEVERMECATPSDKQGMFVLSL 583
Db 566 CEGDDCQPPVYTYNNITCASPEEVAGLDRDL 597

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RESULT 9
T17461
disease resistance protein D - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17461
R:Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A>Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resistance gene
A:Reference number: Z18801; MUID:99254130; PMID:10318973
A:Accession: T17461
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-853 <PAR>
A:Cross-references: UNIPROT:O9ZS82; EMBL:AF119040; NID:94235640; PID:94235641; PIDD:AA00
C:Genetics:
A:Gene: NL0D

Query Match          7.3%; Score 302; DB 2; Length 853;
Best Local Similarity 24.6%; Pred. No.3,1e-11;
Matches 185; Conservative 102; Mismatches 280; Indels 184; Gaps 33;

OY 17 KNLDSF-----PRLHGSYSPFPELOVLDLRCEIGTIEGAYQSLSHLTILTG 71
   |||||:
DB 111 KRLLSYNDFTGSP-----SPKGFESNLTDLDFDSFTGTLIPEISHSKLYLRTST 166
   |||||:

OY 72 NPQSLALG-----AFSGLSLQKLVAVETNLASLENFPIGHLKTKELNVANHLIQSF 125
   |||||:
DB 167 DYPVGLSGPHNFELLKNLTQLRELNLVDNLSS--TIPENFSHLTNRLAVTELRGI 224
   |||||:

OY 126 KLPEYFSNLTNLEHDLSSNKIQSIYCTDLVHOMPLINSLDLSLNPNPFIQGAFFE 185
   |||||:
DB 225 -LPEFFFLSNLESIDLSFNPQLTVRFPTTKWSSASLVNLYL-AGVNIADRI-PESFSH 281
   |||||:

OY 186 IRLHKLTRNNFDSLNVAKTCIQGLAGLEVRLYVGEPRNEGNLEKPKSALBEGCNLT- 244
   |||||:
DB 282 L-----TALKHLNMGYTNLSGPIPK-----PLMNLTH 308
   |||||:

OY 245 IEEPRLAYLD-YLDDIDLFNCLTNVSSFSLVSATIE-RVKDSSYNFGMHLLEY- 298
   |||||:
DB 309 IESL---FLVDNHLLEGPISSHFTIPEKLSLGLGNPNPFGGRLEPLSPFRSMWKLRLDPSS 365
   |||||:

OY 299 NCKRGQFPT-LKLSKLRLFTTSNK-GGNAPSEY-DLPSLEFIDLSRNGLSFK- 348
   |||||:
DB 366 NFLGPIPSNVSGIQLQQLILSSNHLNGTIPSWIFSLPSLTIVNLSDNTLSGKIOERKS 425
   |||||:

OY 349 -----GCCSDPFGTTLKYLILDSFNGV-TMSSNPLGLEQLEHLDFOGHN 393
   |||||:
DB 426 KTLVFSLEQNKLECPITRSLINQOFLQALLSHNNISGHISSAICNKTPTILNLNLSNN 485
   |||||:

OY 394 LK-----OMSESVPLSLRNLILYLDISHTRVAVNGIENGLSILEVAKMAGNSFOE 445
   |||||:

```

[illegible]

Db	124	ICHTHIEROULSTALGTFAHTPALASIGLSNNRLSTLEBDLPGLGSLMTDLNCGNSIA	183
Qy	64	ISTLITVGNPISGLAARFS-----GLSLGKLVAVETNIA	99
Db	64	NITRLPDGPGGTQALMDGNNTSSVPPAFQUNLSIGFLNTGGGQLSLERPALGLLEN	123
Qy	4	NFYKIPDNLPFTTKNDLSFNPRLRHGYSFSPFPELQVLDLSRCETGTIEDGAYQSLSH	63
Db	156	Matched 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;	
Qy	4	NFYKIPDNLPFTTKNDLSFNPRLRHGYSFSPFPELQVLDLSRCETGTIEDGAYQSLSH	63
Db	156	Matched 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;	
Qy	64	ISTLITVGNPISGLAARFS-----GLSLGKLVAVETNIA	99
Db	124	ICHTHIEROULSTALGTFAHTPALASIGLSNNRLSTLEBDLPGLGSLMTDLNCGNSIA	183

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QY 100 SLENPIGHLKTLKEINVAHNLIOSEKLPYEFYNLTNLEHLDLSSNKIQSYCTDLRVLA 159
DB 184 VLPDAAPFGSLGSLRELIVLAGNRL-AVLQALPSGLAELELDLSSNALRAI---KANVY 239
QY 160 QMPLNLSDLSLNPMPNFIQGAFFKIR-LHKLTLRNNFDSLNMKTCTIOGLAGEVHRL 218
DB 240 QLPRLQ-KLYDLRNLIAAVALPAGFLGKALRWLDLSHN-RVAGLLEDFEPGLGLHRL 297
QY 219 VLGERNBNENLEPKSALLEGONLTIEBFRLAYDYVDIIDLFNCLTNVSSPLSV 278
DB 298 -----SHNATASLRPRYKOL-----HLEEL-----QLGN 324
QY 279 TIERVYDSYNGWOMHLELVNCKFCQFPYLKLSKRLFTS--NKGNAFSEVDLPSE 336
DB 335 RIRQLAERSFE-GLQGLVLTLDHNOQGVKAGAFGLGNVAVMLSGCLAR-NLPEVY 381
QY 337 FLIDLR-NGLSFKGCC-----SQDPGTTSLKYLDLSENGVITMGSNPL-GLEQLHLD 389
DB 382 FRGLCKLSHLEGSCLGRIRPHTFTGLSLRRLFLKONGLVIGIEQSLMGLAELELDL 441
QY 390 QHSNLKQNSSEFVFLSLRLIYLDISHHTTRVAFNGIEFNGLSLEVLKMAGNSFOENPL 449
DB 442 TSNOL-----THLP-----HFLFGGLCKLEYLLISRRLAB--LP 474
QY 450 -DIFELRLNLTFLDLSQCOLEQSPFAFNSLSLQVLMNSHNNFSLDTPPYKCLNSIQV 508
DB 475 ADALPFLQRAFLVDVSHNRLALPNSILAPLGLRLTSLRRN---SLRFTTQ----- 524
QY 509 LDYSLNHTWTSKKQLQHPSSLAFLNLTQNDPACTCEHOSFLQWTKD-----QRO 559
DB 525 -----PGLERLMEGNPMDCCP-----LKALRDPALQNSAVPRF 561
QY 560 LLEVERMECATPSPDKQMPVLSINTQMNKTIIGVSV 598
DB 562 VOACEBGDCQPPATYTN-----NITCASPEVVGDL 594

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RESULT 11

T42218

slit-1 protein homolog - rat

N:Alternate names: MEGR4 protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T42218

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A:Reference number: Z14126; MUID:98360089; PMID:9693030

A:Accession: T42218

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1531 <NAK>

A:Cross-references: UNIPROT:Q88279; EMBL:AB011530; NID:G3449289; PID:BA32460.1; PID:G3

A:Experimental source: strain Sprague-Dawley; brain

C:Genetics:

A:Gene: MEGR4

C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 7.1%; Score 296; DB 2; Length 1531;
 Best Local Similarity 22.2%; Pred. No. 1.6e-10;
 Matches 158; Conservative 94; Mismatches 241; Indels 218; Gaps 25;

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QY 8 IPDNLPFTKMLDLSNPLRHLSGSFFSPFELQVLDLSRCEIQTEEDGAYQSLSHLSTL 67
DB 303 IPANLPETWTRLELNGIKSIPPGAFSPYRKLRRLDLSNNOIAETAPDAFQGLNSLSL 362
QY 68 ILTGNPIQSLAAGSGLSLQKLVAVETNLASLENFPIGHKTLKEINVAHNLIOSEKLP 127
DB 363 VLYGNKTLTPRGVFGGLVTLQELL-----LNA--NKINCIR- 397
QY 128 PEYFSNLTNLEHLDLSSNKIQSYCTDLRVLAHOMPLNLSDLSLNPMPNFIQGAFFK 184

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DB 398 PDADFOLDNLISLYDNKIOSLAKGTTSLRAIO-----THLAONP--FTDCNLK 448
QY 185 EIRLHKLTLRNNFDSLNMKTCTIOGLAGEVHRLV---LGERNBNENLEPKSALLEG 241
DB 449 WLA-----DFLRNTIET--TGARCSRRRLANKRIGQKS---KKPSCAKE--- 491
QY 242 NLTIEFRLAYDYVDI-----DIIDLFNCLTNVSSPLSVTIERVYDSYNGWOMHLE 296
DB 492 ---QYFIPTGEDYHIANSECTSDVACPCKRCSEASVECSGLKSKRPE-RIPQSTTELR 546
QY 297 LVNCKP-----GQPTLKLSKRLTFTSNKKGNAFSEVDLPSEFLDLSNNGSFKGC 350
DB 547 LNNEISILEATGPKR-KLSHLKKNLSNNK---VSEIDGTE----- 586
QY 351 CSQDPGTTSLKYLDLSENGVITMGSN-FLGLEQLHLDFOHSNLKQNSSEFVFLSLRL 409
DB 587 -----GATSVSELHTNQLSESVSGMFRGLDGLRTLMRLNRRNSCIHNS-FLGLNRY 639
QY 410 IYLDISHHTTRVAFNGIEFNGLSLEVLKMAGNSFOENF----- 447
DB 640 RLISLYDNHITTSIPGARDTLOALSTLNLANPFCNCQALWLGDLRKRKIVTGNPRCQ 699
QY 448 -----L 448
DB 700 NPDFLRQIPLQDVAPDFRCBEGQEVGCLPRPQCPQBCACIDTVVRCNKHQALPKGI 759
QY 449 PDIFTEL-----RLNLTFLDLSQCOLEQSPFAFNSLSLQVLMNSHNN 491
DB 760 PRNVTLELDNGQFLVVGQSLSTFKYLOLVLDNSNNKISLSSFTNMSQTLTLLISYVA 819
QY 492 FFSLDTPPYKCLNSIQVLDYSLNHTWTSKKQLQHPSSLAFLNLTQNDPACTCEHOSFL 551
DB 820 LQCIPLPLAFQGLRSRLTLSHGNDVSTLQEGIFADV-TLSLSLAIGANPLYCDCHLRWLS 878
QY 552 QMIKQRLQVLEVERMECA-----TPSDK---QGMVPLSINTC 587
DB 879 SWVKTYGR---EPGIARCAQPEMEGKLLTTPAKKFCQGPSPILAQAAC 926

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RESULT 12

H96510

probable disease resistance protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H96510

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talon,

ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H96510

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-994 <STO>

A:Cross-references: UNIPROT:Q9C637; GB:AB005173; NID:g11321768; PID:AA034245.1; GSPDB:C

C:Genetics:

A:Gene: F2G19.6

A:Map position: 1

Query Match 7.1%; Score 292; DB 2; Length 994;
 Best Local Similarity 23.6%; Pred. No. 1.6e-10;
 Matches 152; Conservative 92; Mismatches 241; Indels 158; Gaps 30;

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QY 1 MEINLYKIPDNLPFTKMLDLSNPLRHLSGSFFSPFELQVLDLSRCEIQTEEDGAYOS 60
DB 281 LKLSLY-----NTSFS-GTIPNSISNKLKHLTS-----LKLQOASAFSGRIPSSLR 324

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QY 61 LSHSLTLITLGNPILQSLALGAFSGLSLQKLVAVETNLASLENP--IGHLKTJKELVNA 118
Db 325 LSHSLNLVLSENPFVGEIIPSSSVNMLKQTLTLPDVSNNING--NPPSSLNLNQLRYDIDC 382
QY 119 HNLIOSFPLPEYFSNLTJLJLHLDLSNNKIQSIYCTDLRVLHQP--LNLTS----LDLSL 172
Db 383 SNHPTGF-LPPTTISQLSNLEFFSACDNSPTG-----SIPSSLPNISLTLTGISTY 431
QY 173 NPMNFIOGAEKEIRLHLKTLRNPFDSLNVKTCIOGLAGLEVHRLVIGEFRNENGEKF 232
Db 432 NQLN-----DTNLI-----KNISLNL 449
QY 233 DKSLLEGJCNLTIEBFRLAYLDYLDLIDLENCCLTNVSSSLYSV--TIERKVDPSYN 289
Db 450 QRLILDN----NNFKASQVD----LDVFLSLKRLVSJLALGILPLSTNITSDBFS 497
QY 290 FGMOHLLELVNCKFGQFPTKLKSLKRLTFTSNKGNAFSEVD----LPSTLEPDLSSNG 344
Db 498 SHLEYELBSGCNIIIEFPBF-IRNQRLNSSIDLSSNNIKGQVPMMLMRPLPSTYDLSNS 556
QY 345 L-SFKGCCSQSGDFGTTSLKLYLDLSPNGVITSSN-----FLGLEQLEHLDFOHSNLKOM 397
Db 557 LIGFNG-----SLKALSGSKIVMLDLSNNAFQGLPMPRPGIYFLGSVNNFICY 606
QY 398 SEFSVFLSLRKLVIYDISHHTTRVAFCNGIFNGL-----SSLEVLKXAGNSFOENFL 448
Db 607 IPPBI-CGLAPLILDLIS-----NNMLHGLIPRCLEAOMSSSVLNLNNLSL-DGSL 656
QY 449 PDIFTELNLNLFELDLSQCQLQLSPTAFNLSLSLOVLMSSNNPFSLDTPFY--KCLNSL 506
Db 657 PNITFNNACVLSLDVSSHNTLEGGKLPASLAGCSALEILVBSNNT--NTPFPFWLNSLEKL 714
QY 507 QVLDVSLNHIITMSKKQELQH-----FPSSLAFLNLTQNDPACTCEHQSEFLQWIKDQRQ 559
Db 715 QVLVLRSNF-----RGLTLHNDVGWGFPP-LRITDVSNDHFVGLTLPBDYFMNMTAISKS 769
QY 560 LLVEVERMECATPSD--KQGMFVLSLNTTCQNMKTTIGSVYL 599
Db 770 ---ETLEQYIGDPEDYGYTSLVLMNKGVSMMEMOIRILKTYVI 809

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[illegible]

```

Db 155 NBLSGP-----HNELLKNTQRLNLDNSNISTTSNPS 194
Qy 133 NLTNEHDLDSNNKIQSI-----YCTDLRVHQPMLNLNLDLSLNEPNIQCAFK-- 184
   ||||| : : : : :
Db 195 HLTNLM--LPYTELNGVPERVFNHLSLDEFLH-----LSYNQLTVRFPTTKWN 241
Qy 165 -EIRHKLTLRNNFSLNWKTCIOGLAGL-EVHRLVGERBRNGNLEKFPKSALEGJCN 242
   ||| : : : : :
Db 242 SGASLTKLVH-----SVNIADRIPESEFHLTSLHALTMGRCLNSGHTRK-----PLWN 290
Qy 243 LT-IEEFLRAYLDYUDDIIDLFNCLTNVSSFSLSVYTIERKDF-SYNFGOMHLELV-- 298
   ||||| : : : : :
Db 291 LTNISLFLG--DNHLEGPQLTRFEKRLKRLSGNNNLHGLLEFLSPNRSMWQLEIYLF 348
Qy 299 --NCKFGQFPT--LKLKSLKRLFTSNK--CGNAFSEV--DPSLEFLDLSRNGLSFK----- 348
   ||||| : : : : :
Db 349 SSNYLTGPISNVNVSGLQNLGWLFLSSNHLNGSIPSWIFSLPSLVLLDLSNNTFSGKIOEF 408
Qy 349 -----GCCSQSDFGTTSLKRYLDLSPFNGVI-TWSSNFLEQLBEHDFOH 391
   ||||| : : : : :
Db 409 KSKTLSTVTLKQNLQEGPIPNLSLNQESLOFLLSHNNISGVISSINLMTIWLDDGS 468
Qy 392 SNKQMSFSEVFLSLNLNLYLDISHTHTVAENGIFNGLSLEVLRKAGNSFOENFLPDI 451
   ||||| : : : : :
Db 469 NNLBEGTIPQCVBERNEYLLDLDSLNNRSLSGTINTTFSIGNSFKAISLHGKLTGK-VPRS 527
Qy 462 FTELNLTLFLDLSQOCEQSLPFAFNSLSLOYLNMHNNPFSLDTPFYKCLNS----- 505
   ||||| : : : : :
Db 528 LINCXYLLKLJLGNNOJLNDTFPWWLGYLSOLKTLISLNSKLHG---PIKSSGSTNLPMR 583
Qy 506 LQVLDYS-----LNHMTSKK--QELQHPFSLA----- 532
   ||||| : : : : :
Db 584 LQILDLSSNGFSGNLPERILGNLQTKMKIDENRFRPEYISDQVEIYYVLLTTITTKQDY 643
Qy 533 -----PLNTQNDFACTCEH--QSFLQMLKDQQLVVEVERMECATSDDKGMPL 581
   ||||| : : : : :
Db 644 DSVRLDSNMIIINLSKRFE--GHIPSIIGDVLGFTLMSRNALBSHPIASFGNLVYL 700
Qy 582 -----SLNITCOMNNTIIGVSVLSVLVSVAVLVYKFFHMLMLAGCIKYGRBENIYD 635
   ||||| : : : : :
Db 701 BSLDLSNRSNRISEBIPQGLASITFLLEVIANLS-----HNHLV--GCIKRGKQ---FD 745
Qy 636 AFVITYSSODEVWRNELVKNLEGVPPQJLC 666
   : : : : :
Db 746 SFGNITSYQGNDR-----GFLPSKLC 767

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RESULT 14
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence _revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1282
R/Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A>Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JC1282; MUID:93058676; PMID:1384485
A/Accession: JC1282
A/Molecule type: mRNA
A/Residues: 1-603 <DAI>
A/Cross-references: UNIPROT:P35859; GB:S46785; NID:G258002; PIDD:AA823770.2; PID:9570593
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F.1-27/Domain: signal sequence #status Predicted <SIG>
F.28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F.267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match          7 0%; Score 290; DB 2; Length 603;
Best Local Similarity 24.1%; Pred. No. 1.1e-10;
Matches 154; Conservative 84; Mismatches 240; Indels 162; Gaps 24;

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Db      64 NLTHTLPIVSTRALMLDGNLSSTPSAFOQLNSLDFLNLQSGSWLRSLFQALIGLON 123
Qy      64 LSTLITLGNPIQSLALGAFSGSLQKLVAVETNLASLENPFGIKTLKELNVA----- 118
Db      124 LYVHLERNRLNLAVALGFTHTPPLASLSLSNLLGRLEEGFQGLSHLMDLNLGNLSLV 183
Qy      119 -----NHLI-----QSFRLPEYFSNLTNLLEHLDSSSNKIQSIYCTDLRYLHQ 160
Db      184 VLPDVTFOGLNHLVLAGNKLTYLQFPALFCGLLELRELDLSRLALRSV---KANVFVA 240
Qy      161 MFLNLISLDSLNPNNFIOPGAFKEIR-LHKLTLLNNFSLNVMKTCIOGLAGLEVHRLV 219
Db      241 LPRLO-KLYLDKNLTLTAAVAFGLMKALRWLDLSHN-RVAGLMETTFGLGLVHLRLA 298
Qy      220 -----LGEFR-NEGNELEKFPKSALEGLCNLTIEFRLAYLDYLDI- 260
Db      299 HNAIALSRPRTFPKDLHLEELQLGHNRIHQGERTFEGGLQLEV---LTINDNQITEVR 354
Qy      261 IDLEFNCNTNVSFSLVSVTI---ERV---KDFSYNFGMHLELVNCKKGQFPYTKLSL 313
Db      355 VGAFSGLEFNVAWNLNSGNCRLSRPFRVFOGLDKLHLSHSLCHVRLHTE--AGLSGL 412
Qy      314 KRLTTSNKGNAFSEVD-----LPSLEFLDLSRNGLSFKGCCSQSDGTTSLKXLDLS 367
Db      413 RRLFRD-----NSISIEBQSLAGLSLELDDLTNRLLTH--LPRQLPGLHGLVLLLS 466
Qy      368 FNGVITMSSNFLGLELEHLDFOHSNLMKMBFSVFLSLRNLIYDISHHTTRVAFNGIF 427
Db      467 YNQLTTLSAEVLG-----PLQRAFWLIDISHNLETLAEGLF 502
Qy      428 NGLSLEVLKMAGNSFOENFLPDITELRNLTFLDLSQCLQSLPFTAFNSLSLQVLNM 487
Db      503 SSLGRVYLSLRNNSLQ--TFSP-----QGLERL----- 530
Qy      488 SHNNFSDTFEPYKCLNSLOVL-DYSLNHNMTSKQELQHPSSSLAFNLQNDPACTCE 546
Db      531 -----WLDANPMDSCCLKALDPALQN-----PGVVPFRPQT-----VCE 566
Qy      547 HOSFLQWIKDQRQLLVEVERMECATPSPDKQGNPVLISLNT 586
Db      567 -----GDDCQPYTYNNITCAGPANVSGLDLNDVSET 598

RESULT 15
Cf-4A protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T07015
R:Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A:Title: Identification and De-tagged isolation of a new gene at the Cf-4 locus of tomato
A:Reference number: z15863; MUID:98335213; PMID:9670557
A:Accession: T07015
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-855 <TAK>
A:Cross-references: UNIPROT:O50024; EMBL:Y12640; NID:e1289424; PIDN:CAA73187.1; PID:e128
C:Genetics:
A:Experimental source: strain Cf-4; isolate MM-Cf-4
A:Gene: Cf-4A
A:Map position: 1

Query Match      7.0%; Score 290; DB 2; Length 855;
Best Local Similarity 24.8%; Pred. No. 1,8e-10;
Matches 187; Conservative 95; Mismatches 281; Indels 190; Gaps 36;
Qy      19 LDLSNPRLR---HLCGYSPFSPPELQVLDLSRCETQTEDGAYQSLSHLSTLITLGNPIQ 75
Db      85 LDIGSQQLQGRKFSNS-SLFPQLSNLRKRLDLSND-----FTGSP- 123
Qy      76 SLALGAFSGLSLQGLVAVETNLASLENPFGIKTLKELNVAHNLQSFKL---PEYF- 131

```

```

Db      124 SPKFGESFDLTHLD---LSDSNFTGVIPSEIHLKHLVRLIS---DQYKLSLGRHNE 176
Qy      132 ---SNLTNLLEHLDSSNKIQ-----SIYCTDLRYLHQ-----MP-----LNLNS-LDL 170
Db      177 LLLKNLTQLQREHLHLSVNISSITIPSNFSPHLLNLASTYELNGVLPFRVHLSNLELDD 236
Qy      171 SLNPNNFIO-----PGAFKEIRLHKLTLLNNF--DSLNVNMTKTCIOGLAGLEVHRLV 221
Db      237 SYNPLQTVRFPTTIWNSSASLVKLYLSRVNLAGNIPDSFSYLTA-----LHLEDNV 287
Qy      222 EFRNNGNEKFPKSALEGLCNLT-IEFRLAYLDYLDIIDLFLNCLTNVSSPFSVSVTI 280
Db      288 YTNLSGPIPK-----PLMNLTNIESLDLDY--NHLBEPILQPLPEFKLSLTLGNNDV 338
Qy      261 ERVKDF-SYNFGMHLELV---NCKFGQFPY--LKLKSLKRLTFTSNK-GNAPSEV-D 331
Db      339 DQGLEFLFPNRSWTQLEELDPSNSLTPGIPENVSGLRNLQSLYLSNNLNGSIPSWMD 398
Qy      332 LPSLEFLDLSRNGLS-----FKGCCSQSDGTTSLKXLDLSFNGV 371
Db      399 LPSLSLDSLNNTFPSGKIQEFKSKTSLIVTLKONQKGPINPSLINOESLQFLLSHNNI 458
Qy      372 I-TWSSNFLGLELEHLDFOHSNLMKMBFSVFLSLRNLIYDISHHTTRVAFNGIFNGL 430
Db      459 SCHISSICNLKILNVLNLDGSSNNLEGTIPQCYVERNEYLSHLDLSNNRSLGTTINTTFSIG 518
Qy      431 SLEVLKMAGNSFOENFLPDITELRNLTFLDLSQCLQSLPFTAFNSLSLQVLNM 490
Db      519 NSFRAISLHGNKLTGK-VPRSLINCKYLTLLDIGNNQLNDTPRNLGYSQKILSLRNN 577
Qy      491 NFPSLDTFPYKCLNS-----LQVLDYS-----LNHNMTSKK-QELQHPSSL 531
Db      578 KLHG-----PIKSSGNTLFLMRLQIIDLSSNGPSGMLPERILGNLQTMKKFDENTRFPBEYI 633
Qy      532 A-----FLNTQNDPACTCEHOSFLQWIKDQRQLL 562
Db      634 SDRIYYLYLTITTTKGQDYDSVRIFTNMTIINLSKNFBEKI--PSIIIGDLVGRITLNL 691
Qy      563 EVERMECATPSPDKQGNPVL-----SLNITCOMNKTIIIGSVLSVAVSVAVLVYKPYF 616
Db      692 SHNVLEGHIPVSLQNLVSLSELDSSNKISGAILPQGLASLFLLEVLNLS-----HN 742
Qy      617 HMLLAGCITKYGRENITDAFYIYSSQDEDMVR 649
Db      743 HLNV---GCIPKQKQ---FDSFGNTSYQQNDGIR 769

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Search completed: March 12, 2005, 19:57:00
 Job time : 28.6156 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 86.9834 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-6

Perfect score: 4335

Sequence: 1 NMPLHLAGTLIMLFLSCL.....GRALNPDETSEEQEATTLT 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2860.5	66.0	839	6	ABU04773 Human exp
2	2860.5	66.0	839	6	ABU04774 Human exp
3	2860.5	66.0	839	6	ABU04775 Human exp
4	2860.5	66.0	839	7	AD078785 Human PRO
5	2860.5	66.0	839	7	AD048826 Human PRO
6	2844	65.6	837	2	AAW86361 Human DNA
7	2844	65.6	837	2	AAW86361 Human DNA
8	2844	65.6	837	6	ABU04776 Human exp
9	2837	65.4	837	5	AAE16116 Human DNA
10	2796.5	64.5	801	8	AD057797 Squirrel
11	2782.5	64.2	795	8	AD057791 Rhesus mo
12	2781.5	64.2	795	8	AD057800 Hamadryas
13	2777	64.1	808	8	AD057803 Chimpanze
14	2773	64.0	808	8	AD057782 Chimpanze
15	2761	63.7	808	8	AD057785 Gorilla t
16	2751.5	63.5	801	8	AD057788 Gibbon co
17	2726	62.9	799	2	AAW86352 Human DNA
18	2726	62.9	799	5	AAE16093 Human DNA
19	2726	62.9	799	5	ABW83162 Human Tol
20	2726	62.9	799	6	ABR42963 Human Tol
21	2726	62.9	799	7	AD039121 Human Tol
22	2726	62.9	799	8	ADP66566 Human Tol
23	2726	62.9	799	8	ADP48597 Human Tol
24	2558.5	59.0	745	8	ADP57799 White-fac
25	2440	56.3	738	8	ADP29455 Human sec

26	898.5	20.7	208	3	AAW88059 Human Tol
27	883	20.4	179	7	AD042707 Murine To
28	761.5	17.6	178	8	ADN12270 IL-1R/TLR
29	602.5	13.9	661	2	AAW28510 Product o
30	602.5	13.9	661	2	AAW87556 B cell su
31	602.5	13.9	661	7	AD038652 Human sec
32	602.5	13.9	661	7	ADP69098 Human MP5
33	595	13.7	650	3	AAW82527 Human RPL
34	588.5	13.6	661	2	AAW47274 Human B-C
35	575	13.3	1032	5	AAO21588 Murine To
36	575	13.3	1032	7	AD085953 Murine To
37	575	13.3	1032	7	ABW01559 Murine To
38	559	12.9	1050	5	AAO21579 Murine To
39	559	12.9	1050	7	AD085947 Murine To
40	559	12.9	1050	7	ABW01556 Murine To
41	546	12.6	1059	5	AAO21587 Murine To
42	546	12.6	1059	7	AD085951 Human Tol
43	546	12.6	1059	8	AD088188 Human 122
44	541.5	12.5	859	6	AAE33341 Mouse Tol
45	541	12.5	1041	2	AAW41768 Human PRO

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
AC	ABU04773;	
DT	29-JAN-2003	(first entry)
DE	Human expressed protein tag (EPT) #1439.	
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
OS	Homo sapiens.	
PN	WO200278524-A2.	
PN	XX	
PD	10-OCT-2002.	
XX	XX	
XX	28-MAR-2002; 2002WO-US009671.	
XX	XX	
XX	28-MAR-2001; 2001US-0279495P.	
XX	PR	21-MAY-2001; 2001US-0292544P.
XX	PR	08-AUG-2001; 2001US-0310801P.
XX	PR	01-OCT-2001; 2001US-0326370P.
XX	PR	04-DEC-2001; 2001US-0336780P.
XX	PR	20-FEB-2002; 2002US-0358985P.
XX	PA	(ZYCO-) ZYCO INC.
XX	PI	Chicz RM, Tomlinson AJ, Urban RG;
XX	DR	WPI; 2003-040607/03.
XX	PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX	PT	cytoskeletal proteins, receptors or transcription factors), useful for
XX	PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX	PT	leukemia.
XX	PS	Example 2; SEQ ID NO 1439; 134p; English.
XX	CC	The invention describes a purified polypeptide, which comprises a
XX	CC	fragment of a kinase, phosphatase, protease, protease inhibitor,
XX	CC	transporter, cytoskeletal protein, receptor or transcription factor. The
XX	CC	polypeptide is useful as an immunogenic composition for eliciting in a


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Db      1 MMSASRLAGTLLPAAAFSLSCVBPESWPCVEVVPNTTYOCMEINLFYKIDNLPFSTKND 60
Oy      60 LSFNPLKIRSYSPFTNFSQLQWLDLRCCEIETIEDKAMGNLQSLTVLTGNPIKSPSPG 119
Db      61 LSFNPLRHLGYSFSPFPELOVLDLSRCEIQTIEDAGVQSLSTLITLITGNPIQSLAG 120
Oy      120 SFGSLTNLENLVAVETKMTSLBGFHIGQISLKKLVANANLHSPKLPYPSNLTNLEHV 179
Db      121 AFSGLSLQKLVAVETNLASLENFPIGHKTKELVANANLQSPFLPEYPSNLTNLEHL 180
Oy      180 DLSYNTIQTISVKDLOFLRENPOVNLSDLSNLPIDISIOAQAQFQIRLHELTLSNPNSS 239
Db      181 DLSNKTIOSTYCTDLRVLHQMPLNLSDLSNPNMFIOPGAFAKEIRLHKLTLRNPNFSL 240
Oy      240 NYLKMCLQMTGHLVHRLILGEPKERNLSPDRSMEGLCNVSIIDEPFLTYINHPSDI 299
Db      241 NMKTCIOGLAGLEVRLVGEFRNGNLEKPDKALBGLCLNLTIEFRLAYLDYLDI 300
Oy      300 YNL-NCLANISAMSTGVHIIKILADVPRHFKWQSLIIRCHLKPEPKSLPELKSMTLT 358
Db      301 IDLFNCLTVVSSFLSVTIERKDPVSNFMQHLVNCQKQFPFLTKKSLKRLTFT 360
Oy      359 NREDISFGOLAPSLRYLDLSRNAMSPRCSSSDGTNNLKYLDLSFNGVILMSANENG 418
Db      361 NKGNAFSEVDLPSELPDLISRNGLSFKGCCSDPTTSLKXLDLSFNGVITMSNFDG 420
Oy      419 LBELEYLDFQHSITLKKVTEFSVFLSEKLTLYLIDISTNTKIDPDGIFLGISLNTKMG 478
Db      421 LROLEHLDPQHSNLMKQMSFVFLSLRNLIYLDISTHTRVAFNGIFNGLSLSEVLKMG 480
Oy      479 NSFCKNTLSNVFTNTNLFTLDSKQLEQISRGVDTLYRLQLMNSHNHLLFDPSHY 538
Db      481 NSFQENFLDIFTELNLFTLDSQCLQSLSTANSLSIQVAMSHNNPFLDTPFY 540
Oy      539 KQIYSIRTDSCFNRIETG-KGILQHPKSLAVFNLTNNSVACTCYQNFQWQKMF 597
Db      541 KCLNLSQVADVSIINHMTSKQELQHPPSLAFNLNTQNDPACTCHOSFLQWIKQOROL 600
Oy      598 LVNVEQMKASPIDMKASLVLDFTNSTCYIKTIIISVSVSVVAVTAVFLYHPEFHLI 657
Db      601 LVEVEHECAITPSDKQMPVLSI-NITCQNNKTIIVSVLSVAVSVAVLYKTFHLM 659
Oy      658 LTAGCKYSRGSBIYDAFYIYSSQNEQWVNLVKNLESGVPRFQCLHYRDFIPGVAIA 717
Db      660 LTAGCTIKYRGEMIVYAFVIYSSQDEDMVRLNKLVEGVPFQCLHYRDFIPGVAIA 719
Oy      718 ANIIOGFHKSRKVIYVSRHPTIOSRWCIPEYETIAQTWQPLSSRSIIPIVLEKYSLL 777
Db      720 ANIIEGFHKSRKVIYVSRHPTIOSRWCIPEYETIAQTWQPLSSRSIIPIVLEKYSLL 779
Oy      778 RQOVELYRLSRNTYLEWEDNLGRHIFMRRLKALLDDKALNPD--ETSEBOQATLL 834
Db      780 RQOVELYRLSRNTYLEWEDSVLGRHIFMRRLKALLDDKSNVBSGTGVCNMQEATSI 839

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XX      XX WO200278524-A2.
PN      XX
XX      XX 105OCT-2002.
PD      XX
XX      XX 28-MAR-2002; 2002MO-US009671.
PF      XX
XX      XX 28-MAR-2001; 2001US-0279495P.
PR      XX
XX      XX 21-MAY-2001; 2001US-0292544P.
PR      XX
XX      XX 08-AUG-2001; 2001US-0310801P.
PR      XX
XX      XX 01-OCT-2001; 2001US-0326370P.
PR      XX
XX      XX 04-DEC-2001; 2001US-0336780P.
PR      XX
XX      XX 20-FEB-2002; 2002US-0358985P.
PA      (ZYCO-) ZYCOS INC.
PI      Chicz RM, Tomlinson AJ, Urban RG;
XX      WPI; 2003-040607/03.
DR      XX
XX      XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX      XX cytoskeletal proteins, receptors or transcription factors), useful for
XX      XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX      XX leukemia.
XX      XX Example 2; SEQ ID NO 1441; 134pp; English.
XX      XX The invention describes a purified polypeptide, which comprises a
XX      XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX      XX polypeptide is useful as an immunogenic composition for eliciting in a
XX      XX mammal an immunogenic response directed against any of the purified
XX      XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX      XX polypeptide, is useful for treating cancer. The polypeptide is also
XX      XX useful for identifying compounds that binds to a naturally processed
XX      XX class I or class II MHC-binding polypeptide. The polypeptides and
XX      XX polynucleotides are particularly useful for treating or preventing
XX      XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      XX CC lymphoma or leukemia. These are also useful for screening agents for
XX      XX CC treating the above mentioned diseases. This sequence represents an
XX      XX expressed protein tag (EPT) isolated from human tissue for translational
XX      XX profiling. Note: this sequence does not appear in the printed
XX      XX CC specification but was obtained in electronic format directly from WIPo at
XX      XX CC ftp.wipo.int/pub/published_pct_sequences
XX      XX
XX      XX Sequence 839 AA;
XX      XX
XX      XX Query Match 66.0%; Score 2860.5; DB 6; Length 839;
XX      XX Best Local Similarity 66.5%; Pred. No. 4.1e-244;
XX      XX Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;
Oy      1 MMSASRLAGTLLPAAAFSLSCVBPESWPCVEVVPNTTYOCMEINLFYKIDNLPFSTKND 59
Db      1 MMSASRLAGTLLPAAAFSLSCVBPESWPCVEVVPNTTYOCMEINLFYKIDNLPFSTKND 60
Oy      60 LSFNPLKIRSYSPFTNFSQLQWLDLRCCEIETIEDKAMGNLQSLTVLTGNPIKSPSPG 119
Db      61 LSFNPLRHLGYSFSPFPELOVLDLSRCEIQTIEDAGVQSLSTLITLITGNPIQSLAG 120
Oy      120 SFGSLTNLENLVAVETKMTSLBGFHIGQISLKKLVANANLHSPKLPYPSNLTNLEHV 179
Db      121 AFSGLSLQKLVAVETNLASLENFPIGHKTKELVANANLQSPFLPEYPSNLTNLEHL 180
Oy      180 DLSYNTIQTISVKDLOFLRENPOVNLSDLSNLPIDISIOAQAQFQIRLHELTLSNPNSS 239
Db      181 DLSNKTIOSTYCTDLRVLHQMPLNLSDLSNPNMFIOPGAFAKEIRLHKLTLRNPNFSL 240
Oy      240 NYLKMCLQMTGHLVHRLILGEPKERNLSPDRSMEGLCNVSIIDEPFLTYINHPSDI 299
Db      241 NMKTCIOGLAGLEVRLVGEFRNGNLEKPDKALBGLCLNLTIEFRLAYLDYLDI 300
Oy      300 YNL-NCLANISAMSTGVHIIKILADVPRHFKWQSLIIRCHLKPEPKSLPELKSMTLT 358

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Db 301 IDLNFCLINVSFSLVSTIERVKDFSYNFGQHLVNVCKFGQFPFLTKSLKRLTETS 360
Qy 359 NREDISFGQALPSLRAYLDLSRNAMSFRCSCSYDPGTNNLKYLDLSFNGVILMSANFNG 418
xx 361 NKGNAFSEVDLPSELEFDLSRNGLSFKCCSQSDPGTSLKYLDSFNGVITMSNPLG 420
Qy 419 LEELEYLDPQHSSTLKKVTEFSVFLSEKLYLDISTYNTKIDPDGIFGLISLNTLKNAG 478
Db 421 LEQLEHDPQHSNLMKQMSSEFVFLSLRNLIYLDISHTHTRVAFNGIFNGLSLEVLKNAG 480
Qy 479 NSFQKNTLSNVFTNTNTNLFLDLSCQLEQISRGVDTLYRLQLNMSHNNLLFLDPSHY 538
Db 481 NSFQENFLPDIFTELRNLTFDLSCQLEQISPTAFNSLQVLNMSHNNFSLDTPPY 540
Qy 539 KQVSLRLTDCSPNRLET-S-KGILQHPKSLAVFNLITNNSVACICEYONFLQWYDQKF 597
Db 541 KCLNSLOVLDYSLNHNMTSKQELQHPESLSLFLNLTQNDFACTCEHQSFLQWIDQRL 600
Qy 558 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVSVLVVATVAFLIYHFFHLI 657
Db 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIIGSVLSVLVSVAVLVYKFFHLM 659
Qy 658 LIAGCKTYSRGSIIYDAFVIYSSQNEDEWVRNELVKNLEBGPFRQCLHYRDPFGVAIA 717
Db 660 LIAGCIKTGRGENIYDAFVIYSSQDEDEWVRNELVKNLEBGPFRQCLHYRDPFGVAIA 719
Qy 718 ANIIOEGFHKSRRKVIYVVSRRHFIQSRWCIFEYEIAQTMQFLSSRSGIIFVLEKYEKSL 777
Db 720 ANIHGPHKSRKVIYVVSQHFIOQRWCIFEYEIAQTMQFLSSRSGIIFVLYQYKEXTL 779
Qy 778 RQVVELYRLLSRNTYLEMEDNALGRHIFWRRLKALLDGKALNPD---ETSEEDQATTL 834
Db 780 RQVVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNWNPBGVGTGCMQGEATSI 839

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KM human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
XX
OS Homo sapiens.
XX
PN W02003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI, 2003-481990/45.
XX
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327bp; English.
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
SQ Sequence 839 AA;
Query Match 66.0%; Score 2860.5; DB 7; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;
Qy 1 MNPPLHAGTLMAL-FLSCLRPSGLNPCIYLPVITTCQMDONLSKIPHDIPYSTKLD 59
Db 1 MMSARLGLTLPAAAFSLCVRPSSEPCVEVPVITYQCEMLNFKLPDLPESTKLD 60
Qy 60 LSFNPLKILRSYSFTNFSQLOMLDLSCREIETIEDKAMHGNOLSTVLITGNPIKSPSG 119
Db 61 LSFNPLRLHLSGYSFSPSEFELQVLDLSREIQTIEDGAQSLSHTLITGNPIQSLALG 120
Qy 120 SPSGLTNLENLVAVETKNTSLIEGPHIGQLSKKLNVANHLIHSFKLPEYFSNLTNEHV 179
Db 121 AFSGLISLQKLVAEVTNLIASENFPIGHLTKLEINVAHNLIQSFKLPEYFSNLTNEHL 180
Qy 180 DLSVNYIOTISVKLOQFRENPOVNLSDLSINPDISIQAAPGCIPLHETLISNPFSS 239
Db 181 DLSNKKIQSIYCTDLRVLHQPPLNLSDLSLNPNNFQPAAPKIRLKLTLRNPFSL 240
Qy 240 NVLKMCLQNTGLHVRRLILEGFKNERLLEFDSVMEGLCNVSIDEBRLTYINHFSDI 299
Db 241 NVMTKCIQGLAGLEVHRVLGEFPNENGLERFDSALEGLCNLTIBERLAVLDYLDI 300
Qy 300 YNL-NCLANISAMSPFTGVHIXIADVPRIHPKQSLISIRCHLKPPLKSLPPLKSWTLTT 358
Db 301 IDLNFCLINVSFSLVSTIERVKDFSYNFGQHLVNVCKFGQFPFLTKSLKRLTETS 360
Qy 359 NREDISFGQALPSLRAYLDLSRNAMSFRCSCSYDPGTNNLKYLDLSFNGVILMSANFNG 418
Db 361 NKGNAFSEVDLPSELEFDLSRNGLSFKCCSQSDPGTSLKYLDSFNGVITMSNPLG 420
Qy 419 LEELEYLDPQHSSTLKKVTEFSVFLSEKLYLDISTYNTKIDPDGIFGLISLNTLKNAG 478
Db 421 LEQLEHDPQHSNLMKQMSSEFVFLSLRNLIYLDISHTHTRVAFNGIFNGLSLEVLKNAG 480
Qy 479 LEELEYLDPQHSSTLKKVTEFSVFLSEKLYLDISTYNTKIDPDGIFGLISLNTLKNAG 538
Db 481 NSFQENFLPDIFTELRNLTFDLSCQLEQISPTAFNSLQVLNMSHNNFSLDTPPY 540
Qy 539 KQVSLRLTDCSPNRLET-S-KGILQHPKSLAVFNLITNNSVACICEYONFLQWYDQKF 597
Db 541 KCLNSLOVLDYSLNHNMTSKQELQHPESLSLFLNLTQNDFACTCEHQSFLQWIDQRL 600
Qy 558 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVSVLVVATVAFLIYHFFHLI 657
Db 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIIGSVLSVLVSVAVLVYKFFHLM 659
Qy 658 LIAGCKTYSRGSIIYDAFVIYSSQNEDEWVRNELVKNLEBGPFRQCLHYRDPFGVAIA 717
Db 660 LIAGCIKTGRGENIYDAFVIYSSQDEDEWVRNELVKNLEBGPFRQCLHYRDPFGVAIA 719
Qy 718 ANIIOEGFHKSRRKVIYVVSRRHFIQSRWCIFEYEIAQTMQFLSSRSGIIFVLEKYEKSL 777
Db 720 ANIHGPHKSRKVIYVVSQHFIOQRWCIFEYEIAQTMQFLSSRSGIIFVLYQYKEXTL 779
Qy 778 RQVVELYRLLSRNTYLEMEDNALGRHIFWRRLKALLDGKALNPD---ETSEEDQATTL 834
Db 780 RQVVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNWNPBGVGTGCMQGEATSI 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

DT 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAF05316, SEQ ID NO 14536.
 XX
 KM Human: pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 OS Unidentified.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR MPI; 2003-268312/26.
 DR GENBANK; AAF05316.
 PT
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Example 1; Page: 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPD at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 839 AA;

Query Match 66.0%; Score 2860.5; DB 7; Length 839;
 Best Local Similarity 66.5%; Pred. No. 4.1e-244;
 Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;

QY 1 MNPDLHAGTIAL-FLSGRPGSLNPELV-NTTYOQMDNLSKIPHDYSTRKND 59
 DB 1 MNSASRLAGTLPAKMAFLSCVPSWBPCEVVPNTTYOQMDNLSKIPHDYSTRKND 60

QY 60 LSFNPLKIRSYSFNFNSOLOMLDLSRCEITIEDKAMHGLNQSTLVITGNPIKFSFG 119
 Db 61 LSFNPLRHLGYSYFSPFEPQLVTLDSRCEITIEBGAAYOSLSHSLTLITGNPIOSLAG 120
 QY 120 SFGSLTNLENLVAVEKMTSLGEPHGLISLKKLVANHLJHSPFLPEYFNSLTLEHY 179
 Db 121 AFSGLSSLOKLAVERNLASLNFPLGHTKTLKELVANLLOSFRLPEYFNSLTLEHY 180
 QY 180 DLSYNYITISVKDLOFLRENPOVNLSDLSNPIDSIOQAPOGIRLHELTLRSNFS 239
 Db 181 DLSNKKIGSITCTDLRYHLQWPLNLSDLSNPNNFIOPGAFKEIRLHKTLRNPFSL 240
 QY 240 NTLKRCLOMGTGLYHRLILGFEKNERNLBSDRSYMBGLCVASIDEPFLTYINHSDDI 299
 Db 241 NNMKTCIOGLAGLEHYRLVIGFEFRNENLEKEDKALBELCNLTIEBFLAYLDYLDI 300
 QY 300 NTLNCLNISMSTFGVHIIKILAVPHRKKOSLIIRCHLKPPFKSLPFLKSTLT 358
 Db 301 IDLFNCLTNVSSFSLSVSTIERVKDPSYNGQHLVYCKFGQFPFLKLSKLTFTS 360
 QY 359 NREDISFGQALPSIRYLDLSRNAMSFRGCCSYDFGTNNLKLYLDFNGVILMSANFG 418
 Db 361 NKGNAFSEVDLPSEFLDLSRNGLSFKGCCQSDPGTSLKXLDLSFVGVTMSNFI 420
 QY 419 LEELEYLDFQHSTLKKVTEFSVLSLEKLLYLDISYTNKIDPDGIFGLISLNTLKMAG 478
 Db 421 LEQLEHLDFOHNLKOMSEFVFLSLRNLIYLDISHTHTRVAFNGIFNGLSLEVLKMG 480
 QY 479 NSFKNLTLSNVTNTNTNLTLFLDSKCOLRQIRGVFDTLRYLQNLMSNNLLFLDRSHY 538
 Db 481 NSFQENFLPDITELRNLTFLDLSCQLEQLSPTAENSLSSQLVNMNSNNPFLDPY 540
 QY 539 KQYSLRTDSCFNFNLETS-KGILQHPKSLAVPLTNNSVACICEYQNFLOWVKQKMF 597
 Db 541 KCLNSLQVLDYDLNHLNIMSKQELHFPBSLAFNLTLQNDPACTCEHGFLOWKIDQRL 600
 QY 598 LVNVEQMKCASPIDMKASLVDFTNSTCYIYTIISVSVSVLVATVAFLIHYFHLI 657
 Db 601 LVEVERMECATPSDKQGMVLSL-NITQMNKTIIGVSLVSVVAVLVYKXFHLM 659
 QY 658 LTAGCKKYSRGSIYDAFVYSQNDWVRNLTNLERGVRFOLCHYRDFIPVATA 717
 Db 660 LTAGCKTKRGSENIYDAFVYSQNDWVRNLTNLERGVRFOLCHYRDFIPVATA 719
 QY 718 ANIIOGFPKSRKVIWVSRHFIQSRWCIFEYELIAQTWQFLSSRSGLIPIVLEKYEKSL 777
 Db 720 ANIIRGFPKSRKVIWVSRHFIQSRWCIFEYELIAQTWQFLSSRSGLIPIVLEKYEKSL 779
 QY 778 RQVELYRLLSNNTYLEWEDNALGRHIFWRLLKALLDQKALNP---ETSEEDQATLL 834
 Db 780 RQVELYRLLSNNTYLEWEDSVLGRHIFWRLLKALLDQKALNPDEGTGCMQWQATSI 839

RESULT 6
 AAW86361
 ID AAW86361 standard; protein; 837 AA.

AC AAW86361;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Human DNAX toll-like receptor DTLR4.

KM DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KM interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KM modulate inflammatory function; morphological effect;
 KM immunological disorder.

OS Homo sapiens.
 XX
 PN WO9805047-A2.
 XX
 PD 12-NOV-1998.

XX 07-MAY-1998; 98WO-US008979.
PF 07-MAY-1997; 97US-0044293P.
XX 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX (SCHE) SCHERING CORP.
PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
PI MPI: 1999-059670/05.
XX N-PSDB; AAV80675.
DR
XX MPI: 1999-059670/05.
PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
XX metabolism, modulate inflammatory function or innate immunity responses.
PS Claim 3; Page 147-149; 171pp; English.
XX
XX The present invention specifically describes human DNAX toll-like
XX receptors 2 to 10 (DTR2-10). The present sequence is human DTLR4 given
XX in the present invention. Also described are: (1) a fusion protein
XX comprising a DTLR protein or peptide; (2) a binding compound, preferably
XX an antibody or antibody fragment which specifically binds to a DTLR
XX protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
XX; (4) an expression vector comprising the nucleic acid of (3); and (5) a
XX host cell comprising the vector of (4). The host cell of (5) can be used
XX to produce the DTLR proteins. The DTLR proteins can be used to alter
XX phosphate metabolism, to modulate inflammatory function, innate immunity
XX responses or morphological effects. The DTLR proteins can be used in the
XX treatment of conditions exhibiting abnormal expression of the receptors
XX of their ligands. These abnormalities are typically manifested by
XX immunological disorders
SQ Sequence 837 AA;
Query Match 65.6%; Score 2844; DB 2; Length 837;
Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;
QY 2 MFLHAGTLIMAL-FLSCLRPSLNPCTEVL-PNTTYOQMDNLKIPHDISTKNDL 60
DB 1 MSASRLAGTLIPAMAFSCVPESWEPCEV-PNTTYQCEMLNPKIPNLPEFTKNDL 59
QY 61 SFNPKILRSYSFTNFSQLOMLDSRCETIETEDKAMGMLNSTLVLTGNPIKSFSPGS 120
DB 60 SFNPKILRSYSFTNFSQLOMLDSRCETIETEDKAMGMLNSTLVLTGNPIKSFSPGS 119
QY 121 FSGLTNLENLVAVETKMTSLSGFPHIGQLISLKKLVANHLISFKLPEYFSNLNLEHYD 180
DB 120 FSGLTNLENLVAVETKMTSLSGFPHIGQLISLKKLVANHLISFKLPEYFSNLNLEHYD 179
QY 181 LSYNYIQTISVKDLOFLRENPOVNLSDLSNPDISIQAGQGRHETLRSFNSNSN 240
DB 180 LSYNYIQTISVKDLOFLRENPOVNLSDLSNPDISIQAGQGRHETLRSFNSNSN 239
QY 241 VLKMLQONTGLAHVRLILGEFKNERNLSPDRSWEGLCNYSIDEFRLTYINHSDDY 300
DB 240 VLKMLQONTGLAHVRLILGEFKNERNLSPDRSWEGLCNYSIDEFRLTYINHSDDY 299
QY 301 NL-NCLANISAMSFTGVHAKIADYPRHFKWQSLIIRCHLKPFLSLPFLKSWTLTN 359
DB 300 NL-NCLANISAMSFTGVHAKIADYPRHFKWQSLIIRCHLKPFLSLPFLKSWTLTN 359
QY 360 REDISFGOLALPSLYLDSRNAMSPGSCSYSDGTNNLKYLDLSPFNVTIMSNPGL 419
DB 360 REDISFGOLALPSLYLDSRNAMSPGSCSYSDGTNNLKYLDLSPFNVTIMSNPGL 419
QY 420 BELLEVLPFOHSTLTKVTEFSVFLSEKLKYLDLSTYNTKIDYDGIPLGLISINTLKMG 479
DB 420 BELLEVLPFOHSTLTKVTEFSVFLSEKLKYLDLSTYNTKIDYDGIPLGLISINTLKMG 479
QY 480 SFKDNVTLNVTNTNLTFLDLISKQLEQISRGVFDLTLYRLQLLNNSHNNLLFLDP SHYK 539

DB 480 SFKDNVTLNVTNTNLTFLDLISKQLEQISRGVFDLTLYRLQLLNNSHNNLLFLDP SHYK 539
QY 540 QVSLRTDSCSFNRIETS-KGILQHPKSLAVFNLNNSVACICEYQNFLOMVKDQKML 598
DB 540 QVSLRTDSCSFNRIETS-KGILQHPKSLAVFNLNNSVACICEYQNFLOMVKDQKML 599
QY 599 VNVBQMKASPIDMKASLVDFTNSTCYIYKTIISVSVSVALVAVATFLLIYHFFHLIL 658
DB 599 VNVBQMKASPIDMKASLVDFTNSTCYIYKTIISVSVSVALVAVATFLLIYHFFHLIL 658
QY 659 IAGCKYRGESIIYDAFYIYSSQNEWDWRNMLVKNLESGVRFQCLHYRPFIFGVALA 718
DB 659 IAGCKYRGESIIYDAFYIYSSQNEWDWRNMLVKNLESGVRFQCLHYRPFIFGVALA 718
QY 719 NIIOBGFHKSRRVIVVSRHFIQSRMCIFFEYIQAQWOFSSRGIIPIYVEKYEKSLLR 778
DB 719 NIIOBGFHKSRRVIVVSRHFIQSRMCIFFEYIQAQWOFSSRGIIPIYVEKYEKSLLR 778
QY 779 QVVELYRLSLNNTYLEWEDNALGRHIFWRRLKALLDQKALNPD---ETSEBQBATTL 834
DB 779 QVVELYRLSLNNTYLEWEDNALGRHIFWRRLKALLDQKALNPD---ETSEBQBATTL 837
RESULT 7
ID AAE16102 standard; protein; 837 AA.
XX AAE16102;
AC AAE16102;
XX 26-MAR-2002 (first entry)
DT Human DNAX Toll like receptor (DTLR) 4 #2.
DE Human DNAX Toll like receptor; DTLR; therapy; immunological disorder;
XX Human; DNAX Toll like receptor; DTLR; screening; immunomodulator; chromosome 9q32-33.
XX Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX Homo sapiens.
XX WO200190151-A2.
XX 29-NOV-2001.
XX 23-MAY-2001; 2001WO-US016766.
XX 25-MAY-2000; 2000US-0207558P.
XX (SCHE) SCHERING CORP.
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
DB MPI: 2002-083085/11.
XX N-PSDB; AAD26292.
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
XX conditions exhibiting abnormal expression of the receptors of their
XX ligands, particularly abnormalities manifested by immunological
XX disorders.
PS Claim 3; Page 41; 297pp; English.
XX The invention relates to mammalian receptor proteins, e.g., primate,
XX human DNAX Toll like receptor (DTLR) protein and their corresponding
XX nucleic acids. The DTLR is useful for treating conditions exhibiting
XX abnormal expression of the receptors of their ligands. Such abnormality
XX is manifested by immunological disorders. In particular, the DTLR is
XX useful for treating various disease or disorders associated with abnormal
XX expression or abnormal triggering of response to a ligand. The DTLR is
XX also useful as an immunogen for the production of antisera or antibodies
XX specific, e.g., capable of distinguishing between other interleukin (IL)-1
XX receptor family members, for the DTLR or its various fragments. The
XX purified DTLR can be used to screen monoclonal antibodies or antigen-
XX binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTR or cells that express it. The present sequence is
CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
CC
CC NOTE: The present sequence SEQ ID NO 26 is stated to be similar to the
CC sequence shown in page 240-243 (AA016116). However these sequences differ
CC at several locations

SQ Sequence 837 AA;

Query Match	Score	DB	Length
65.6%	2844	5	837

Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6

[illegible]

ID	ABU04776 standard; protein; 837 AA.
AC	ABU04776;
XX	
XX	
DT	29-JAN-2003 (first entry)
DE	Human expressed protein tag (EPT) #1442.
XX	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX	protease; protease inhibitor; transporter; cytoskeletal protein;
KW	receptor; transcription factor; cancer; MHC;
KW	major histocompatibility complex; melanoma; colon cancer; gastric cancer;
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX	
OS	Homo sapiens.
XX	
PN	MO200278524-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002WO-US009671.
XX	
PR	28-MAR-2001; 2001US-0279495P.
XX	
PR	21-MAY-2001; 2001US-0292544P.
XX	
PR	08-AUG-2001; 2001US-0310801P.
XX	
PR	01-OCT-2001; 2001US-0326370P.
XX	
PR	04-DEC-2001; 2001US-0336780P.
XX	
PR	20-FEB-2002; 2002US-0358985P.
XX	
PA	(ZYCO-) ZYCOS INC.
XX	
PI	Chicz RM, Tomlinson AJ, Urban RG;
XX	
DR	WPI; 2003-040607/03.
XX	
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX	cytoskeletal proteins, receptors or transcription factors), useful for
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX	leukemia.
XX	
PS	Example 2; SEQ ID NO 1442; 134dp; English.
XX	
XX	The invention describes a purified polypeptide, which comprises a
XX	fragment of a kinase, phosphatase, protease, protease inhibitor,
CC	transporter, cytoskeletal protein, receptor or transcription factor. The
CC	polypeptide is useful as an immunogenic composition for eliciting in a
CC	mammal an immunogenic response directed against any of the purified
CC	polypeptide. The purified polypeptide, or the antibody that binds to this
CC	polypeptide, is useful for treating cancer. The polypeptide is also
CC	useful for identifying compounds that binds to a naturally processed
CC	class I or class II MHC-binding polypeptide. The polypeptides and
CC	polynucleotides are particularly useful for treating or preventing
CC	lymphoma or leukaemia. These are also useful for screening agents for
CC	treating the above mentioned diseases. This sequence represents an
CC	expressed protein tag (EPT) isolated from human tissue for translational
CC	profiling. Note: This sequence does not appear in the printed
CC	specification but was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 837 AA;
XX	
XX	Query Match 65.6%; Score 2844; DB 6; Length 837;
XX	Best Local Similarity 66.5%; Pred. No. 1.2e-242;
XX	Matches 558; Conservativity 114; Mismatches 159; Indels 8; Gaps 6;
QY	2 MPELHAGTLMAL-FLSCLRPGSLNCLIEVLNNTTQCNDNSKIPHDIPYSTRKNDL 60
DB	1 MSASRLGTTLLPAMAFSLCVBPESWEPCEVY-PNITVOCEMLNFKYKIPDNPFSRKNIDL 59
QY	61 SENEPLKIRASFLNFSQLOWLDISRCIEITIEKAMHGNQSLTIYVLTGNPKISFSPGS 120
DB	60 SFNPLRHUGASTSFPSPFLQVLDISRCIEITIEKGAAYOSHSHTLITGNPKISLALGA 119

QY	121	ESGLTLENLVAIVETOMTSLSEGHIIQOLISLTKLNAVHNLIHSPKLPETYSNLTNLEHVD	186
Db	120	FGGLSSLOQLVAAEINLVLASLENPFIHLKTLTKELNAHNLIOGFKLPETYSNLTNLEHLD	1797
QY	181	LSYNYIQTISVVDLOFLRENPQVNLSDLSLNFIDSIOAQAFQIGIRLHELTLSNFSSN	2464
Db	180	LSNNKIQSYICVDLRLVHQMPLNLNSDLSTNPMNPQPAFAKEIRLHKLTLRNPNPSLN	2393
QY	241	VLXMCLONNTGJLHVHRLIIGEPFNEBNLBSFDSSVMEGLCNVSIDERLTYVIMHPSDIY	3000
Db	240	VNKTCIOGLAGLEVHRLVIGEFNEGNLEKFKDSALEGICNLTYEERLAVLDYLDII	2299
QY	301	NL-NCIANISAMSEFGVNHKHTADVBRHFMQSLSIIRCLKRPKPLSLPELKSMTLTN	3552
Db	300	DLFNCITNWSSTSLVSVTIERVDFSYNGWQHLVNCCKFGQPTLKTKSLKRLTFTSN	3559
QY	360	REDISFGQALPRLRYLDSRNAMSEPGCCSYSDPGTNLKLVDLSFNGVILMSANMGL	4191
Db	360	KGNAFSEVDLSLEFLDLSRNLSTKCCGCSQSDPGTISLKYDLSNGVITMSSNPLGL	4199
QY	420	ELEVLDPGHSTLKKATBESVFLSEKLYLDISYNTKIDPGLIFGLISLNTLKMAGN	4797
Db	420	BOLEHLDPOHSNMLKOMSEFSVFLSLRNLIYLDISHHTREVAFNGIFNGLSLSEVLKMAGN	4797
QY	480	SPKDNLSVNFNTNTNLTELDLSKCOLQOISRGVPTLYRLQOLMNSHNLLFLDPSHYK	5399
Db	480	SPQENFLPDIFTELRLNLTFLDSQCEQLSPAFNSLSLQVLMNSHNHFPSLDTPPYK	5399
QY	540	QLYSRLTLDSCSFNRLETS-KGILQHPKSLAVENLTNNSVACICEYONFLQWKOQMF	5989
Db	540	CLNSLOVLDYSLNHIMTSSKKQELQHPSSLAPLNLQONPACICEHOSFLQWIKDOROL	5999
QY	599	VNVEQMKCASPLDMKASLVLDFPNSSTCYIYKTIISVSVSVLVAVTAVFLIYHPYHLL	6588
Db	600	VEVERMECATPBDKQMPVLSL-NITCOMNKTIIGVSVLSVLVSVAVLYYKFFHML	6588
QY	659	IAGCKKYSGESIYDAFVIYSSONEMVAVNELVONLEEGVPRQCLAHYADPLPGVATIA	7181
Db	659	LAGCKIKYRGSEIYDAFVIYSSODEBVMRELKVLBEGVPRQCLAHYADPLPGVATIA	7181
QY	719	NIIOGFHKSRCRIVVSSHFIQSRWCICEYEYEAQTQWFLSSRSGIIFIVLEKVESLIR	7781
Db	719	NIHHEGFHKSRCRIVVSGHFQSRWCICEYEYEAQTQWFLSSRSGIIFIVLQVEKTLIR	7781
QY	779	QOVELYRLLSRNTTYLEMEDNALGRHIFMRRLKALLDGRALND---ETSEEQEATTL	8341
Db	779	QOVELYRLLSRNTTYLEMEDSVLGRHIFMRRLKALLDGKSNPEGTIVGTCNNQOEATSI	8371
RESULT 9			
AAE16116			
ID	AAE16116 standard; protein, 837 AA.		
XX	AAE16116;		
AC			
DT	26-MAR-2002 (first entry)		
XX			
DE	Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.		
XX			
KW	Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;		
KW	interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	Misc-difference 211		
FT	/label= unknown		
XX	/note= "Encoded by AAY"		
XX	W0200190151-A2.		
XX			
DD	29-NOV-2001.		

[illegible]

QY 420 EELEYLDPOHSTLTKVTERSVFLSLKLYLDISTYNTKIDDPGIFLGISLNTLMKAGN 479
 Db 420 EQLHLDPOHSLMKOMSEFSVFLSLRNLITLDISHTRVAFNGIFNGISLSEVLKMGN 479
 QY 480 SFKDNLTSLVFNNTNLTFLDLSKCOLBOISRGVPTLRLQULMNSHNLLFLDPSSHK 539
 Db 480 SFGNFTLPDIFELNLTFLDLSQCOLBQUSPTAFNSLSLOVLNNSHNFFSLDTPFK 539
 QY 540 QLYSLRTLDSCFNRIETS-KGILQHPKSLAVENLTNNSVACICEYONFLQWVKQKML 598
 Db 540 CLNSLOVDLYSLNHTMTSKQELQHPSPSLAFNLINQDNFACTCEHQSLQWIKQORLL 599
 QY 559 VVVEQMKASPIDMKASLYLDFTNSTCYTKTITISVSVSUVVATVAFILYHFFHLL 658
 Db 600 VEEVMECATPSPDKCMPLSL-NITCQNNKTIIGSVLSVAVSVAVLYKFFHML 658
 QY 659 IAGCKYSGESIYAFVYSSQDNEDWVNELVKOLEBGPFCOLCHYRDPFGVATAA 718
 Db 659 IAGCTKRGENTYAFVYSSQDEBWNELVKNLEBGPFCOLCHYRDPFGVATAA 718
 QY 719 NIIQGFHKSRYIVVSNHPIQSRWCIFVEYIAQTWQPLSSRSGIIFVLEKVEKSLR 778
 Db 719 NIIHGFHKSRYIVVSNHPIQSRWCIFVEYIAQTWQPLSSRSGIIFVLEKVEKSLR 778
 QY 779 QQVELYRLSLRNTYLEMEDNALGRHIFWRRLKALLDGCALNPD--ETSEBQATTL 834
 Db 779 QQVELYRLSLRNTYLEMEDSVLGRHIFWRRLKALLDGCALNPD--ETSEBQATTL 834

RESULT 10

AD057797 standard; protein; 801 AA.

AD057797;

12-AUG-2004 (first entry)

Squirrel monkey toll-like receptor 4 SEQ ID NO:18.

XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 XX sepsis; severe sepsis; septic shock; asthma; squirrel monkey.

OS Saimiri sciureus.

FH Key Location/Qualifiers

FT Misc-difference 14

FT /label= leu, phe

PN WO2004042365-A2.

PD 21-MAY-2004.

PE 03-NOV-2003; 2003WO-US036247.

PR 01-NOV-2002; 2002US-0423113P.

PA (EVOL-) EVOLUTIONARY GENOMICS LLC.

PI Messier W;

DR WPI; 2004-400726/37.

DR N-PSDB; AD057795, AD057796.

XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 FT sequence of the Old World monkey with that of a human.
 XX Dieclourel; SEQ ID NO 18; 111pp; English.

CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World

CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents squirrel monkey TLR4.

XX Sequence 801 AA;

Query Match 64.5%; Score 2796.5; DB 8; Length 801;
 Beet Local Similarity 67.7%; Pred. No. 1.8e-238;
 Matches 539; Conservative 105; Mismatches 149; Indels 3; Gaps 3;

QY 31 VLPNTTYQCMQNDLSKIPHDIPYSTRKNDLSFNPPLKIRSYPTFNSOLQWMDLSRCETE 90
 Db 1 VVPNTTYQCMELNKKIKDINIPSTRKNDLSFNPPLRHGSHSFNFPBLOVLDLSRCDIQ 60
 QY 91 TIEDKAMHGLNQLSTLVLTGNPIKSPSPGSGFLTNLENLVAETKMTSLGEGHIGOLIS 150
 Db 61 TIEDGAYQSLSHSLSTLITGNPIQWALGARGSLQKLVAVETHLSLENFPIGHLKT 120
 QY 151 LKLVANANLHSPFLPEYFENLTLEHVDLSYNTYQITISYKVDLOFLKBNQVNLSDLS 210
 Db 121 LKDLNVANNLQSPFLPEYFENLTLEHVDLSYNTYQITISYKVDLOFLKBNQVNLSDLS 180
 QY 211 LNPIDSIQAOAFQGRRLHELTLSNFNSNVLKQCLQWMTGLHYRLHILGEGKNERNES 270
 Db 181 LNPIDFIQPGAFKEIRLKLTLRNPFSLNMMKKTIOGLAGLEVRLVGLGERRNRNED 240
 QY 271 FDRSVMEGLCNVSDIDEFLTYINHFSDIYNI-NCLANISAMSPFGVHIKHIADYPRHFK 329
 Db 241 FDKSALBGLCNUTINEFLAYLIDPLDIDILFNLAVSSFLNVHIIKREDPSYNR 300
 QY 330 WQSLIIRCHLKPPKLSLPLFKSWTLTTNRBDSFGQLAPSLRYLDLSRANSFRGCC 389
 Db 301 WQHELNVNCFQOPPLKSLKRLTFANKGRNHFSDVDPSEFLDLSRNGSLFKGCC 360
 QY 390 SYSDEGTNNLKYLDLSFNGVILMSANFGLBELEYLDPOHSTLTKVTERSVFLSEKLY 449
 Db 361 SOSDEGTISLKYLDLSFNDVITMGSNFGLQLEHLDQHSNLMKOMSFSVFLSLRNLIT 420
 QY 450 LDISYNTKIDPDGIFLGISLNTLKVAGNSPKONTLSNVEFTNTNTLFLDLSKCOLBOI 509
 Db 421 LDISHTRVAFNGIFNGIFSLKVLKVAGNSFQGNFLIEDIDFLDNNLLFLDSECOLBOL 480
 QY 510 SRGVPTDITLYRLQNLMSHNLLFLDPSTYKOLYSRTIDCSFNRIETSKG-ILQHPKSL 568
 Db 481 SPTAFDLSLPRLRILNMSHNFFALDTPPYKLYSLQVLDYSILNHTGTSKQELQHPPSL 540
 QY 569 AVFNLTNNSVACICEYONFLQWVNDQKMLVNVNOMKASPIDMKASLYLDFTNSTCY 628
 Db 541 AFLNLQDNDFACTCEHOSFLOMIXDQRLVLEVEOMEBATNLRKGIPLVL-NITCQMS 599
 QY 629 KTIISVSYSVAVVATVAFILYHFFHLLIAGCKYSGESIYDAFYISSQDNEDWRN 688
 Db 600 KTIIGSVLSLVVSVAVVAVLYKFFHMLLAGCKYRGENTYDAFYISSQDEBWRN 659
 QY 689 ELVKNLEBGPFCOLCHYRDPFGVATAANIIOBGFHKSRYIVVSNHPIQSRWCIFE 748
 Db 660 ELVKNLEBGPFCOLCHYRDPFGVATAANIIEHGFHKSRYIVVSNHPIQSRWCIFE 719
 QY 749 YEIAQTWQPLSSRSGIIFVLEKVEKSLTROOVLELYRLSLNNTYLEMEDNALGHIIFRR 808
 Db 720 YEIAQTWQPLSSRSGIIFVLEKVEKSLRQOVELYRLSLNNTYLEMEDSVLGRHIFWR 779
 QY 809 LKCALLDGCALNPDPT 824
 Db 780 LKCALLDGRPMNPGT 795

RESULT 11

AD057791
ID AD057791 standard; protein; 795 AA.
XX AC AD057791;
XX
XX
DT 12-AUG-2004 (first entry)
DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
XX toll-like receptor 4; TUR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS Macaca mulatta.
FH Key Location/Qualifiers
FT Misc-difference 635
FT /label= Lys, Asn
FN WO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Meslier W;
XX
XX WPI: 2004-400726/37.
DR N-PSDB; AD057789, AD057790.
XX
XX
XX Identifying a nucleotide change in a TUR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TUR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX
XX Disclosure; SEQ ID NO 12; 111pp; English.
XX
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TUR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TUR4 polynucleotide sequence of the Old World
CC monkey with corresponding TUR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TUR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents rhesus monkey TUR4.
XX
XX
XX Sequence 795 AA;
SQ
Query Match 64.2%; Score 2782.5; DB 8; Length 795;
Best Local Similarity 67.5%; Pred. No. 3.1e-237;
Matches 537; Conservative 109; Mismatches 146; Indels 3; Gaps 3;
QY 31 VLPNITTYOCMDONLSKIPHDIPSTKNDLSFNPILKILRSYSPYNSOLQWDLSCREIS 90
DB 1 VVFNITTYOCMEINPFKIPNLPSTKNDLSFNPILRHLSISYFSPFPELQVUDLSRCEIQ 60
QY 91 TIEDKAMHGLNQLSTVLVTGNPIKSPSPGSGLTNLENLVAETKMTSLSGFHIQGLIS 150
DB 61 TIEDGAYGSLSHLSTLITGNPIQSLDGAFGSLQGLVAVERNILASLENFPIGHUKT 120
QY 151 LKKNAVANHLLHSFKLPEYFSNLTLNLEHDLSTYNTIGTISVADLQFLKRNPOVNLSDIS 210
DB 121 LKELNVANHLLIOSFKLPEYFSNLTLNLEHDLSSNKIQNTYCKDLQVLHQMPLSNLSLDS 180
QY 211 LNPIDISIQAFQGRILHELTLSRNPNSGNVLKMGCLQNNNTGJLHVRLTIGEFKERNIES 270
DB 181 LNPINPIQGFATKIRLHKULTRSNFDLNVKTKICQGLAGLJVRHLVIGEFERNERLEE 240

QY 271 FDRSVMGLCNVSIIDEPRLTYINHPSDDIYNL-NCLANISAMSTGVHIIKIAVPRHFK 329
DB 241 FDKSLBGLCNLTJTEBFLTYLDYLDNIIDLFCNLANVSSPISVSIKREVEFSSVNR 300
QY 330 MOSLITRCHLKPPPKSLPLFLKSMWLTLTNEDISFQGLAPSLRYLIDLSNNMSRCC 389
DB 301 WQHELVNCKEQQPPTLEBSLKRLTFPANGNAPSVSDVPSLEFDLSTNGISFKGCC 360
QY 390 SYSPDGTNLLKYLDLSPFNGVILMSANFMELEBELEDFQHSSTLKVKTEFSVFLSEKLLY 449
DB 361 SQSDPGTISLKLKLDLSPFDVITMSNPLGLEKLEHDPQHNLLQMSQFSVFLSRNLIY 420
QY 450 LDISYTNKIDPDGIFGLISLNTLKVAGNSFKONTLSNFTNTNLTFLDLSKQGLEOI 509
DB 421 LDISHTHRAVFNGLFDGLSLKVLKVAAGNSFQENFLPDIPTDLKNLTFPLDLSQGLEOL 480
QY 510 SRGVPTLYRLQULNMSNNLLPLDPSHYKQULYSKRLDGFNRLERSKG-ILQHFPSSL 568
DB 481 SPFAEDTLNKLQVLNMSNNPFSIDTFPEYKCLPSLQVLDYSLNHTMSNNQELQHPSSL 540
QY 569 AVFNLTNNSVACICEYQNFQWMDQKMFVNVBOMKCAPIDMKASLVLDPSTNCTYIY 628
DB 541 AFLNLTQNDPACTGCHGSLQWMDQKQVLVBAERMECATPSDQGMVLSL-NITQGM 599
QY 629 KTIISVSYSVLYVATVAFILYHFFPHLILIAQCKKTSRGESIYDAFYISSQNEDEVNR 688
DB 600 KTIIGSVYSVLYVAVVAVLYKKEYPHMLIAGCIXYGRGENIYDAFYISSQNEDEVNR 659
QY 689 ELVKNLEBGRPRLCLHYRDFIPGVAAANIIOGFFKSKRVVWVSRHFIQSRWCFE 748
DB 660 ELVKNLEBGRPRLCLHYRDFIPGVAAANIHEGFFKSKRVVWVSRHFIQSRWCFE 719
QY 749 YEIAQTWQLSSRSGIIFIVLEKYKSLRQOVELYRLSHNTYLEMEDNALGHIEMWR 808
DB 720 YEIAQTWQLSSRSGIIFIVLQYKXKTLRQOVELYRLSHNTYLEMEDSVLGGHIFWR 779
QY 809 LKKALLDQKALNPDE 823
DB 780 LKKALLDGRSWNPDE 794
RESULTS
AD057800
ID AD057800 standard; protein; 795 AA.
XX
XX AD057800;
XX
XX 12-AUG-2004 (first entry)
XX
XX
XX Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
XX toll-like receptor 4; TUR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS Papio hamadryas.
XX
XX WO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Meslier W;
XX
XX WPI: 2004-400726/37.
DR N-PSDB; AD057798, AD057799.
XX

PT Identifying a nucleotide change in a TUR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TUR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
PS Disclosure; SEQ ID NO 21; 11bp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TUR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TUR4 polynucleotide sequence of the Old World
CC monkey with corresponding TUR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TUR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents hamadryas baboon TUR4.
XX
SQ Sequence 795 AA;
Query Match 64.2%; Score 2781.5; DB 8; Length 795;
Best Local Similarity 67.7%; Pred. No. 3.9e-237;
Matches 538; Conservative 106; Mismatches 148; Indels 3; Gaps 3;
QY 31 VLPNITTCQMDQNTSKIPHDIPYSTKNLIDSPNPKIIRSYSTFNFSQLOLWDLSCREIE 90
DB 1 VVPNITTCQMDLNFYKIPDNIPFSTKNLIDSFNPRHIGSYFELFPELOVLDLSRCEIQ 60
QY 91 TIEBKAMHGLNQLSTLVLTGNPIKSFSPGSGLTNENLVAVENTKMTSLGPHIGOLIS 150
DB 61 TIEBGAVYSLHSLTLITGNPIQSLALGARSGLSLQKLVAVETNLASLENFPIGHLKT 120
QY 151 LKTLNVAHNLHSPFLPEYFENLTLNLEHVDLSYNYIQTISVYKLOFLRENQOVNLSLDS 210
DB 121 LKELNVAHNLQSFRLPEYFENLTLNLEHVDLSNNKIQIYCKDQVLMPLNLSLDS 180
QY 211 LNPIDSTIAQAPQGIHRLHETLRSNFNSNVLKMLQNMGTGLHVRLLIGEFKERNIES 270
DB 181 LNPINFIOPGAFKEIRHKLTLRSNFDLNVWKTICIGLAGLEHVRLLIGEFERNERNIE 240
QY 271 FDRVMEGLCNVSDIEPFLTYINHESDIYNL-NCLANISMSFTGVHKKIADVPKHX 329
DB 241 FDKALBEGCNLTLEEFRLTYLDYLDNIIDLFCNLAASSFLSVNIKREDSYNYFR 300
QY 330 WQSLIIRCHLKPFPKLSLFLKSWTLTTNREDISFGQALPSRLYDLSSRNAMSFRCGC 389
DB 301 WQHLVAVNCKEFPQPTLLESLKRLTFANKGNAFSEVDPLSEFLDLNRNGLSFKGCC 360
QY 390 SYSDFGTNNLKYLDLSPNGVILMSANFNGLEBEYLDFOHSTLKKVTEFSVFLSEKLLY 449
DB 361 SOSDFGTTSLKYLDLSPNDVITMGSNFLGLBQLEHLDFOHSLKMQSQFSVFLSLRNLIY 420
QY 450 LDISTYTNKIDPDGFLGLISINTLKMGNSFKNTLSNVPNTNLTFLDLISKQLFOI 509
DB 421 LDISHHTYTVAFNGTDELTLKVLKMGNSFOENFLDIDFLDKNLTLFLDLISQQLBQL 480
QY 510 SRGVEDTLYRLQLNMSHNNLLFLDPSHYKOLYSLRTDSCFNRIETSKG-ILQHPKSL 568
DB 481 SPTAFDITANKQVLNMSHNNFSLDVPYKCLPSIQVLDYLSLNTMTKNOBEPQHPSSL 540
QY 569 AVENLTNNSVACICEYQNFQWVDQKMLFVNVEQMKCASPIDKASLVLDTNSTCYIY 628
DB 541 AFLNLTQDPFACGCEHQSFLQMIKQROTLVEABREMCATPSDKGMFVLG-VNITTCQMN 599
QY 629 KTIISVSVSIVAVATVAFLYHPEFHLILTAGCKKRGESINYAFVITYSQNDWVRN 688
DB 600 KTIIGVSFVSIVAVAVAVLYKFEFHLMLLAGCCKYRGENTYDAFIYSSQDDWVRN 659
QY 689 ELVKNLEBGRVPOFCLHYRDFIPGVAIAANIIOGFHKSRYIVVVRSHFIOSEWCFE 748
DB 660 ELVKNLEBGRVPOFCLHYRDFIPGVAIAANIHHGFHKSRYIVVVSQHFIQSNWCIFE 719
QY 749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLRQOVELYRLLSRNTYLEWEDNALGRHIFWRR 808

DB 720 YEIAQTWQFLSSRSGIIFIVLEKVEKTLRQOVELYRLLSRNTYLEWEDSVLGQHIWRR 779
QY 809 LKKALDQKALNPDE 823
DB 780 LKKALDGRSWNPBE 794
RESULT 13
AD057803
ID AD057803 standard; protein; 808 AA.
XX
XX AD057803;
AC AD057803;
XX
XX 12-AUG-2004 (first entry)
DT
XX Chimpanzee toll-like receptor 4 SEQ ID NO:24.
DE
XX toll-like receptor 4; TUR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
XX Pan troglodytes.
OS
XX W02004042365-A2.
EN
XX
XX 21-MAY-2004.
PD
XX
XX 03-NOV-2003; 2003WO-US036247.
PE
XX
XX 01-NOV-2002; 2002US-0423113P.
PR
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
PA
XX
XX Messier W;
PI
XX WPI: 2004-400726/37.
DR
XX N-PSDB; AD057801, AD057802.
XX
XX
PT Identifying a nucleotide change in a TUR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TUR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
PS Disclosure; SEQ ID NO 24; 11bp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TUR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TUR4 polynucleotide sequence of the Old World
XX monkey with corresponding TUR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TUR4 polynucleotide sequence of an Old World monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents chimpanzee TUR4.
XX
SQ Sequence 808 AA;
Query Match 64.1%; Score 2777; DB 8; Length 808;
Best Local Similarity 66.7%; Pred. No. 9.9e-237;
Matches 540; Conservative 113; Mismatches 150; Indels 6; Gaps 4;
QY 31 VLPNITTCQMDQNTSKIPHDIPYSTKNLIDSPNPKIIRSYSTFNFSQLOLWDLSCREIE 90
DB 1 VVPNITTCQMDLNFYKIPDNIPFSTKNLIDSFNPRHIGSYFELFPELOVLDLSRCEIQ 60
QY 91 TIEBKAMHGLNQLSTLVLTGNPIKSFSPGSGLTNENLVAVENTKMTSLGPHIGOLIS 150
DB 61 TIEBGAVYSLHSLTLITGNPIQSLALGARSGLSLQKLVAVETNLASLENFPIGHLKT 120
QY 151 LKTLNVAHNLHSPFLPEYFENLTLNLEHVDLSYNYIQTISVYKLOFLRENQOVNLSLDS 210

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Db      121 LKELNVAHNLQSFGLPEYFNSLNLNLEHLDLSSNKIKQSYCTDLRVLHQMPLNLSDLS 180
Qy      211 LNPIDSIOAOPQGIIRLHELTLRSNPNSSNVLKMCLOMMTGIAVHRLILGEFKERNIES 270
Db      181 LNPMPFIQPAFAKRIHLKHLTLRNNFDSLNVWKTCIOGLAGLEVARIVLGEFRNENLEK 240
Qy      271 FDRSMVEGLCNVSIDEFRLTYINHSDDIYNL-NCLANISAMSTGVHIIKHIAVPRHPK 329
Db      241 FDKSALBGLCNLTIEFRLAYLDYLDIIDLNFCLTNVSSFSILSVTIKSVKDSYNFG 300
Qy      330 WQSIIIRCHLKPPKLSLPLKSWTLTTNREDISFGOLAPSLAYLDSRNAMSFRGCC 389
Db      301 WQHLVAVCKRQGPFTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSNGLSFGGCC 360
Qy      390 SYSDFGNNLKYLDLSFNGVILMSANFMGLBELEYLDPOHSTLKKTVEFSVLSLEKLY 449
Db      361 SOSDFGTTSLKXLDLSFNGVILMSNFIQLBGLHLDPOHSLKQMSSEFSVLSLRNLIY 420
Qy      450 LDISYTNKIDPDGIFLGLISLNTLTKMAGNSFKDNTLSNVPTNTNLTFPLDLSKQLEQI 509
Db      421 LDISHHTRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIETELRNLTFPLDLSQCLEQL 480
Qy      510 SRGVDLTLYRLQOLNMSHNNLLFLDPHYKQYSLRTLDCSPNRLETS-KGILGHFPRSL 568
Db      481 SPTAFNSLSLQVLNMSHNNFSLDTPPYKCLNSLQVLDSLNHIMTSKQELQHPSSL 540
Qy      569 AVFNLTNNSVACICEYONFLOWVDQKMFVNVQMKCASPIDMKASVLDPFTNSCYIY 628
Db      541 AFLNLQNDFACTGCHQSFLOMKIKQROLIVEVERMECATPSDKQGMVLSL-NITCQMN 599
Qy      629 KTIISVSVAIVVATVAFLIYHFYFHLILLAGCKKYSRGSISYDAFVIYSSQEDWVRN 688
Db      600 KTIIGSVLSVAVVAVLVYKFFHMLLAGCIKYGGENIYDAFVIYSSQEDWVRN 659
Qy      689 ELVKNLEBGVRFQCLHYRDPFPGVATAANIIOGCFHKSRYIVVSRHFIQSWCTFE 748
Db      660 ELVKNLEBGVRFQCLHYRDPFPGVATAANIIEGPHKSRYIVVVSQHFIOQSWCTFE 719
Qy      749 YEIAQTWQFLSSRSGLFIYVLEKYEKSLRQOVELYRLSRNTYLEWEDNALGRHIFWR 808
Db      720 YEIAQTWQFLSSRAIFIVLQKVEKTLIRQVELYRLSRNTYLEWEDSVLGRHIFWR 779
Qy      809 LKKALLDGRKALNPD---ETSEBQATTL 834
Db      780 LRKALLDGRKSWNPBGTVGTCNMQCATSI 808

RESULT 14
AD057782
ID      AD057782 standard; protein; 808 AA.
XX
AC      AD057782;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS      Pan troglodytes.
XX
PN      MO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PE      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVL- ) EVOLUTIONARY GENOMICS LLC.

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PI      Messier W;
XX
XX      WPI; 2004-400726/37.
DR      N-PSDB; AD057780, AD057781.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1; SEQ ID NO 3; 111pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiaesthetic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX
SQ      Sequence 808 AA:
XX
Query Match          64.0%; Score 2773; DB 8; Length 808;
Best Local Similarity 66.7%; Pred. No. 2,2e-236;
Matches 540; Conservative 112; Mismatches 151; Indels 6; Gaps 4;

31 VLPIITTYQCDMDNSKIPHDIPYSTKNLDSFNPDLKILRSYFTNFSQOLMDLSRCEIE 90
   1 VVPNITTYQCDMDNSKIPDNLPFSTKNLDSFNPDLKILRSYFTNFSQOLMDLSRCEIE 60
Db      1 TIEDKAMHGNQSLTILVNGNPIKSPGSGTNTLENVAVETKMTSGEFGIQLIS 150
Qy      61 TIEDGATQSLSHSLTILVNGNPIKSPGSGTNTLENVAVETKMTSGEFGIQLIS 120
Db      151 LKELNVAHNLHSPKLEPEYFNSLNLNLEHLDLSSNKIKQSYCTDLRVLHQMPLNLSDLS 210
Qy      121 LKELNVAHNLQSFGLPEYFNSLNLNLEHLDLSSNKIKQSYCTDLRVLHQMPLNLSDLS 180
Db      211 LNPIDSIOAOPQGIIRLHELTLRSNPNSSNVLKMCLOMMTGIAVHRLILGEFKERNIES 270
Qy      181 LNPMPFIQPAFAKRIHLKHLTLRNNFDSLNVWKTCIOGLAGLEVARIVLGEFRNENLEK 240
Db      271 FDRSMVEGLCNVSIDEFRLTYINHSDDIYNL-NCLANISAMSTGVHIIKHIAVPRHPK 329
Qy      241 FDKSALBGLCNLTIEFRLAYLDYLDIIDLNFCLTNVSSFSILSVTIKSVKDSYNFG 300
Db      330 WQSIIIRCHLKPPKLSLPLKSWTLTTNREDISFGOLAPSLAYLDSRNAMSFRGCC 389
Qy      301 WQHLVAVCKRQGPFTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSNGLSFGGCC 360
Db      390 SYSDFGNNLKYLDLSFNGVILMSANFMGLBELEYLDPOHSTLKKTVEFSVLSLEKLY 449
Qy      361 SOSDFGTTSLKXLDLSFNGVILMSNFIQLBGLHLDPOHSLKQMSSEFSVLSLRNLIY 420
Db      450 LDISYTNKIDPDGIFLGLISLNTLTKMAGNSFKDNTLSNVPTNTNLTFPLDLSKQLEQI 509
Qy      421 LDISHHTRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIETELRNLTFPLDLSQCLEQL 480
Db      510 SRGVDLTLYRLQOLNMSHNNLLFLDPHYKQYSLRTLDCSPNRLETS-KGILGHFPRSL 568
Qy      481 SPTAFNSLSLQVLNMSHNNFSLDTPPYKCLNSLQVLDSLNHIMTSKQELQHPSSL 540
Db      569 AVFNLTNNSVACICEYONFLOWVDQKMFVNVQMKCASPIDMKASVLDPFTNSCYIY 628
Qy      541 AFLNLQNDFACTGCHQSFLOMKIKQROLIVEVERMECATPSDKQGMVLSL-NITCQMN 599
Db      629 KTIISVSVAIVVATVAFLIYHFYFHLILLAGCKKYSRGSISYDAFVIYSSQEDWVRN 688
Qy      600 KTIIGSVLSVAVVAVLVYKFFHMLLAGCIKYGGENIYDAFVIYSSQEDWVRN 659

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QY 689 ELVKULEEVPFQCLHPRDPIPGVAIAANIIOGEGHKSRYIVVSRHFIQSRWCIFE 748
DB 660 ELVKULEEVPFQCLHPRDPIPGVAIAANIIEGEGHKSRYIVVSRHFIQSRWCIFE 719
QY 749 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDNALGRHIFMR 808
DB 720 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDSVLGRHIFMR 779
QY 809 LKKALLDGRKALNPD--ETSEEOEATTL 834
DB 780 LKKALLDGRKSWNEGTGTCNMQDEATSI 808
RESULT 15
ID ADO57785 standard; protein; 808 AA.
AC ADO57785;
XX 12-AUG-2004 (first entry)
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX toll-like receptor 4; TLR4; Old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; gorilla.
OS Gorilla gorilla.
XX MO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003WO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
PA Mesier W;
XX MPI: 2004-400726/37.
DR N-PSDB; ADO57783, ADO57784.
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX Example 1; SEQ ID NO 6; 11bp; English.
PS The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;

Query Match 63.7%; Score 2761; DB 8; Length 808;
Best Local Similarity 66.5%; Pred. No. 2,6e-235;
Matches 538; Conservative 112; Mismatches 153; Indels 6; Gaps 4;

QY 31 VLPNTTYQCMQDNLSKIPHDIPYSTKNDLSFNPLKILTSYSTFNPSQOMLDSRCETE 90
DB 1 VLPNTTYQCMQDNLSKIPHDIPYSTKNDLSFNPLKILTSYSTFNPSQOMLDSRCETE 60
QY 91 TIEDKAMHGLNQLSTLVLTGNPIKSFSGSLTNLENLVAVETKMTSLGEGHIGQLIS 150

DB 61 TIEDKAYOSLSHLSSTLITGNPIQSLALGAFGLSSLOQLVAVENTNLASLENFPIGHILKT 120
QY 151 LKKLVANHLJISFPLPEYFSNL/TNLEHVDLSYNTIQTISVVDLOFLRENPOVNLSDLS 210
DB 121 LKELVANHLJISFPLPEYFSNL/TNLEHVDLSYNTIQTISVVDLOFLRENPOVNLSDLS 180
QY 211 INPIDIOAQAFOGIRLHELTLRSNPNSSNVLKMLQONTGSHVRLJIGEFKERNLES 270
DB 181 INPMFIIOPGAFKEIRLKHULTLRNNFDSLNVMKTCIOGLAGLEVRLVIGEFKERNLES 240
QY 271 PDRSMVEGICNVSIDEFRLTYINHSDDIYNL-NCLANI SAMSFGVHAKHIAVPRHKK 329
DB 241 PDKSALBGLCNLTIEFRLAYLDYLDIIDLFCNLTIVSSPSLVSTIERKVDPSYNG 300
QY 330 WOSLSIIRCHLKPFPKLSLPFLKSWTLTNRDISFGOLAPSLRLVDSRVNAMSPPGCC 389
DB 301 WOLBELVNCRGQFPFLKLSLKRLTFSNKGANFSEVDLPSEFLDSRNGLSFKGCC 360
QY 390 SYSDEGTNNLKYLDLSFNGVILMSANFMGLBELLYLDFQHSYTLKKTVEPSVFLSEKLDY 449
DB 361 SOSDFGTSLSKYLDSFNGVITMSNPLGLBQLBHLDPQHSNLMKQMSFVSFLSRLNLY 420
QY 450 LDIYSTNTKIDPDGIFLGLISLNTKMAKNSFKDNLNVFTNTNLTPLDLSKQLEOI 509
DB 421 LDISSHTRVAFNGIFNGLSLEVKMAGNSFOENFLPDIFELNLTPLDLSQCLEOL 480
QY 510 SRGVFDTLRYLOLMSHNNLLFLDPHKKOLYSRTLDSCSNRLETS-KGILHPPKSL 568
DB 481 SPTAFNSLSLQVLMNSHNNFSLDTPFKCLNSLRVLDYSLNHMTSKKOLHPHPSL 540
QY 569 AVFNLTNNSVACICEYQNFQWVKDQKMFVNVEQKCAPIDMKASVLDLDTNSTCYTY 628
DB 541 AFLNLTQNDFACTGCHQSFQWIKDQRLVVEVMECATPDKQGMPLSL-NITQCKN 599
QY 629 KTIISVSVSVLVATVAFIYHFFHLLIAGCKKISRGESITYAPVYSSQNBWVN 688
DB 600 KTIIGSVSVSVLVAVLVYKFFHMLLAGCTKYGGENVYDAFVYSSQNBWVN 659
QY 669 ELVKULEEVPFQCLHPRDPIPGVAIAANIIOGEGHKSRYIVVSRHFIQSRWCIFE 748
DB 660 ELVKULEEVPFQCLHPRDPIPGVAIAANIIEGEGHKSRYIVVSRHFIQSRWCIFE 719
QY 749 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDNALGRHIFMR 808
DB 720 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDSVLGRHIFMR 779
QY 809 LKKALLDGRKALNPD--ETSEEOEATTL 834
DB 780 LKKALLDGRKSWNEGTGTCNMQDEATSI 808

Search completed: March 12, 2005, 19:55:04
Job time : 90.9634 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-6

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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 - 6: /cgn2_6/prodata/1/iaa/backfilset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2779.5	64.1	844	4	US-09-949-016-9438
2	602.5	13.9	661	1	US-08-514-014-4
3	602.5	13.9	661	2	US-08-833-823-4
4	502	11.6	784	4	US-09-982-308B-23
5	439.5	10.1	775	4	US-09-949-016-8799
6	300.5	6.9	605	3	US-09-063-950-5
7	290.5	6.7	603	1	US-08-190-802A-50
8	290.5	6.7	603	3	US-08-473-346-50
9	290.5	6.7	603	4	US-08-473-089-50
10	290.5	6.7	603	4	US-08-487-072A-50
11	288.5	6.7	1112	3	US-09-353-585-2
12	288.5	6.7	1112	3	US-09-353-585-3
13	281.5	6.5	605	1	US-08-190-802A-49
14	281.5	6.5	605	3	US-08-473-346-49
15	281.5	6.5	605	3	US-08-473-089-49
16	281.5	6.5	605	4	US-08-487-072A-49
17	281.5	6.5	605	4	US-09-538-092-1087
18	281.5	6.5	623	4	US-09-949-016-10995
19	279	6.4	1480	3	US-09-191-647-7
20	279	6.4	1480	3	US-09-540-245A-7
21	279	6.4	1480	3	US-09-540-153-7
22	279	6.4	1480	5	PCT-US91-09055-2
23	277	6.4	1480	3	US-09-182-024A-5
24	274.5	6.3	1119	4	US-09-907-794A-294
25	274.5	6.3	1119	4	US-09-905-125A-294
26	274.5	6.3	1119	4	US-09-902-775A-294
27	274.5	6.3	1119	4	US-09-906-700-294

28	274.5	6.3	1119	4	US-09-903-603A-294	Sequence 294, App
29	274.5	6.3	1119	4	US-09-904-920A-294	Sequence 294, App
30	274.5	6.3	1119	4	US-09-909-064-294	Sequence 294, App
31	274.5	6.3	1119	4	US-09-905-381A-294	Sequence 294, App
32	274.5	6.3	1119	4	US-09-906-618-294	Sequence 294, App
33	272.5	6.3	958	4	US-09-706-594-5	Sequence 5, App1
34	265.5	6.1	1016	3	US-09-180-439-8	Sequence 8, App1
35	264.5	6.1	968	3	US-09-180-439-3	Sequence 3, App1
36	264.5	6.0	1325	3	US-09-180-439-4	Sequence 2, App1
37	259	6.0	1525	3	US-09-540-245A-2	Sequence 2, App1
38	259	6.0	1525	3	US-09-540-153-2	Sequence 2, App1
39	259	6.0	1525	3	US-09-512-283C-396	Sequence 396, App
40	259	6.0	1529	4	US-08-592-500-2	Sequence 2, App1
41	256	5.9	560	3	US-08-195-006-2	Sequence 2, App1
42	256	5.9	560	3	US-09-063-950-4	Sequence 4, App1
43	256	5.9	560	3	PCT-US94-07644A-2	Sequence 2, App1
44	256	5.9	560	3	US-09-182-024A-2	Sequence 2, App1
45	255.5	5.9	1523	3		

ALIGNMENTS

```
RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match      64.1%; Score 2779.5; DB 4; Length 844;
Best Local Similarity 65.8%; Pred. No. 76-246;
Matches 546; Conservative 112; Mismatches 161; Indels 11; Gaps 5;

QY      10 TLIALFLSLRPGSLNPTIEVLTTCQMDQNSKIPHDIPYSTKQNDLSFNPILKIR 69
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      21 TPIPLLACR-----FTBEVAVPNITYQCMINPFIKIPDNPFPSTKNDLSFNPILRHG 75

QY      70 SSSFNPSQLOMLDLSRCIEITEDKAWHGNQSLTLVLTGNPIKSPSSGSGSLTNLEN 129
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      76 SISFSFPELQVLDLSRCIEITEDKAWHGNQSLTLVLTGNPIKSPSSGSGSLTNLEN 135

QY      130 LVAVEITKMTSLRGFIQGLISLKLNVANLTHSFLEPEYFSGNTLNEHVDLSYNYQTI 189
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      136 LVAVEITKMTSLRGFIQGLISLKLNVANLTHSFLEPEYFSGNTLNEHVDLSYNYQTI 195

QY      190 SYKDIQFLRENOVVLSDLSINPDIQAOAFQGRILHELTIRSNFNSNVLAKMLQNM 249
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      196 YCTDRLVHQLMVLNLSLSDLSINPDIQAOAFQGRILHELTIRSNFNSNVLAKMLQNM 255

QY      250 TGLHVRILIGFKNERNLSPDRSVMSEGLCVSIDEFLTYINHSDDIYNL-NCLANI 308
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      256 AGLVHVRILIGFKNERNLSPDRSVMSEGLCVSIDEFLTYINHSDDIYNL-NCLANI 315

QY      309 SAMSFYGVHAKIADVPRRHFKWQSLIIRCHLKPPKLSLPFLKSWTLTTRNEDISFGOL 368
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Dh 316 SFSFIVSVIERKVDSDSNVFMQHLLELVNCKFCGQFPFLTKLKSJLRLFTFSNKGANAFSEV 375
Oy 369 ALPSLRVYLDLSGNAMSFRCGCCVSDEGTNNLKYLDLSFNGVILMSANFMGLJELEYDFO 428
Dh 376 DLPSLSEFLDLSNRGSLFKGCCSQSDGTGSLKTLDSLSPNGVITMSSNLFLELEQLEHLDFO 435
Oy 429 HSTLKKVTEFSVFLSLEKLLLYLDLSYTNTKIDPDGIFLGLISINTLKMAGNSFKDNTLSN 488
Dh 436 HSNLKQMSSEFSVFLSLRNLIYLDLSHTHTRVANGIFNGLSLEVLKMAGNSFOENLPD 495
Oy 489 VFTNTNLTFLDLKQLEQLEISRGVDTLYRLQLLMSHNNLLFLDPSHYKOLYSRLTD 548
Dh 496 IFTEDRLNLTFLDLKQLEQLESEPTANSLSSLOVIMNSHNNPFSLSLTFPKYCINLSLOVLD 555
Oy 549 CSFNRLET-S-KGILHFFPKSLAVFNLTNNSVACICEQONLQMWKQJMEVLNVWEOKCA 607
Dh 556 YSLNHTMYSKQELQHFPSLSLAFNLNTQNDFACTCHOSLQNIKQORQLLVEVERMECA 615
Oy 608 SPIDMKASIVLDPFTNSCYIYKTTISVSVSVLVVAIVAFLIYHFFHLLIAGCKKYSR 667
Dh 616 TFSDDKQGMVLSL-NITCQMNKTIIGSVLSVLVSVAVLVAFLYKFFHMLLLAGCITKGR 674
Oy 668 GESIYDAPATYSSQNEWDWVRNELVKNLEEGVPRFOCLHRTDITPGVAILAANTIQSFPK 727
Dh 675 GNITDAFATYSSQDEWDVRNELVKNLEEGVPRFOCLHRTDITPGVAILAANTIHSQFPK 734
Oy 728 SRKVIIVVSRHHSIQSRWCIFFEYELAQTWQFLSSRSGIIFVLEKVEKSLRQCVELYRL 787
Dh 735 SRKVIIVVVSQHRIQSRCWCIFFEYELAQTWQFLSSRAGIIFVLOKVEKTLRQCVELYRL 794
Oy 788 SNTYTLMEWDNALGRHIFWRRLKALLDGRALNPD--ETSEEDQATTL 834
Dh 795 SNTYTLMEWEDSVLGRHIFWRRLKALLDGRSNPBGTVGTGCMQOATSI 844

RESULT 2
US-08-514-014-4
US-Sequence 4, Application US/08514014
US-Patent No. 5707829
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514, 014
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI6000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

```

[illegible]

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 13.9%; Score 602.5; DB 2; Length 661;
Best Local Similarity 28.2%; Pred. No. 3e-46;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

28 CIEVLPNITYGCGDDQLSKIPHDIPYSTKNLDSFNPPLKILRSYFTNFSQLOMDLSRC 87
28 CIEKANKYKNCENGLSEIPDTLPTEPLEFSFNPPLIHKRISRLMNTFLDLTLC 87
88 BIETIEDKAMHGLNQLSTLVLTGNPIKSPSPSGSLTNLEMLVAETKNTSLGPHIQ 147
88 QINMIHEDTFQSHQSTLVLTGNPLIFMAETSLNPKSKLHFLQTSISNLEFIPVNH 147
148 LISLKLVAHNLHSHFKLPEYFSNLTNLEHVDLSNYIQTISVKLOFLRENPQVNL 207
148 LNLLESLYGSNHSISIKFPKQFP-ARNLKVLPQNNALHYISREIMRSLEQ--AINLSL 204
208 DLSLNPIDSIQAOAFGIRLHELTLRSNPNSSNVLKMCQDMTGHHVHLLIGEPKNE 267
205 NENGNVKGIEGAFSTVFOSL---NFGGTPNLSVITNGLDNSTTQSLMSTGFEDID 260
268 LESFDRSVMGICNVSIDFRLTYINHPSD-DIYNLNCIANISAMSGTGVHIGIADVP 326
261 -EDISSAMKGLCEMSVESLNLQE-HRFDISSTTQCTQLOEDLVTTHLK---GLPS 315
327 HRKWSLSLIR-----CHLKP--FPKLSLPLKSWTLTTRNEDISFGOL-ALP 371
316 GNR--GLNLKLVLSVNHFDQLQISANFSLTLYIRG--NVKYLHLGVGCLERK 370
372 SLRYLDSNNAMFRGCCSYSDGNTNLYLIDLSFNGVI-LMSANFMGLELEYLDFQS 430
371 NLOTLDSNNDI EASCCSLQKLNLSHLOTNLNLSHEPIGLSQOAKCECPQLELDLAF 430
431 TLKVTESVFLSLEKLLYLDISYNTKIDPDGIFGLISLNTLKAGNSFKDNTL-SN 488
431 RLHINAPQSPQNLHFLQVNLNLYCFLDLSNGHLAGLVPVLRHLNKGHNFQDGTITKN 490
489 VETNTNTNLTFDLSCQLEQISRGVDTLYRLQLMNSNNLI--FLDP-SHYKOLYSR 545
491 LIQTVGSLEVLILISCGSLISIQOAFHSIGKMSHVDLSHNSLTCDSIDLSHLKGIY-- 547
546 TLDCSNRIETSGILQHFPKSLAVFNLTNNSVACICEYONFLQWKQDKMFLVNEQMK 605
548 -LMLANSINIIISPRLLPTLSQOSTNLNLSHNPIDCTCSNIHFLTWKEMLHKLGSEET 606
606 CASPIDMKASLVLDFTNS---TCYIYKTIISVSVLVVAFLVAFLLIHFYFHL 656

DB 607 CANPSPSLRGVLSLVKLSGCIYTAIGFFLIVLELLAILLFPFAVKYLLRMKYOHI 661

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Dalié, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavadny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: J06010C
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 11.6%; Score 502; DB 4; Length 784;
Best Local Similarity 24.9%; Pred. No. 6.5e-37;
Matches 210; Conservative 136; Mismatches 324; Indels 172; Gaps 32;

43 NLSKIPHDIPYSTKNLDSFNPPLKILRSYFTNFSQLOMDLSRCEIETIEDKAMHGLNQ 102
42 SLNLSIPSGTEAVKSLDLSNNRIYISN-----SDIQRCY-----N 77
103 ISTLVLTGNPIKSPSPSGSLTNLEMLVAETKNTSLGPHIGOLISLKLVAHNLH 162
78 LQALVLTSGNINTIEDSPSSLSGLSLEHLDLSYNYLSSSWFKPLSLTFLNLTGNPYK 137
163 SPKLPEYFSNLTNLEHVDL---SYNYQTISVKLOFLRENPQVNLSDLSLNPIDSIQ 218
138 TLGETSLPSHLTKQDILRVGNMDTFTKIQKDFAGITPLEE-----LEIDASDQSYE 190
219 AQAFOGIR-----LH---ELTLRSNPNSSNVLKMCQ---NMTGLVHRLILGEFKY- 264
191 PKSLKSIQVSHLILHMKOHILLLEIFVDYVSSVECLERDQDLDTFHSELSGTGETNL 250
265 -----ERNLESFDRSVM-----GLCNVSIDFRLTYINH-SDDIYNLNCIANIS 309
251 IKKTFPRNVKTI DESLFGVMKLLNQISGLELEFPDCTLNGVGNFRASDNDRVIDPGKVE 310
310 AMSFTGVHIGIADVPFRHKWSLSITIRCHLKPFPKLSLP---FLKSWTLTTRNEDISF 365
311 TLTIRRLH-----PREFLYDLSLTLVSLERVAKRTIVENSKVLPCLLSQH----- 358
366 GQLALPSRLYLDLSNNAMFRGCCSYSDGNTNLYLIDLSFNGVILMSANFMGLELEYL 425
359 -----LKSLEYLDLSNNLV-----EYLKNS-----ACEBAMSLQTLILR 395
426 DFQSTLTKVTEFSVFLSLEKLLYLDISYNTKIDPDGIFGLISLNTLKAGNSFKDNT 485
396 QNHLSLSEKTEG--TLTLTKLNTNIDIS-----KNSF--HS 427
486 LSNVFTNTNLTFDLSCQLEQISRGVDTLYRLQLMNSNNLI--LP-LDPSHYKOLY- 542
428 MPETCWDEKMKYKLNLSSTRHSVTCIPKT---LEILDVSNNNLNLPSLNLPOLEKELYI 484

QY 543 -----SLRTDCSFNRIFT-SKGILOHPKSLAVENLTNNSVACICEYON 586
DB 485 SRNKLMTLPDASLLPMLVLKISRVAITTFSEKQULDSF-HTLKTLEAGNNFICSCFELS 543
QY 587 FLOWVKDQKMFVNV---QMKCASPIDMKASLVLD-FTNSTCYIKTIISVSVSLVA 641
DB 544 FTQ--EQQALAKVLIDWPANTLCSFSPHVRCQOVQVRLSVSECHRIALVSGMCCALFTL 601
QY 642 VATVALYHVF---YFHLI--LIAGCKKYSRGS---YDAFVIYSSQNMEDVNEELVK 692
DB 602 ILTGVLCGRFPGWLWYMKMMAMLOAKRPRKAPSNICYDAFVYSERDAYVENVLMWQ 661
QY 693 NIEBQVPRQCLHTRDFIPGVALAANIIOEGFHMSKRYIVVSRHFIOISRCIFEYELA 752
DB 662 ELENRPFPKLCIHRKDFIPGKMIIDNII-DSIEKSHKTVFVLSENFVSEWCKEYELDFS 720
QY 753 QWOFSSSGIIFVLEKVESLLRQO-VELYRLSRMTYLEWEDNALGRHIFWRKXK 811
DB 721 HRLFDENDDAAILLLEPIEKKAIPORPCUKIKMTKTYLEWPMDEAKOREGFVNLRA 780
QY 812 AL 813
DB 781 AL 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 10.1%; Score 439.5; DB 4; Length 775;
Best Local Similarity 24.7%; Pred. No. 3.5e-31;
Matches 201; Conservative 122; Mismatches 292; Indels 199; Gaps 32;
QY 43 NLSKTPHIDIPYSTKNLDSFNPLKILRSYFTNFSOLOMLDLSRCEIETIEDKAMHGLNQ 102
DB 77 SLNLSIPSGITBAVKSIDLNNRITYISN-----SDQRCV-----N 112
QY 103 LSTVLGTGNPIKSPGSPSGGLTNLENLVAVETKMTSLEGPHIGQLISLKKLVANHLIH 162
DB 113 LQALVLVTSNGVITTEBDSFSLGSLHLLDLSYNYLSSSSWPKPSSLTFTNLGNPKY 172
QY 163 SFKLDEYSNLTNLHVDL---SYNYIOTISVKDLOFLRENPOVNLSDLINPIDSTQ 218
DB 173 TLGERSLPSHLTKLOLRVGNNDFTFKIQRKDPAGITPLEF-----LEIASDLQSYE 225
QY 219 AOAFCGIR-----LH---ELTIRSNENSSNVLKMCLO---NMTGLHVRHLLILEFKN- 264
DB 226 PKSLKSIQVSHLILHMKQHILLLEIFVDVTSVSECTLEBDTDLDTFHFSELSGTETNSL 285
QY 265 -----ERNLESFDRSVM-----GLCNVSIDEFRLTYINMF-SDDIYNLANCLANIS 309
DB 286 IKKFTFRNVKTI DESLFOVMKLLNOI SGLLELEFDDCTLNGVGNFRASPNDRVIDPGKVE 345

QY 310 AMSFTGVHIIKHADVPRHFKMQSISIIIRCHLKPPPKSLP-----FLKSWTLTTNNEDISF 365
DB 346 TLTIRRLHI-----PRFYLPYDLSLTVSLERVARIRIVENSKVFLVCLLSQH----- 393
QY 366 GQALPSIRLYDLSRNMSFRGCCSYSPDGNNLKIYDLSPNGVILMSANFMGLELEYL 425
DB 394 ----LKSLEYLDLSENLMV-----BEYLKNS-----ACEDAMPSTLOTILR 430
QY 426 DQHSHTKKVTEFSVFLSEKLLYLDISYTNKIDPOGIPLGLISLNTLKMAAGSFKONT 485
DB 431 QNHLSLEKTEG--TLTLTKMLTNIDIS-----KNSF--HS 462
QY 486 LSNVFTNTNLTFLDLSKCOLEQISRGVFDLYRLQLMNSHNL-LF-LDPESHKOLY- 542
DB 463 MPETQWPEKMKYINLSSTRHSHVTCIPIKT---LEILDVSNNNLNFSLNLPOLKELYI 519
QY 543 -----SLRTDCSFNRIFT-SKGILOHPKSLAVENLTNNSVACICEYON 586
DB 520 SRNKLMTLPDASLLPMLVLKISRVAITTFSEKQULDSF-HTLKTLEAGNNFICSCFELS 578
QY 587 FLOWVKDQKMFVNV---QMKCASPIDMKASLVLDFTNSTCYIKTIISVSVSLVA 643
DB 579 FTQ--EQQALAKVLIDWPANTLCSFSPHVRCQOVQVRLSVSECHRT---ALVSGMCCA 632
QY 644 TVAFLYHVFYHLLIAG--CKKY-----SRGESIYDAFYIY 678
DB 633 -----LFLILLTGVLCGRFPGWLWYMKMMAMLOAKRPRKAPSR-NICYDAFVSY 682
QY 679 SQNEDWRNELVKNLEBQVPRQCLHTRDFIPGVALAANIIOEGFHMSKRYIVVSRH 738
DB 683 SERDAYVVENLMVOLEFNPNPFPKLCIHRKDFIPGKMIIDNII-DSIEKSHKTVFVLSN 741
QY 739 FIOSRCIFEYEIAQWOFSSSGIIFVLEKV 772
DB 742 FVKSBEWCKYEIDFHSFRLFDENDDAAILLEPI 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRGG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 6.9%; Score 300.5; DB 3; Length 605;
Best Local Similarity 23.9%; Pred. No. 1.3e-19;
Matches 155; Conservative 81; Mismatches 236; Indels 175; Gaps 20;
QY 39 CMDQNLKIPHDIPYSTKNLDSFNPLKILRSYFTNFSOLOMLDLSRCEIETIEDKAMH 98
DB 60 CSSRLTLPDGIIGGTALMLDNNSSISIPAFRNLSLAFNLQGGQGLSLEPQALL 119
QY 99 GINQSLTVLTGNPIKSPGSPSGGLTNLENLVAVETKMTSLEGPHIGQLISLKKLVANAH 158
DB 120 GLENCHILHLEARNOLRSILAFTVTPATALLGSHNNRISLREBGLFEFGCLNMDLINGW 179
QY 159 NLHSFKLPE-YFENLTNLHVDLSYN---YIOTISVVDLOFLRENPOVNLSDLINLPI 214
DB 180 NSL--AVLPDAFAGLGLRELVLAGNRLAYLQALPSSGLAEIR-----LDLSRNAL 230


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QY 123 -----GLTNLENLVAETKMTSLGEGFHIGQLISLKKLVANHLIHSFYLPEYF 170
DB 180 NSLVVLPDPTVQGLGNLHLYLAGNKLTYLQPALFCGELRELDLSRNALRSVK-ANVF 238
QY 171 SNLTNLEHVDLSYNYIQTIS-----VVDLOFLRENPOVNLSDLSINPDISIQAAQOG 224
DB 239 VHLPRLOQLYDLRNLITAVAPGAFIEMKALRW-----LDLSHRVAGIMEDTPEG 288
QY 225 -IRLHELTLRSNPNSSNVLKMCLOMMTGIL-VHRLILGEFK-----NERNLSEFDSVMEG 278
DB 289 LIGLHVLALAN-----ALASLRPRTPKOLHLEELQLGHNRIROGERTFEGLEGLEVT 344
QY 279 LCNVSIDEFRL-TYINHPSDIYNL--NCLANISAMSTGVHIKIADVPRHFKMQSLSI 335
DB 345 LINDNQTETVRVGAFFGLFNVAVMNLGNCRLSPRVFQGLDKLH-----SLHLSCLGH 400
QY 336 IRCHLKPPKLS--LPLFKSWTLTTNREDISFGQALPSLYLDLSRNAMS-----FR 386
DB 401 VRLH--TPAGLSGLRRLFLRDNSSISIEQSLAG--LSELELDLTTNRLTHLPRQLFQ 455
QY 387 GCCSYSDFTNNLKYLDLSPNGVILMSANFMGLELELYLDFOHSTLKKVTERSVLSLEK 446
DB 456 -----GLGHELYLISYNQLTLSAEVLG-----PLQR 483
QY 447 LLYLDISYNTKIDPDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTNLTFLDLSKQL 506
DB 484 AFWLDISLNH-----LPLDPSHYKOLYSRLTDCSFNNIE 555
QY 507 EQLSGVVDTLVRLQOLNMSHNL-----LPLDPSHYKOLYSRLTDCSFNNIE 555
DB 495 ETLAEGFLSSIGRVRVYLSLRNNSLOTFSPQGLERLMDAMPW-----DCS----- 540
QY 556 TSKGILQHP-KSLAVFULTNNSVACICEYQNFLOWVD--OQMFLVNVQOMCASPI 610
DB 541 -----CPKALRDFALQHPGV--PRFVQVCEGDCCQVYTYN-NITCAGPA 585
QY 611 DMKASLVLDFTNSTCYIY 628
DB 586 NV-SGLDRDVSETHFVH 602

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RESULT 10
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500

```

```

; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; US-08-487-072A-50

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Query Match 6.7%; Score 290.5; DB 4; Length 603;
Best Local Similarity 22.4%; Pred. No. 1,1e-17;
Matches 152; Conservative 99; Mismatches 204; Indels 223; Gaps 26;

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QY 39 CMDQNLKIPHDIPYSTKNDLSFNPILKRSYFTNFSQLOMDLSRCEITIEDKAWH 98
DB 60 CSSKVLTLPLDIPVSTRALMDGNNLSSIPSAFQNLSDPLNLQGSWLRSLPEQALL 119
QY 99 GLNQSLTVLGNPKSPSPS----- 122
DB 120 GLQNLVYLHLBRNRRLNLAVALFTHTPSLASLSLSSNLGLREBGLFQGLSHLMDNLGW 179
QY 123 -----GLTNLENLVAETKMTSLGEGFHIGQLISLKKLVANHLIHSFYLPEYF 170
DB 180 NSLVVLPDPTVQGLGNLHLYLAGNKLTYLQPALFCGELRELDLSRNALRSVK-ANVF 238
QY 171 SNLTNLEHVDLSYNYIQTIS-----VVDLOFLRENPOVNLSDLSINPDISIQAAQOG 224
DB 239 VHLPRLOQLYDLRNLITAVAPGAFIEMKALRW-----LDLSHRVAGIMEDTPEG 288
QY 225 -IRLHELTLRSNPNSSNVLKMCLOMMTGIL-VHRLILGEFK-----NERNLSEFDSVMEG 278
DB 289 LIGLHVLALAN-----ALASLRPRTPKOLHLEELQLGHNRIROGERTFEGLEGLEVT 344
QY 279 LCNVSIDEFRL-TYINHPSDIYNL--NCLANISAMSTGVHIKIADVPRHFKMQSLSI 335
DB 345 LINDNQTETVRVGAFFGLFNVAVMNLGNCRLSPRVFQGLDKLH-----SLHLSCLGH 400
QY 336 IRCHLKPPKLS--LPLFKSWTLTTNREDISFGQALPSLYLDLSRNAMS-----FR 386
DB 401 VRLH--TPAGLSGLRRLFLRDNSSISIEQSLAG--LSELELDLTTNRLTHLPRQLFQ 455
QY 387 GCCSYSDFTNNLKYLDLSPNGVILMSANFMGLELELYLDFOHSTLKKVTERSVLSLEK 446
DB 456 -----GLGHELYLISYNQLTLSAEVLG-----PLQR 483
QY 447 LLYLDISYNTKIDPDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTNLTFLDLSKQL 506
DB 484 AFWLDISLNH-----LPLDPSHYKOLYSRLTDCSFNNIE 555
QY 507 EQLSGVVDTLVRLQOLNMSHNL-----LPLDPSHYKOLYSRLTDCSFNNIE 555
DB 495 ETLAEGFLSSIGRVRVYLSLRNNSLOTFSPQGLERLMDAMPW-----DCS----- 540
QY 556 TSKGILQHP-KSLAVFULTNNSVACICEYQNFLOWVD--OQMFLVNVQOMCASPI 610
DB 541 -----CPKALRDFALQHPGV--PRFVQVCEGDCCQVYTYN-NITCAGPA 585
QY 611 DMKASLVLDFTNSTCYIY 628
DB 586 NV-SGLDRDVSETHFVH 602

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RESULT 11
US-09-353-585-2
; Sequence 2, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S

```

Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2
Query Match 6.7%; Score 288.5; DB 3; Length 1112;
Best Local Similarity 23.5%; Pred. No. 4.4e-17;
Matches 158; Conservative 93; Mismatches 243; Indels 179; Gaps 26;
QY 23 GSINPCIEVLNIT--YOCMDONLSKIPHDIPY--STKNLDSPFKLILSYSTNTNSQ 78
DB 397 GSIPASLNLNNLSLYLNNQSGSIPSEEGYLSLTYYLDSNNISINGFLIPASGNNMN 456
QY 79 LQWDLRSCEIETEDKAMHGLNQSLTVLGNPIKSPSPSGSLTNLEMLVAETQWT 138
DB 457 LAFLELYENQGLASSVPEIGYIRSLNVLDLSENLNGSIPASFGNLNLSRLNLYNNQDS 516
QY 139 SLEGHGIGQLISLKKLVANHLHSFKLPEYFSNLTNLEHVDLSYNYIQTISVNDQFLR 198
DB 517 GSIPSEIGYLSRLNVLDSENLNG-SIPASFGNLNLSRLNLYNNQSGSIPSEIGYLR 575
QY 199 ENPQVNS-----LDLSLNP 214
DB 576 SLNDGLSENALNGSIPASLGNLNLNMLYNNQSGSIPSEIGYLSLTYYLSLGNNSL 635
QY 215 DSIOAQAFOGIR-LHELTFRS-----NFNSSNVLMK-----CLQWMT 250
DB 636 NGLIPASPYANRRNLQALILNDNNNLIGETIPSSVCNLTSLLEVLMPRRNLKGVPOCLNIS 695

QY 251 GLVHRLILGEFKNE-----RULES-----FDRSMWGL-----C--NNSIDFRLTYINH 295
DB 696 NLQVLSMSSNSFSGELPSSISNLTSLQILDGRRNNLBGAIPQCGNISLSLEVPDMQNNKL 755
QY 296 SDDI---YNLNCNLNISMSTGVHIXHIAVPRHF-----WQGLSIRCHLK--PFRPL- 346
DB 756 SGTLPNTNSIC--SLISLNDHGNLELD--EIPSLDNCCKLQVLDLGDNDQNLNPTFPMWL 811
QY 347 -SLPFLKSWTLTTNRED-----ISFGQALPFLRYLDSIRNMSPRGCCSYSDFGTNNLKY 401
DB 812 GTLPFLRYLRLTSKTKHNPRISSRAELMFPLRLIIDSRRNFS-----QDLPLSLEPH 864
QY 402 LDLSFNGVILMSANFMGLELELYLDFQHSITKKTVESVFLSEKLYLDISYNTKIDF 461
DB 865 L-----KGMRTVDKT--MEEPSYESYDDSVVVVTK----- 893
QY 462 DGIFGLISLNTLTKMAGNSFKDNTLSNVFTNTTLTFLDLSKQQLQEQISRGVFTLYRLQ 521
DB 894 -GLELEIVRLISL-----YTVLDLSSNFKEGHIPSVLDLDAIR 931
QY 522 LLMNSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKGILLQHPKSLA-----VFNLTN 575
DB 932 ILNVSNNALOGYIYISSLSGLSILSLDSFVQLS-----GEIPQLASLTFLEFINLSH 985
QY 576 NSV-ACICEYQNF 587
DB 986 NYLQICIPQGPQF 998
RESULT 12
US-09-353-585-3
Sequence 3, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:


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SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

Query Match      6.7%; Score 288.5; DB 3; Length 1112;
Best Local Similarity 22.0%; Pred. No. 4.4e-17;
Matches 173; Conservative 116; Mismatches 282; Indels 217; Gaps 31;

QY 23 GGLNLCIEVLPNIT--YQCMDNLSKIPIDIPY--STKMLDLSFNPCLKIRSYSPFNBSQ 78
DB 397 GSIPLASIGNLNINLSRLYLNNQLSGSIPBEIGLSLTLYLDLSNNNSINGFIPASFGNMEN 456
QY 79 LQMLDSRCEIETIEDKAWHGLNOLSTLYLTGPNIPSPGSGGLTNLENVAVETKMT 138
DB 457 LAFLEYENQLASSPBEIGYLRSLNVLDSENALNGSIPASFGNINLSRLNVLNNQLS 516
QY 139 SLEGPHIGQLISLKLNVANHLHSPKLPPEYFNSLTNLEHVDLSYNYIQTISVKDLQFLR 198
DB 517 GSIPBEIGYLRSLNVLDSENALNG-SIPASFGNINLSRLNVLNNQLSGSIPBEIGYLR 575
QY 199 ENPQVNL-----LDSLNP 214
DB 576 SLNDGLSENALNGSIPASIGNLNINLSMLYNNQLSGSIPBEIGYLSLTLYSLGNNSL 635
QY 215 DSIOAOFQIGIR-LHELTLS-----NENSNVLKMW-----CLQNT 250
DB 636 NGLIPASFGNMENLQALINDNNLIGETISSVCNLTSLLEVLYMPNNLKGYPOCLGNIS 695
QY 251 GLAHVRLIIGEFKNE-----RNLES-----PDRSVMEGL--C-NVSIDEFRLTYINHF 295
DB 696 NLQVLSMSNSPSGELPSISNLTSLQILDFGNNLEGAIPQCFGNISLSEVFDQNNKL 755
QY 236 SDDI---YVNLCLANISAMSPGVAKIADYPRHF---KNQOSITICHLK-PPPKL- 346
DB 756 SCTLTLTNEFIGC--SLISLNLHGNELD--EIPRSLDCKKQLQVLDLGNQNLDTFFPWL 811
QY 347 -SLPFLKSWTLTFTNED---ISFGQALPSLRVYLDLSNNAMSPRGCCSYSPGNTNKKY 401
DB 812 GTLPFLRVLRILTSNKLHPIRSSRAEIMFPDLRIIDLSNAFS-----QDLPTSLFEH 864
QY 402 LDSLFRGVILMSANFPGLELELYLDFQHSCLKKTEFSVFLSLKLLYLDISYTWTKIDF 461
DB 865 L---KGRMTVDKT---MEPSYESYDDSVVVYIK----- 893
QY 462 DGIPLGLISLNTLTKRAGNSFKDNTLSNVFTNTNTLTFDLDSKQQLQELSRGVFDLYRLQ 521
DB 894 -GLELEIYVILSL-----YVILDSNNKEFGHIPVSLGDLIAIR 931
QY 522 LLMNSHNMLFLDPBHYKQYLSLRTLDSPNRIETSKGLQHPFKSLA-----VFNLTN 575
DB 932 ILNVSHNALQGYIPSSLGLSLILSLSLDSFNQLS-----GEIPQDLASTLELEFNLSH 985
QY 576 NSV-ACICEYQNFLOW-----VKDQKFLVNVQMKCASPI 610
DB 986 NVLQGGICPGGPQFRFFESNSYEGNDGLRGYPVSKGCGKDPVEBKNTVATLADQESNSF 1045
QY 611 --DMKASLVLDFTNSTCYIKTITISYSVVLV---VATVAPLYHYFFHLILLAGCK 664
DB 1046 FNDPFKAAALMGSGSLC-----IGISIIYIILISTGNLRLWLAIIELHKKIMGR--RK 1097
QY 665 YSRGESIY 672
DB 1098 KORGQKNY 1105
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RESULT 13
US-08-190-802A-49
Sequence 49, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived peptides and uses
TITLE OF INVENTION: Theeocf
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Denlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match      6.5%; Score 281.5; DB 1; Length 605;
Best Local Similarity 23.5%; Pred. No. 7.4e-17;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;

QY 39 CMDQNLSTKIPHDIPYSTKNLDSFNPCLKIRSYSPFNBSQQLQMLDSRCEIETIEDKAWH 98
DB 60 CSSRLVRLPDGVPCGTALWLDGNLSSVPPAFOQLSSIGFLNLQGGQLSLBQALL 119
QY 99 GLNQLSTVLTGNPIKSPSPGSGGLTNLENVAVETKMTSLEGPHIGQLISLKLNVANH 158
DB 120 GLENCHLHLENQRLSLALGTFATTPALASIGLSNNLSRLBEDGLFEBLSLMDNLQW 179
QY 159 NLIHSPKLP-EYFSNLTNLEHVDLSYN---YIQTISVKDLOFLRNPQVNLSDLSLNP 214
DB 180 NSL--AVLPDAAFRGSLRELYLAGNRLAYLQPALFSGIAELRE-----LDSRLNAL 230
QY 215 DSIOAOF--QGRILHELTLSRFSNSNVLMKQLQMTGILHVRLLIGEFKNERNLESFPR 273
DB 221 RAIKANVTVQLPRQLKYL-----DRNL----- 253
QY 274 SYMEGLCNVSIDEFRLTYINHSDDIYNINCLANISAMSPGVAKIADYPRHFQKWSL 333
DB 254 -----IAVAAPAFGL-----KALRWLDL 273
QY 334 SITRCHLKPFPKLSLPFLKSWTLTITNR-----EDISFGQALPSLRVYLDLSNNAMSPRGCC 388
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Db 274 S-----HNRVAGLEDTFFGLI--GLRVLRISHNAIASLRP 307
QY 389 CSYSDFGTNNLKYLDSLFGV-ILMSANPMGLELEYLDFQHSITLKVTEFSVLSLEKL 447
308 RTFKDL--HFLEELQGHNRIRQLARSPREGIGLEVLTLDNHQLOEV-KAGAFGLTLNV 364
QY 448 LYLIDISYNTKIDFGDIFGLISLNTLKMAGNS-----FKDNTLSN 488
Db 365 AVMNLSGNCLRNLPQGVFRGLGKLSHLEGSCLGRIRPHTFTGSLGRLLFLKONGLVG 424
QY 489 V-----FTTNTNLTFLDLSCQLEQISRGVPTLYRLQLNMSHNNLLFLDPSHYQLYSL 544
Db 425 IEEQSLMGLELELDTLSNQLTHLPRLFGIGLKLTYLLSRNLAEILPADALGPLQRA 484
QY 545 RTLDSPFRITSKGILOHFPKSLAVFNLTNNSVACICEYQNFLO--WYDQKMFVNV 602
Db 485 FWLDVSHNRLEALPNSLAPLGRRLYSLRNNSLRTFTPOPGLERLWLEG-----N 536
QY 603 QMKCASPID-----MKASLVLDFTNSTC-----YIKTIISSVSVSVL 640
Db 537 PWDCCGPELKALRDFALQNPASVPRFVOALCEGDDCQPPAYTYNNITCASPPREV 590

RESULT 14
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49
Query Match 6.5%; Score 281.5; DB 3; Length 605;

Best Local Similarity 23.5%; Pred. No. 7.4e-17;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;
QY 39 CNDONLSKIPHIPIPTSKNLDLSPNPKILNSYFTNSQLOLWDSRCEIETEDKMH 98
60 CSSRNLTRPDGVPDGTQALMDGNLSSVPPAAQNLSSIGFLWQGGQSLSPQALL 119
QY 99 GINQSLVLTGNPKSPSPGSGTLNLEMLVAVETKMTSLGPHIGQLISLKLNVAH 158
Db 120 GLENLCHLHBRNQRLSALGTFAHTPALASIGLSNNRLSRLEDGLFGSLGSLMDNLGW 179
QY 159 NLHSEFKLPE-YFSNLTUHEVDSLNV--YIQTISVQDLOFLRNPQVNLSDLSLPI 214
Db 180 NSL--AVLPDAFRLGSLRELVLQGNRLAYLQPLFSGLELRN-----LDSRLAL 230
QY 215 DSIOQAF--QGIHRELTLRSNFSNVNLKMCLOMTGTHVHRLTGFGEKRNLESFDR 273
Db 231 RAIKANVFQLPRLKLYL-----DRNL-----253
QY 274 SYMEGICNVSIDEPRLTYINHSDDIYNINCLANISAMSFTGVHAKH1ADVPRRHKQSL 333
Db 254 -----IAAVAQAFGL-----KALRWLDL 273
QY 334 SITRCHLKPPKLSLPTLKSWTLTNR-----EDISFQALAPSLRYDLDSRNSPFGC 388
Db 274 S-----HNRVAGLEDTFFGLI--GLRVLRISHNAIASLRP 307
QY 389 CSYSDFGTNNLKYLDSLFGV-ILMSANPMGLELEYLDFQHSITLKVTEFSVLSLEKL 447
Db 308 RTFKDL--HFLEELQGHNRIRQLARSPREGIGLEVLTLDNHQLOEV-KAGAFGLTLNV 364
QY 448 LYLIDISYNTKIDFGDIFGLISLNTLKMAGNS-----FKDNTLSN 488
Db 365 AVMNLSGNCLRNLPQGVFRGLGKLSHLEGSCLGRIRPHTFTGSLGRLLFLKONGLVG 424
QY 489 V-----FTTNTNLTFLDLSCQLEQISRGVPTLYRLQLNMSHNNLLFLDPSHYQLYSL 544
Db 425 IEEQSLMGLELELDTLSNQLTHLPRLFGIGLKLTYLLSRNLAEILPADALGPLQRA 484
QY 545 RTLDSPFRITSKGILOHFPKSLAVFNLTNNSVACICEYQNFLO--WYDQKMFVNV 602
Db 485 FWLDVSHNRLEALPNSLAPLGRRLYSLRNNSLRTFTPOPGLERLWLEG-----N 536
QY 603 QMKCASPID-----MKASLVLDFTNSTC-----YIKTIISSVSVSVL 640
Db 537 PWDCCGPELKALRDFALQNPASVPRFVOALCEGDDCQPPAYTYNNITCASPPREV 590

RESULT 15
US-08-473-089-49
Sequence 49, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.9956 Seconds

(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-6

Perfect score: 4335
Sequence: 1 MPMPLHLAGTILMALFLSL.....GKALNPDETSEREQATTLT 835Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Published Applications_AA.*
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2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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11:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2726	62.9	799	10	US-09-950-041-8
3	2726	62.9	799	14	US-10-128-166-7
4	2726	62.9	799	16	US-10-732-563-8
5	2726	62.9	799	16	US-10-732-796A-8
6	602.5	13.9	661	13	US-10-114-893-10
7	602.5	13.9	661	15	US-10-038-854-134
8	597.5	13.8	661	15	US-10-038-854-135
9	597.5	13.8	661	15	US-10-037-417-107
10	575	13.3	1032	10	US-09-954-987B-192
11	575	13.3	1032	14	US-10-272-502A-31
12	575	13.3	1032	15	US-10-407-952-32
13	559	12.9	1050	10	US-09-954-987B-175

14	559	12.9	1050	14	US-10-272-502A-22	Sequence 22, Appl
15	559	12.9	1050	15	US-10-407-952-26	Sequence 26, Appl
16	546	12.6	1059	10	US-09-954-987B-187	Sequence 187, Appl
17	546	12.6	1059	15	US-10-407-952-30	Sequence 30, Appl
18	546	12.6	1059	17	US-10-753-267-30	Sequence 30, Appl
19	541.5	12.5	859	14	US-10-125-692-6	Sequence 6, Appl
20	541	12.5	1041	9	US-09-168-978-3	Sequence 3, Appl
21	541	12.5	1041	9	US-09-978-295A-498	Sequence 498, Appl
22	541	12.5	1041	9	US-09-978-697-498	Sequence 498, Appl
23	541	12.5	1041	9	US-09-978-192A-498	Sequence 498, Appl
24	541	12.5	1041	9	US-09-999-832A-498	Sequence 498, Appl
25	541	12.5	1041	10	US-09-978-189-498	Sequence 498, Appl
26	541	12.5	1041	10	US-09-978-608A-498	Sequence 498, Appl
27	541	12.5	1041	10	US-09-978-585A-498	Sequence 498, Appl
28	541	12.5	1041	10	US-09-978-191A-498	Sequence 498, Appl
29	541	12.5	1041	10	US-09-978-403A-498	Sequence 498, Appl
30	541	12.5	1041	10	US-09-978-564A-498	Sequence 498, Appl
31	541	12.5	1041	10	US-09-999-833A-498	Sequence 498, Appl
32	541	12.5	1041	10	US-09-981-915A-498	Sequence 498, Appl
33	541	12.5	1041	10	US-09-978-824-498	Sequence 498, Appl
34	541	12.5	1041	10	US-09-918-585A-498	Sequence 498, Appl
35	541	12.5	1041	10	US-09-999-834A-498	Sequence 498, Appl
36	541	12.5	1041	10	US-09-978-423A-498	Sequence 498, Appl
37	541	12.5	1041	10	US-09-978-193A-498	Sequence 498, Appl
38	541	12.5	1041	10	US-09-999-830A-498	Sequence 498, Appl
39	541	12.5	1041	10	US-09-978-757A-498	Sequence 498, Appl
40	541	12.5	1041	10	US-09-978-187B-498	Sequence 498, Appl
41	541	12.5	1041	10	US-09-978-643A-498	Sequence 498, Appl
42	541	12.5	1041	10	US-09-978-375A-498	Sequence 498, Appl
43	541	12.5	1041	10	US-09-978-288A-498	Sequence 498, Appl
44	541	12.5	1041	10	US-09-978-188A-498	Sequence 498, Appl
45	541	12.5	1041	10	US-09-978-681A-498	Sequence 498, Appl

ALIGNMENTS

RESULT 1

US-09-950-041-26

Sequence 26, Application US/09950041

GENERAL INFORMATION: US20030032090A1

Best Local Similarity 66.5%; Pred. No. 1.3e-222;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;

QY 2 MPLHLAAGLWAL-FLSCLRPGLSAPICIEVLNITTYOQMDNLSEKIPHDIPYSTKNDL 60
Db 1 MSASLALAGTLIPAMAFSCVPRSEMEPCVEV-PNITTYQCEMLNPFKIPDNLEFSTKNDL 59
QY 61 SPNPKILRSYSFTNFSQLOWLDLSRCEIETIEDKAMGLNOLSTVLVTGNPIKSPSGS 120
Db 60 SFNPLRHIGSYSPFSPELQVLDLSRCEIQTIEDGAYQSLSHLSTLITGNPISQALGA 119
QY 121 FSGGLNLENLVAVERKMTSLSEGFHIGQLISLKLNVANHLHSFCLPEYFSULTLEHYD 180
Db 120 FSGSLSLQKLVAVETNLASLENFPFGHLKTKELNVANHLIQSFCLPEYFSULTLEHYD 179
QY 181 LSYNYIQTISVQDLQFLRENPOVNLSDLSNPIDISIOAQFQRLHLETLRSFNSN 240
Db 180 LSSNKIQSITCYTDLRLVHQMPILNLSLDLSLNPMPFIQPGAFKEIRLHKTLIRNPFSLN 239
QY 241 VLKMCLOMTGLVHRLILGEFKNERNLSEFDRSVMEGLCNVSIDEFRLTYINHSDDIY 300
Db 240 VMKTCIQGLAGLEVHRLVYGEFRNEGNIKEFKDSALEGLCNLTIEFRLAYLDYLDII 299
QY 301 NL-NCLANISAMSFTGVHIKHIADVPRHFKMOSLSIICHKLKPFKLSLIPKSTLITN 359
Db 300 DLFNCLTNVSSFSVLVETIERVKDFSYNFGWQHELVNCKFGQFPTLKLKSLKRLTPTSN 359
QY 360 REDISFGQALPSELVLDLSRNAMSPGCCSYSDGTTNNLKYLDLSPNGVILMSANFGL 419
Db 360 KGNNAFSEVDLPSELFDLSRNGLSFKGCCSQSDGTTSLKTLDSFNGVITMSNPFGL 419
QY 420 ELEVLDPQHSSTLKKVTEPSVFLSEKLLYDISYNTKIDPBGILPLGISLNTLKMAQN 479
Db 420 EQLHLDPQHSSTLKKMSEFSVFLSLRNLIIYLDISHTRVAFNGIFNGLSLEVLKMAQN 479
QY 480 SPKONTLSNVPTNTNLTFLDLSKQLEQISRGVDTLYRLQLMSHNNLLFLDPSHYK 539
Db 480 SPQENFLPDIFFELRNLTFLDLSQCLQLESPJANSLSLQVLMASHNNPFLDTPRYK 539
QY 540 QVLSRTLDSCFNRIETS-KGILQHPKSLAVFNLTNNSVACICEYONFLQWQKQKML 598
Db 540 CLNSIQVLDYSLNHMTSKKQELQHPSSSLAFNLNTQNDFACTCHQSPLOMKQKQRL 599
QY 599 VNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSYSVLVAVATFALVYHFYHLL 658
Db 600 VEVERMECATPSDKQMPVLSL-NITCQNMKTIIGVSYLSVLVAVATFALVYKFYHLL 658
QY 659 IAGCKYRGESITYAFVITYSSQNDWYNELVKNLESGVPRFQCLAHYRDPISGVALIA 718
Db 659 LAGCTYRGENITYDAFVIYSSQDEDWYNELVKNLESGVPRFQCLAHYRDPISGVALIA 718
QY 719 NIIOGFHRSKRVIVVSRHFQSRMCI FEYEIAQTQWFLSRSGLIFVLEKVEKSLIR 778
Db 719 NIHFHRSKRVIVVSOHFIQSRMCI FEYEIAQTQWFLSRSGLIIFVLEKVEKSLIR 778
QY 779 QQVELYRLLSRNTYLEMEDNALGRHI FWRRLKALLDGKSNPBGSTVGTGCMWQATSI 834
Db 779 QQVELYRLLSRNTYLEMEDSVLGRHI FWRRLKALLDGKSNPBGSTVGTGCMWQATSI 837

RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W. K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX07244X1

; CURRENT APPLICATION NUMBER: US/09/950, 041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Query Match 62.9%; Score 2726; DB 10; Length 799;
Best Local Similarity 66.5%; Pred. No. 5e-213;
Matches 532; Conservative 111; Mismatches 151; Indels 6; Gaps 4;

QY 40 MDONLSKIPHDIPYSTKNDLSPNPKILRSYSFTNFSQLOWLDLSRCEIETIEDKAMHG 99
Db 1 MEINPYKIPDLPSTKNDLSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYQS 60
QY 100 LNOJSTLVLTGNPIKSPSGSFGGLTNLENLVAVERKMTSLSEGFHIGQLISLKLNVAAH 159
Db 61 LSHSTLITGNPISQALGAFSGSLSQKLVAVETNLASLENFPFGHLKTKELNVAAH 120
QY 160 LIHSEKLPYEVSNLTNLEHNDLSYNYIQTISVQDLQFLRENPOVNLSDLSNPIDISIOA 219
Db 121 LIQSFKLPEYFSNLTNLEHNDLSNKKIQSICYTDLRLVHQMPILNLSLDLSLNPMPFIQ 180
QY 220 QAFQIRLHLETLRSNFSNVLMKMCLOMTGLVHRLILGEFKNERNLSEFDRSVMEGL 279
Db 181 GAFKEIRLHKTLIRNPNDSLNVMKTCIQGLAGLEVHRLVGEFRNEGNIKEFKDSALEGL 240
QY 280 CNVSIDEFRLTYINHSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFKMOSLSIIRC 338
Db 241 CNLTIEFRLAYLDYLDIIDLFNCLTNVSSFSLVGVTIERVDFSYNFGWQHELVNVC 300
QY 339 HAKPPTLSLPELKSMTLTNRBDISFGQALPSELVLDLSRNAMSPGCCSYSDPGTNN 398
Db 301 KFGQFPTLKLKSLRLFTFSNKGNAFSEVDLPSELFDLSRNGLSFKGCCSQSDPGTTS 360
QY 399 LKYLDLSPNGVILMSANFMGLELELYLDPQHSSTLKKVTEPSVFLSEKLTYLDISYNTK 458
Db 361 LKYLDLSPNGVITMSNFPGLGLELEHLDFOHSNLMKQSEFSVFLSLRNLIIYLDISHHTTR 420
QY 459 IDPGCIFLGLISLNTLKMAQNSFKONTLSNVFTNTLTLFLDLSKQLEQISRGVPTLY 518
Db 421 VAFNGIFNGSLSLVLMKAGNSFOENFLPDIFFELRNLTFLDLSQCLQLEQSPJANSLS 480
QY 519 RLQOLNMSHNNLLFLDLSHYKQLYSRLTDCSFRIETS-KGILQHPKSLAVNLTNNS 577
Db 481 SLQVLMASHNNPFSBLDTPFYKCLNSLDVLDYSLNHMTSKKQELQHPSSSLAFNLNTQND 540
QY 578 VACICEYONFLQWQKQKMLVNEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVS 637
Db 541 PACCEHQSFLQKIDQKQRLVVERMECATPSDKQMPVLSL-NITCQNMKTIIGVSYL 599
QY 638 SVLVAVATFALVYHFYHLLIAGCKYRSRGSITYDAFVIYSSQNDWYNELVKNLEEG 697
Db 600 SVLVAVATFALVYKFYHLLMILACIKYRGENITYDAFVIYSSQDEDWYNELVKNLEEG 659
QY 698 VPRFQCLAHYRDPISGVALIANNIOGFHRSKRVIVVSRHFQSRMCI FEYEIAQTQW 757
Db 660 VPRFQCLAHYRDPISGVALIANNIHGFHRSKRVIVVSOHFIQSRMCI FEYEIAQTQW 719

OY	758	LSRSRGIFVLEKRYEKSLLRQVELYRLSNNTYLEMDNALGRIWRRLTKALLDGK	814
Dd	720	LSSRAGIIFVLQVKEXTLLRQVELYRLSNNTYLEMDESVLGRIHFWRLRLALLDGK	779
OY	818	ALMPD--ETSEEEORATLL	834
Dd	780	SANPEGTGVTCNMQDEPATIS	799

```

RESULT 3
US-10-128-166-7
Sequence 7, Application US/10128166
Publication No. US20030077279A1
GENERAL INFORMATION:
APPLICANT: ARDITI, MOSHE
APPLICANT: RAJAVASHISTH, TRIPATHI
APPLICANT: SHAH, PRADIMAN K.
TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
FILE REFERENCE: 81476-0255398
CURRENT APPLICATION NUMBER: US/10/128,166
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ. ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO. 7
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-10-128-166-7

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Query Match	62.9%	Score 2726	DB 14	Length 799
Best Local Similarity	66.5%	Pred. No. 5e-213		
Matches 532	Conservative 151	Mismatches 151	Indels 6	Gaps 4

[illegible]

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Db      54  FACTCEHOSPLQWIKDQBPDLVEVERMFCATSPDKQGMFVLSL-NITCQNMKTIIGVSVL 599
Qy      638  SULVATVAFLYHFFHFIHLILAGCKTKYSRGESITADAVITYSSQNMEDVNRVETKYNLEEG 697
Db      600  SYLVASVSVALVYKFFHMLTAGCIKYGRGENIYDAFVITYSSODEDVRNVLVKNLEEG 655
Qy      698  VPRFOLCLHVRDPIPCVATAIANIIOEGFKSRKVIWVSRHFIOSRMCFIPEYELAQTMQF 757
Db      660  VPRFOLCLHVRDPIPCVATAIANIIEGHFKSRKVIWVVSQHFIOSRMCFIPEYELAQTMQF 719
Qy      758  LSSRSGLIIFIVLEKVEKSLLRQOVELYRLLSRNTYLEMEDNALGHIIFWRRLKALLDGK 817
Db      720  LSSRAGIIFIVLOKVEKTIILRQOVELYRLLSRNTYLEMEDSVLGRHIFWRRLRYALLDGK 779
Qy      818  ALNPD---ETSEBEOBATLL 834
Db      780  SAMPBEGTVGTCNMQWETSII 799

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RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58193W003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

```

Query Match	62.9%	Score 2726	DB 16	Length 799
Best Local Similarity	66.5%	Pred. No. 5e-213		
Matches 532	Conservative 111	Mismatches 151	Indels 6	Gaps 4

[illegible]

Db 421 VAFNGIENGSLSEVLKMAAGNSFOENFLPDITELRNITFLDLSOCCOLEQSLPTAFNSLS 480

Qy 519 RLQOLNMSHNNLLFLDPESHYKQLYSLRTLDSCFNRIRTS-KGIIQHPFKSLAVFNLTNNS 577

Db 481 SLQVLMNSHNNPFSIDTPEPKCLNSLOVLDYSLNHNMTSKQELQHPFSSALFNLITOND 540

Qy 578 VACICEYONFLOWYDQKMPLVNEOMKASPIDMKASIVLDFTNSTCYIKYITIISSVV 637

Db 541 FACTEHOSFLOMIDKQQLVEVERBECATPSDKQGPVLSL-NITQNMKTIIGVSLV 599

Qy 638 SVLVAVATAPLIIHYFFPHLIIAGCKKYSRSEIYDAFVIYSSQNMEDWVRNELYKNLEEG 697

Db 600 SVLVAVAVAVLVYKFFPHLMALAGCIKYGGENIYDAFVIYSSQNMEDWVRNELYKNLEEG 659

Qy 698 VPRFOLCHYRDFIPGVAIAANNIOEGFHKSRKVIWVSRHFIQSRWCIFEYELAQTMQF 757

Db 660 VPRFOLCHYRDFIPGVAIAANNIHEGFHKSRKVIWVSRHFIQSRWCIFEYELAQTMQF 719

Qy 758 LSSRSGIIFIVLEKYEKSLRQOVELYRLSNTYILEMEDNALGRHIFWRRLKALLDQK 817

Db 720 LSSRAGIIFIVLOKYEKTLRQOVELYRLSNTYILEMEDSVLGRHIFWRRLKALLDQK 779

Qy 818 ALNPD--ETSEEBQEAATL 834

Db 780 SWNPEGTGTCGNMOEATSI 799

RESULT 5

US-10-732-796A-8

Sequence 8, Application US/10732796A

Publication No. US20040197865A1

GENERAL INFORMATION:

APPLICANT: Gupta, Shalley K.

APPLICANT: Ghosh, Taron K.

APPLICANT: Fink, Jason R.

TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines

FILE REFERENCE: 5818285004

CURRENT APPLICATION NUMBER: US/10/732,796A

CURRENT FILING DATE: 2003-12-10

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.2

SEQ ID NO 8

LENGTH: 799

TYPE: PRT

ORGANISM: Homo sapiens

US-10-732-796A-8

Query Match 62.9%; Score 2726; DB 16; Length 799;

Best Local Similarity 66.5%; Pred. No. 56-213;

Matches 532; Conservative 111; Mismatches 151; Indels 6; Gaps 4;

Qy 40 MDQNLKIPHDIPYETKNDLSFNPDKLIRSYFTNFQOLQWLDLRCEIETEDKAMHG 99

Db 1 MEINPKYKIPDNLPESTKNDLSFNPDKLIRHIGSYFSPFELQVLDLRCEIETEDGAYQS 60

Qy 100 LNOJSTLVLTGNPKISFSPGSGLTJNLENVAVETKMTSLGEPHIGQLISLKLNVAN 159

Db 61 LSHSTLITLGNPISLALGAFSGSLQKLVAVETNLASLENPFIHGLKTLKELNVAN 120

Qy 160 LIHSFKLEPYSNLTNLNHLVDLSYVYIOTISKDIQFLRENQVNLSDLSNPFDSIOA 219

Db 121 LIQSKLEPYSNLTNLNHLVDLSYVYIOTISKDIQFLRENQVNLSDLSNPFDSIOA 180

Qy 220 QAFQGRILHELTLRNPNSSNVLMKCLONMTGLAHVRLILGEFKERNLIESPDRSVMGL 279

Db 181 GAFKRIKHLKLTNRNPNSSNVLMKCLONMTGLAHVRLILGEFKERNLIESPDRSVMGL 240

Qy 280 CNVSIIDEPRLTYINHFSDIYNL-NCLANISAMSGVHIKIIADVPRHFKQSLISIR 338

Db 241 CNLTIIEPRFLAVLDYLDIIDLFNCLTNVSSFSLSVSTIERVKDFSYNFGQHLELVNC 300

Qy 339 HLKPPKSLPPLKSWTLTTRNEDISFQGLALPSLRVYDLSNNANSPFGCCSYSPFGTNN 398

Db 301 KFGEPFLKLSKLRILFTSKNGNAFSEVDLPSELFLDLSRNGISFPFGCCSQSDPGTTS 360

Qy 399 LKYLDLSENGVILMSANFMWGELELYLDPQHSTLKATYEFVSFLSEKTLVLDISTYNTK 458

Db 361 LKYLDLSENGVITMSSNKLGLGEHLDPQHSNKLKQMSFVSFLSLRNLVLDISHTTR 420

Qy 459 IDPDCIFLGLISLNTLKAAGNSFKDNTLSNFTNTNITFLDLSKQQLBQISRGVDTLY 518

Db 421 VAFNGIENGSLSEVLKMAAGNSFOENFLPDITELRNITFLDLSOCCOLEQSLPTAFNSLS 480

Qy 519 RLQOLNMSHNNLLFLDPESHYKQLYSLRTLDSCFNRIRTS-KGIIQHPFKSLAVFNLTNNS 577

Db 481 SLQVLMNSHNNPFSIDTPEPKCLNSLOVLDYSLNHNMTSKQELQHPFSSALFNLITOND 540

Qy 578 VACICEYONFLOWYDQKMPLVNEOMKASPIDMKASIVLDFTNSTCYIKYITIISSVV 637

Db 541 FACTEHOSFLOMIDKQQLVEVERBECATPSDKQGPVLSL-NITQNMKTIIGVSLV 599

Qy 638 SVLVAVATAPLIIHYFFPHLIIAGCKKYSRSEIYDAFVIYSSQNMEDWVRNELYKNLEEG 697

Db 600 SVLVAVAVAVLVYKFFPHLMALAGCIKYGGENIYDAFVIYSSQNMEDWVRNELYKNLEEG 659

Qy 698 VPRFOLCHYRDFIPGVAIAANNIOEGFHKSRKVIWVSRHFIQSRWCIFEYELAQTMQF 757

Db 660 VPRFOLCHYRDFIPGVAIAANNIHEGFHKSRKVIWVSRHFIQSRWCIFEYELAQTMQF 719

Qy 758 LSSRSGIIFIVLEKYEKSLRQOVELYRLSNTYILEMEDNALGRHIFWRRLKALLDQK 817

Db 720 LSSRAGIIFIVLOKYEKTLRQOVELYRLSNTYILEMEDSVLGRHIFWRRLKALLDQK 779

Qy 818 ALNPD--ETSEEBQEAATL 834

Db 780 SWNPEGTGTCGNMOEATSI 799

RESULT 6

US-10-114-893-10

Sequence 10, Application US/10114893

Publication No. US20020193567A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John M.

APPLICANT: Lavallee, Edward R.

APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Evans, Cheryl

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Bowman, Michael R.

APPLICANT: Spaulding, Vikki

APPLICANT: Carlin-Duckett, McKeough

APPLICANT: Kelleher, Kerry S.

APPLICANT: Genetic Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: GI 6000-10A

CURRENT APPLICATION NUMBER: US/10/114,893

CURRENT FILING DATE: 2002-04-02

EARLIER APPLICATION NUMBER: 09/413,232

EARLIER FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 321

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 661

TYPE: PRT

ORGANISM: Homo sapiens

US-10-114-893-10

Query Match 13.9%; Score 602.5; DB 13; Length 661;

Best Local Similarity 28.2%; Pred. No. 4,66-40;

Matches 185; Conservative 127; Mismatches 236; Indels 47; Gaps 18;

Qy 28 CIEVLPNTYTCMOONSKIPHDIPYETKNDLSFNPDKLIRSYFTNFQOLQWLDLRCEIETEDKAMHG 87

Db 28 CIEKANTYVNCENIGLSEIPDTLPNTTPELFSEFNPDLPTIHNRTFSRLMNLVLDLITRC 87

[illegible]

RESULT 8
US-10-038-854-135

```

Sequence 135, Application US/10038854
Publication No. US20040022781a1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Elsen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malvankar, Uriel M
APPLICANT: Shinkets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderma, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoli, Bha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Steacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomoit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/253,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/286,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,663
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus

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US-10-038-854-135

Query Match	13.8%;	Score 597.5;	DB 15;	Length 661;
Best Local Similarity	27.9%;	Pred. NO. 1.2e-39;		
Matches 187;	Conservative 125;	Mismatches 314;	Indels 45;	Gaps 15

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0Y 12 IMALFSCIR--PGSLNPCEIYLPITVQCMDOYNSKPHDI PYSTKNLDLSPFLILR 69
Db 10 LVALFPLASGRATTSOQKICEKVVAKYTNCGNLGNELPGTLPNSTCELESFVPLTIQ 69
0Y 70 SYSFTNFSOLQWLDLRCEIETIEDKAMHGLNOUSTVLTGNPIKTSFGSGLTNLEN 129
Db 70 NTFPSLINTFLPDLTRCOIYWIHEDTPOSOHRLDTVLTPANPLI PAEYALSGPKALKH 129
0Y 130 LVAVERTKMSLSGPHIGOLISLKKLVANVANIHSFKPEYNSNLTNLEHVDLSVNYQTI 189
Db 130 LFTIQGJISIDPFIPLHNOKTLESYLXSNHISIKLPGKPP--EKLKATVDFOUNAITHYL 189
0Y 190 SVKDOFLPRENOVNLSDLSLNPIDSIOQAFOGIRLHELHETLRSNPNSSNVLKMCLONM 249
Db 189 SKEDMSLSLOO--ATNLSLNTLNGNDIAGIEPGAFAFSAVFOSL---NFGFOTNLVIFKGL 242
0Y 250 TGLHVRRLIGSPKERNLESFDRSVMGECNVSIDERFLTYINHPSDDIYINLANLIS 309
Db 243 KNTSIOSLWLGFPE--DMDEDISPAVFGLCEMSVESINLOKHYPFNISNTFHCFSGLQ 301
0Y 310 AMSFTGVAKHAKIAD-----VPRHFKMOSHISIRCHLKP--EPKSLPPLKSWTL 356
Db 302 ELDLTATHLSLSELPBGVLGVGLSTLKKVLVSANFENL---QOISASNPFLSLHLSIKO--- 354
0Y 357 TTNREDISFGOLA-LPSLRATYLDLSNNAMSFPGCCSYSDPOTNNLKYUJDLSPNGVT-LMSA 414
Db 355 NTRRLELGGCCLENNENIRELDSHDDIETSDCCNLQLRNLSHQISNLSNTEPLSLKTE 414
0Y 415 NFMGELLEYLDFOHSTLKVTEPVSFLSKLKYUJDLSPNTRKIDPDGIFLGISLNTL 474
Db 415 AFPECCQBLDLDAFTRKLVKADQASPFQNNHLKYUJLNSHLDLISSEQLFDGLPALQHL 474
0Y 475 KWAGNSFKDNTL--SNVFTNTNTLFTDLDSKCOLBOISRGVDTLYRLQLLNMSHNLLF 532
Db 475 NLOGNSHPKGNIOKNTSLQTLGRLEIIVLSCDSDSIDQHAFSLKMMNHVDSLHNRLTS 534
0Y 533 LD---PSHAKOLYSLRTDSCFNRLETSKGLQHPKPSLAVPNLTNNSVACICEYQNEFLQ 589
Db 535 SSIETALSUKGIY---LNLASNHSITLPSLRLPLISOQRTINRQNPDLCTGNSIYELB 590
0Y 590 VWEVDQRMPLVANEOMKCAPIDMKASLVLDFETNSICY---IYKTIISVSVSVLVAVATV 645
Db 591 WYKXENQKLEDTEDTLCENPPLLRGVRLSDVTLSGMSMAVAGIFPLIVFLVPAILLIFAV 650
0Y 646 APLIHYFPHL 656
Db 651 KYFLRWKYOH 661

```

RESULT 5
ITS-10-03

US-10-037-417-107
: Sequence 107, Application US/10037417
: Publication No. US20040052806A1
: GENERAL INFORMATION:
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Alsobrook II, John P
: APPLICANT: Tchernov, Vellizar T
: APPLICANT: Liu, Xiaohong
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Patuturajan, Meeta
: APPLICANT: Grose, William M
: APPLICANT: Lepley, Denise M
: APPLICANT: Burgess, Catherine E
: APPLICANT: Vernet, Corine A.M.
: APPLICANT: Li, Li
: APPLICANT: Gorman, Linda
: APPLICANT: Edinger, Shlomo R


```
Db          359 SKLRSLKXKLHLRGVYRELKKKHFEHLQSLPNL-ATINLGINFTEKIDPKAQ----- 410
Qy          231 TLRSPNSNVLMKCLQMTGLHVRLLIG-EFKNERNL-----ESP----- 272
Db          411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSWRNLKRPKSLTDDDEFDPHNVFYS 461
Qy          273 -RSVMEGLCNVSIDFRLLTYINH-----SDDIYNLANCIANSAMSPGVHAKIA 322
Db          462 TKPLIKPQCTAYGAKALDLSLNNIFILGSGQFEGFQIACILNLSFNANTQVNGTEPS--- 518
Qy          323 DVPRRFKMOSLSIRCHLKPFPKLSPLKSWTLTTNREDI-----SFGQALPSLRYLDL 378
Db          519 -----SMPHIKYLDLTNNRLDPDNNAFSD--LHDEVLVDL 552
Qy          379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS-----ANFMGLEELEYLDFQHS 430
Db          553 SHNAHFSAIGVTHRGFIQNLINLRVNLSHNGIYTLTBESBELKSLKELVPSGNRLD 612
Qy          431 TLKKYTE--FSVFLSKELLYLDISYNTKIDPDGIFLG-LSLNTLMAGNS--FKDN 484
Db          613 HLMNANDGKWSIFKSLQNLIRLDSLNNLQOIPNGAFINLPQSLQELLISGNKLRFFNW 672
Qy          485 TLSNVFTNTNLTFLDLSKQLEQISRGVFDLYRLQLLNMGNHNLFLDPSHYKQLYSL 544
Db          673 TLLQYF--PHLHLLDLSRNLVFLPNCLSKFAHSLFTLLSHNFSHLPSGFLSEARNL 729
Qy          545 RTLDSPNRLE-TSKGILQHPK-SLAVFNLTNNSVACICEYQNFLOWKQOMF---L 598
Db          730 VHLDSLFTNTIKMINSSLOTKKTNSILBHGNYDCTCDSIDPSWIDENLNTITPCL 789
Qy          599 VNVEQMKASPIDMKASLVLDFTNSTC-----YIKTIISVSYSVLVAVATFLIY 650
Db          790 VNV---ICSNPDQSKSINSLDLTTCVSDTTAAVLFPLTFTTSM--VMLAALVHHLFY 844
Qy          651 ---HFYFHL--ILAGCKKYSRGESITYDAFYYSQN---EDWYNELVKMLEEGVPR-F 701
Db          845 MDWVFTHMCSAKLKGYRTSSTQTFYDAYISYTDASVTWVNLNRYHLESEDEKSV 904
Qy          702 QCLHVRPFIQVAIAANIIOGFFHRSKRVIVVSHFIQSRWCIFEYIACTQWFLS-- 759
Db          905 LILCEERMDPGLPIIDIMQ--SINOSKTIIFVLTKY-----AKSWPKTAF 951
Qy          760 -----SRSGIIFVLEKVEKSLRQOVELYRLSRNTYLEMEDNALGRHIFWRLL 809
Db          952 YLALQRLMDENMDVILFILEPVLQ--YSQYLRLRORICKSSILQWPNPKAENLFWQSL 1009
Qy          810 KKALL 814
Db          1010 KNVVL 1014

RESULT 11
US-10-272-502A-31
; Sequence 31, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Vollmer, Doreg
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; FILE REFERENCE: C01039.70065 US
; CURRENT APPLICATION NUMBER: US/10/272,502A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
```

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; LENGTH: 1032
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-272-502A-31

Query Match      13.3%; Score 575; DB 14; Length 1032;
Best Local Similarity 25.1%; Pred. No. 1.5e-37;
Matches 242; Conservative 153; Mismatches 318; Indels 252; Gaps 40;

Qy          32 LPNTFYQGDQGN-LKIRHPDIPYSTRKNDLSFN----- 63
Db          120 LRLNLVLLLEDNQLTYTTIAGLPESLKELSLIONNIPOYTKNTFGLRMLERYLYGMNCF 179
Qy          64 -----PLKILRSYSFTNF-----SOLQWLDLSRCEIETIEDKAMH 98
Db          180 KGNQTFKVEDGAFKYLHLKVL-SLSFNNLFFVPPKLPSPSLRKLPLSNAKINNIIOGEPK 238
Qy          99 GLNQSTLYLVGN-----PIYSFS-----PSFGSLTNLEMLVAVETQWTSLE 141
Db          239 GLENTTLTLDLSCNCRCYNAPPTCPCKENSIIHHPILAFOSITQLLYLNLSTSLRTIP 298
Qy          142 GFHIGQLSLIKKLVANAH-LIHSFPLREYFSNLTLNLEHVDLSYN-----YIQTISV--- 191
Db          299 STWFENLSNLKELHLEFNYLVQELASGAFITKLPSTLQDLSFNFQYKRYELOFINISSNF 358
Qy          192 -----KDLQFLRENQVNLSDLSPINFLDISIOAQAFQGIHLHEL 230
Db          359 SKLRSLKXKLHLRGVYRELKKKHFEHLQSLPNL-ATINLGINFTEKIDPKAQ----- 410
Qy          231 TLRSPNSNVLMKCLQMTGLHVRLLIG-EFKNERNL-----ESP----- 272
Db          411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSWRNLKRPKSLTDDDEFDPHNVFYS 461
Qy          273 -RSVMEGLCNVSIDFRLLTYINH-----SDDIYNLANCIANSAMSPGVHAKIA 322
Db          462 TKPLIKPQCTAYGAKALDLSLNNIFILGSGQFEGFQIACILNLSFNANTQVNGTEPS--- 518
Qy          323 DVPRRFKMOSLSIRCHLKPFPKLSPLKSWTLTTNREDI-----SFGQALPSLRYLDL 378
Db          519 -----SMPHIKYLDLTNNRLDPDNNAFSD--LHDEVLVDL 552
Qy          379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS-----ANFMGLEELEYLDFQHS 430
Db          553 SHNAHFSAIGVTHRGFIQNLINLRVNLSHNGIYTLTBESBELKSLKELVPSGNRLD 612
Qy          431 TLKKYTE--FSVFLSKELLYLDISYNTKIDPDGIFLG-LSLNTLMAGNS--FKDN 484
Db          613 HLMNANDGKWSIFKSLQNLIRLDSLNNLQOIPNGAFINLPQSLQELLISGNKLRFFNW 672
Qy          485 TLSNVFTNTNLTFLDLSKQLEQISRGVFDLYRLQLLNMGNHNLFLDPSHYKQLYSL 544
Db          673 TLLQYF--PHLHLLDLSRNLVFLPNCLSKFAHSLFTLLSHNFSHLPSGFLSEARNL 729
Qy          545 RTLDSPNRLE-TSKGILQHPK-SLAVFNLTNNSVACICEYQNFLOWKQOMF---L 598
Db          730 VHLDSLFTNTIKMINSSLOTKKTNSILBHGNYDCTCDSIDPSWIDENLNTITPCL 789
Qy          599 VNVEQMKASPIDMKASLVLDFTNSTC-----YIKTIISVSYSVLVAVATFLIY 650
Db          790 VNV---ICSNPDQSKSINSLDLTTCVSDTTAAVLFPLTFTTSM--VMLAALVHHLFY 844
Qy          651 ---HFYFHL--ILAGCKKYSRGESITYDAFYYSQN---EDWYNELVKMLEEGVPR-F 701
Db          845 MDWVFTHMCSAKLKGYRTSSTQTFYDAYISYTDKASVMDWVNLNRYHLESEDEKSV 904
Qy          702 QCLHVRPFIQVAIAANIIOGFFHRSKRVIVVSHFIQSRWCIFEYIACTQWFLS-- 759
Db          905 LILCEERMDPGLPIIDIMQ--SINOSKTIIFVLTKY-----AKSWPKTAF 951
Qy          760 -----SRSGIIFVLEKVEKSLRQOVELYRLSRNTYLEMEDNALGRHIFWRLL 809
Db          952 YLALQRLMDENMDVILFILEPVLQ--YSQYLRLRORICKSSILQWPNPKAENLFWQSL 1009
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Qy 810 KALL 814
Db 1010 KVVVL 1014

RESULT 12

US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauser, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Query Match 13.3%; Score 575; DB 15; Length 1032;

Best Local Similarity 25.1%; Pred. No. 1.5e-37;
Matches 242; Conservative 153; Mismatches 318; Indels 252; Gaps 40;

Qy 32 LENITYQCDON-LSKIPHDIPYSTKNLDLSFN----- 63
Db 120 LKNLVLLLEDQVITIPAGLPESLKEKSLIGNNIPOVTKNTPGLRNLERLYLGNVCV 179
Qy 64 -----PKIKRSYSFTNF-----SOLMLDSRCETIEDKAMH 98
Db 180 KCONTPKVEDGAFKNLILHKLVL-SLSFNNLPYVPPKLPESLKRKLFLSNAKINMIGOEDEK 238
Qy 99 GLENOSTIVLGN-----PIKFSF-----PSFSGLTJNLENVAETKMTSL 141
Db 229 GLENITLJLDGNCRCYNAPPTCPCKENSSIHHPILAFQSLTQLYLINISSTSLRTIP 298
Qy 142 GHHIGQLISLKKLVANHN-LHSFKLPEYFNMJTNLEHVDLSYN-----YIQTISV----- 191
Db 229 SWFPMENLSLKKLHLEFNYLVEIASGAFYTKLPISQIIDLSPNQYKRYLOFININSNP 358
Qy 192 -----KDLQFLRENPOVNLSLDISLNPIDISIQAFQGIRLHEL 230
Db 359 SKLRSLKLLHRLRGVYFRELKKHFEHLQSLPML-ATINGINFIEKIDFKAFQ----- 410
Qy 231 TLKSPNNSNVAKMCLQNTTGLVHRLILG-EFKKERNL-----ESPD----- 272
Db 411 -----NPSKLDVI-----YLSGNRIASVLDGTDYSSWRNRLKRPSTDDDFPHVNFYS 461
Qy 273 -RSVMEGLCNVSIDEFRLTYINHF-----SDIYVLANCIANISAFGVHAKHA 322
Db 462 TKPILKPOCTAGXKALDLSINNIPIIGSQBPBGODIACINSPANQVFGTGRS--- 518
Qy 333 DVPRHFKMOSLSIRCHLKPFPKLSLPIKSWTLTTNREDI-----SFGOLALPSLRKYDL 378
Db 519 -----SMFHIXYLDLTNNRDLDPDNNAFSD--LHDLVLVDL 552
Qy 379 SRNA--MSFRGCCSYSDPGTN--NLKYLDLSFNGVILMS-----ANFMGLEELEYDFOHS 430
Db 553 SNNAHYFSLAGVTHRLGFTQNLINLRVLNLSHNGIYTLTESELSISLKEIVFSGNRID 612
Qy 431 TLKKYTE--FSVFLSLEKLYLDISYNTKXIDPDGIFGL--ISLNTLTKAGNS--FKDN 484
Db 613 HMMNNDGKYSWIFSLQNLIRLUDSYNNLQOIPNCAFNLPOSLQDELLISGNKLRFFMW 672
Qy 485 TLSNVFTNTTNLTFDLDSKQLEQISRGVPTLYRLQLLNMGNHNLFLPDPHYKQLYSL 544

Db 673 TLLQYF-----PHULDLSSRNELYFLPNCLSKFANSLFETLLSHNHFSLPGSFLSEARNL 729
Qy 545 RLDCSFNRIB-TSKGILQHPK-SLAVFNLTNNSVACICEYONFLQWKQKMF-----L 598
Db 730 VHLDSFNTIKINSSIQTKMKNLSTLELHGNVFDCTCQSDSRSMDEMLNTTIPKL 789
Qy 599 VNEQMKASPIDMKASVLDFTNSTC-----YIKTIISSVSVLVVATVAFELIY 650
Db 790 VNV-----ICSNPDQSKSISMSLDLTTCVSDTAAVLFTLFTLSM--VMLAALVHHLFY 844
Qy 651 ---HFYFL--ILLGCKKYSRGEISYDAFYVSSQN---EWMVNELVKNLEEGVPR-F 701
Db 845 MDWFIYHMCASAKKGYRTSSTQTFYDAVISYDTRKASVTDWVINELRHLEESDEKSV 904
Qy 702 QLCIHRDFIPGVAIAANIIQGFHKSRRVIVVSRHRTQSRWCIFEYEAQTQWFLS-- 759
Db 905 LILCEERWDQPLPIIDNMQ-SINOSKTIYFLTKY-----ASNVFKTAF 951
Qy 760 -----SRSGIIFVLEKREKSLRQVELYRLSRNTYLEMEDNALGRHIFWRRL 809
Db 952 YLALQRLMDENMDVIFILFEPVLQ--YSQYLRRLQRICKSILQWPNPKALEMFWQSL 1009
Qy 810 KALL 814
Db 1010 KVVVL 1014

RESULT 13

US-09-954-987B-175
; Sequence 175, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Magner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-987B-175

Query Match 12.9%; Score 559; DB 10; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3.1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

Qy 4 LHLAAGTILMALFSLCRLPGSLNPCIIEVLPNI-----TYQCDONLSKIPHDIPYSTKNL 58
Db 13 LIFLNMVLVSRVFGFRWPKPL-PC-EYKVINPEAHVIVDCTDKHLTEIPBGIPNTTNL 70
Qy 59 DLSFNPPLIKRSYSTNSQLOMDL-----SKCEIFT-----IEDKAMHGLNQSL 104
Db 71 TLTINHIPISSPDSFRRLNHLLEIDLRCNCVPLVGSKAVCTKXLQIRPGSFGSLDLK 130
Qy 105 TTVLGNPFIKSPS--PSFSGLTJNLB--NLVAVF-----TKMTSLGEGHIGQ----- 147
Db 131 ALYLDGNQLLEIPDLPSSLH-LLSLEANNIFSIKENTELVNIETLYLQGNCCYRRNCP 189

QY 148 -----LISTKLANVA-----HN- 160
Db 190 NVSYIEKDAFLVNRNKLKSLKDNVAVPTTLBPNNLELYNNI1KKIOENDFNNTLN 249
QY 161 -----IHSFKL-----PEY 169
Db 250 ELQVLDLSGNCRCVNVYPCTPCENNSPLOIHDAFNSTELKYLRLHSNLSQHVPPW 309
QY 170 FSNLTNLEHVDLSYNYIQTISVKDLOFLRENQVNLSDLSNPIDSIOQAFOGIRLHE 229
Db 310 FKNMNTLOEIDLSONYLAR-EIEBAKFLHFLPNL-VELDFSPN---YELQVYHA---S 359
QY 230 LTLRNNNSNVLMKC-----LQNTGLAHVRL-----ILGEFKN 264
Db 360 ITPHLSLSLENLKLIRVKGYPFKELKNSLSLVHLKLPRLVLDLGTNFIKIDINIFKH 419
QY 265 ERNLESFDRSVME-----GLC---NVSIDEFR---LTYINHFSDDIYNLNC-LAN 307
Db 420 FENMLKLDLSVNVKISPSBESREVGFCPNQOTSVDNRHPOVLEALHAFRYDEYARSCRPN 479
QY 308 ISAMSFVTGVHKLHADVPRHFKWQSLIIRCH---LKPPKLSLPFLKSWTLTTNREDIS 364
Db 480 KEPPSFLPLN---ADC-HIYGQTLDSRNNIFFIKPSDPQHLSPFKCLNLSGN---T 529
QY 365 FGQI-----ALPSLRYLDSRNAMSPFGCCSYSDPGTNNLKLYLDLSPNGVILMSANFM 417
Db 530 IGQTLNGSELMPRLRELYLDPSNNRLD-----LTYSTAFE 564
QY 418 GLEBELEYD-----FOHSTLKVTESFVPLS-LEKLLY-LDISYNTK-IDPDGIFL 466
Db 565 ELQSLLEVLDLSNSHYFOABEGITMNLNFTKKRLDLKLMANDNDISTSSSRMESD--- 620
QY 467 GLISLNTLMKAGNSFK-----DNTLSNVFTNTNLTFPLDSKCOLBOISRGVDP----- 515
Db 621 ---SLRIEFGNHLDVLMRAGDNRYLDPFKULFNLBVLDISRNSLSNPPEVFEFGMPN 677
QY 516 -----TLRYQLMNSHNL-----LFDPSHYK 539
Db 678 LKNLSLAKNGKSPFMDRLQLLKLEIIDLSSHQTLKYPERLANCSKSLTTLILKHNOIR 737
QY 540 QL-----YSLRTLDSPFNRIETSKILO--HPPK---SLAVENLTNNSVACICEYQ 585
Db 738 QLTKEFLBDAQRLVLDISSNKIQ---VIQKTSFPEVNLNLEMLVHHNRFLCNCAV 793
QY 586 NPLQWVQDKMFLVNV-EQMKCASPIDMKASLVDFTNSTCYIYKT---IISVSVSYL- 640
Db 794 WFWVNVNHTDVTIPLYATDVTGCVGGAHKGQSVISLDLYTCELDTNLIILSVSISVLF 853
QY 641 --VYATVAFI-----YHFYPHLILIAQCKKYSRGEISTYDAFYISSQNE--DWYRNEI 690
Db 854 LNVVNTTSHLFFWDMVYIYFPAKIKGYOHLQSMESCVDAFIYVDTTGNASVATEVVLQEL 913
QY 691 VKNLEEGVPR---FOLCLHYRDFIPGVAIAANIIOEGFHKSRYVWVSRHPIOSRCIF 747
Db 914 VAKLED--PREKHFLCLBERDMLPGQVLEHLSQ-SIQLSKTYFVNTQYAKAKESKRM 970
QY 748 EYELAQWQFLSSRSGLIFVLEKYEKSLRQO-VELYRLSRNTVLEMEDNALGRHIFW 806
Db 971 AFVLSHQ-RLDEKVDVILIF--LEKPLQSKFLQKLKRLCRSSVLEMPANPQAHPRFW 1027
QY 807 RLKALK 813
Db 1028 QCLKNAL 1034

RESULT 14

US-10-272-502A-22
; Sequence 22, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Schaeffer, Christiaan
; APPLICANT: Bratzler, Robert L.

; APPLICANT: Vollmer, Jorg
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; TITLE OF INVENTION: MIDAZOLINOLINE COMPOUNDS
; FILE REFERENCE: C01039.70065.US
; CURRENT APPLICATION NUMBER: US/10/272.502A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1050
; TYPE: PRN
; ORGANISM: Mus musculus
US-10-272-502A-22

Query Match 12.9%; Score 559; DB 14; Length 1050;

Best Local Similarity 24.4%; Pred. No. 3.1e-36;

Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

QY 4 LHLHAGTILMLFLSLCPGSLNPCIYLPNI-----TYQCMQNLKIPHDIPSTKUL 58
Db 13 LIFLMMLVSRVFGFRWFPKTL-PC-EVKVNIPEAHVIVDDTDKHLTEIPGIPPTNTNL 70
QY 59 DLSFNPFLKILRSYFTNPSOLQWLDL-----SRCIEET-----IEDKAMHGLNOTS 104
Db 71 TLTINHISIPDSFRLNHLBEIDRCNCYVPLGSKANVCTRLQIRPSSFGSLDLK 130
QY 105 TLVITGNPIKSPS---PGSFGTLNLE--NLVAVE---TYOTSLEGFHIQO----- 147
Db 131 ALVLDGNQLRLIPQDLPSLSLH-LLSLEANNIFSTKENUTELVNIETLYQNCYRNP 189
QY 148 -----LISTKLANVA-----HN- 160
Db 190 NVSYIEKDAFLVNRNKLKSLKDNVAVPTTLBPNNLELYNNI1KKIOENDFNNTLN 249
QY 161 -----IHSFKL-----PEY 169
Db 250 ELQVLDLSGNCRCVNVYPCTPCENNSPLOIHDAFNSTELKYLRLHSNLSQHVPPW 309
QY 170 FSNLTNLEHVDLSYNYIQTISVKDLOFLRENQVNLSDLSNPIDSIOQAFOGIRLHE 229
Db 310 FKNMNTLOEIDLSONYLAR-EIEBAKFLHFLPNL-VELDFSPN---YELQVYHA---S 359
QY 230 LTLRNNNSNVLMKC-----LQNTGLAHVRL-----ILGEFKN 264
Db 360 ITPHLSLSLENLKLIRVKGYPFKELKNSLSLVHLKLPRLVLDLGTNFIKIDINIFKH 419
QY 265 ERNLESFDRSVME-----GLC---NVSIDEFR---LTYINHFSDDIYNLNC-LAN 307
Db 420 FENMLKLDLSVNVKISPSBESREVGFCPNQOTSVDNRHPOVLEALHAFRYDEYARSCRPN 479
QY 308 ISAMSFVTGVHKLHADVPRHFKWQSLIIRCH---LKPPKLSLPFLKSWTLTTNREDIS 364
Db 480 KEPPSFLPLN---ADC-HIYGQTLDSRNNIFFIKPSDPQHLSPFKCLNLSGN---T 529
QY 365 FGQI-----ALPSLRYLDSRNAMSPFGCCSYSDPGTNNLKLYLDLSPNGVILMSANFM 417
Db 530 IGQTLNGSELMPRLRELYLDPSNNRLD-----LTYSTAFE 564
QY 418 GLEBELEYD-----FOHSTLKVTESFVPLS-LEKLLY-LDISYNTK-IDPDGIFL 466
Db 565 ELQSLLEVLDLSNSHYFOABEGITMNLNFTKKRLDLKLMANDNDISTSSSRMESD--- 620
QY 467 GLISLNTLMKAGNSFK-----DNTLSNVFTNTNLTFPLDSKCOLBOISRGVDP----- 515
Db 621 ---SLRIEFGNHLDVLMRAGDNRYLDPFKULFNLBVLDISRNSLSNPPEVFEFGMPN 677
QY 516 -----TLRYQLMNSHNL-----LFDPSHYK 539
Db 678 LKNLSLAKNGKSPFMDRLQLLKLEIIDLSSHQTLKYPERLANCSKSLTTLILKHNOIR 737

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QY 540 QI-----YSLRTLDCSFNRIETSKGILQ--HPEK-----SLAVFNLTNNSVACICEYO 585
DB 728 QLTXYFLDALQRLTYLIDISSNKIQ-----VIQKTSFPENVNLNLEMLVHHRNPLCNCDAV 753
QY 586 NPLQWVKQKMFVNV--EQMKCASPIDMKASLVDPFTNSTCYIKT---IISVSVSVL- 640
DB 794 WFWWWVNHNTDVTIPIYLATDVTVCVGPANHKGQSVISLDLYTCBLDNLNLLFSVSISSVLF 853
QY 641 --VVAIVAFLI-----YHFYFHLIIAGCKKYSRGSIDAFVYSSONE---DWVRNL 690
DB 854 LMVWMTTSHLFPWDMWYIYFWKAKIKGYOHLQSMESCDAFIYDTKASAVTEWLOEL 913
QY 691 VNLEEGVPR---FOLCLHYRDFIPGVAIAANIIQEGFHKSRYIVVSRHFIOGRWCIF 747
DB 914 VAKLED--PREKHFNLCLEERDMLPGQPVLENLSQ--SIQSKTYVFWMTQKAKTESFPM 970
QY 748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLRQO--VELYRLLSRNTYLEMEDNALGRHIFW 806
DB 971 AFYLSHQ--RLDEKVDVILILF--LEKPLQSKSFQRLRRLCRSSVLEWPAHPQHPYFW 1027
QY 807 RLKRLAL 813
DB 1028 QCLKNAL 1034

RESULT 15
US-10-407-952-26
; Sequence 26, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Baurer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-containing Oligonucleotides
; FILE REFERENCE: C01041.70037 US
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent version 3.1
; SEQ ID NO 26
; LENGTH: 1050
; TYPE: PRN
; ORGANISM: Mus musculus
US-10-407-952-26

```

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Query Match 12.9%; Score 559; DB 15; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3,1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

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QY 4 LIHLAGTILMALFLSLCLPRGSLNPCIIEVLNPI---TYQCMDONLSKTPHDIPIYSTKUL 58
DB 13 LIFIMMLLVSRVFGFRWPEKTL-PC-EVKVINPEAHVIVDCDCKHLELPEIGIPNTTNL 70
QY 59 DLSFNPCLKIRSYSTNFSQLOMLD-----SRCEIT---IEDKAMHGINOLS 104
DB 71 TLTINHIISIPDSFRRNLHLEEDIRCNVCVULLGSKRANVCCTKRLQIRPFSGLSDLK 130
QY 105 TLVLGNPIKFS--PGSFGIYNLE--NLVAVB---TKMTSLGPHIQO----- 147
DB 131 ALYLDGNQLLEIPQLPSPSLH--LISLEANNIPSITKENLTELVTLETVLGQNCYRNP 189
QY 148 -----LISIKLANVA----- 160
DB 190 NVSYSEKDAFLWENLKVLSLKDNNVAVPTLPLPNLELYNNIIKKIOENDENNIN 249
QY 161 -----IHSFPL-----PEY 169
DB 250 ELQVLDLSGNCRCYVNPYPCPCENNSPLQIHDAFNLSLTELKVALRHSNSLQHVPTW 309

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QY 170 FSNLTNLEHVDLSNYIQTISVKDLOFLRENDQVNLSDLSLNPIDSIQAOAFQIGIRLHE 229
DB 310 FKNMNLQELDLSQVYLAR--EIEBAKFLHLEPNL--VELDFSFN-----YELQVYHA-----S 359
QY 230 LTLRENFNSNVLKMC-----LQNTGHLVRL-----ILGEFKN 264
DB 360 IYLPHSLSLENLKITLRKGVYFKEKLNSSLSVLHKLPRLEVLDTGTFIKIADLNIFFH 419
QY 265 ERNLESFDRSVME-----GLC---NVSIDEFR---LTYINHFSDDIYNLNC--LAN 307
DB 420 FENLKLIDLSVVKISPSERSREVGFCPNAQISVDHNGPQVLEALHYFRDEVARSCRFPKN 479
QY 308 ISAMSPFGVHIXHADVPRHFQKQSLIIRCH---LKEPKLSLPLKSWTLTTNREDIS 364
DB 480 KEPPSFLEPLN---ADC--HIYGQTLIDLSRNNIPIKPSDFQHLFLKCLNLSGN-----T 529
QY 365 FQOL-----ALPRLRYLIDSRNMSRGCSSYDFGNNLKYVLDLSNGVILSANFM 417
DB 530 IQOTLNGSELMPRLRLRYLDFSNRLD-----LTSYTAIE 564
QY 418 GLEEELEYD-----FOHSTLKVTERSVFLS--LEKLY--LDISYTNWK--IDPDGIRL 466
DB 565 ELQSLLEVLDLSNSHYFOABGITHMLNFTKKRLDKLMDNDNDISTASRTMESD----- 620
QY 467 GLISLNTLMAGNSRK-----DNTLSNFTNTNLTFLIDLSKQLEBQISRGVFD----- 515
DB 621 ---SLRIIEFRGNHDLVLRAGDNNRYLDFPKULFNILEVLDISRNSLNSLPPEVFEQMPN 677
QY 516 -----TLYRQOLNMSHNNL-----LELDBSHK 539
DB 678 LKNLSLANGLKSPFWDRLQQLKHLLELDLSHNOJLTKVERLANCSKSLTTLILKHNQIR 737
QY 540 QI-----YSLRTLDCSFNRIETSKGILQ--HPEK-----SLAVFNLTNNSVACICEYO 585
DB 728 QLTXYFLDALQRLTYLIDISSNKIQ-----VIQKTSFPENVNLNLEMLVHHRNPLCNCDAV 793
QY 586 NPLQWVKQKMFVNV--EQMKCASPIDMKASLVDPFTNSTCYIKT---IISVSVSVL- 640
DB 794 WFWWWVNHNTDVTIPIYLATDVTVCVGPANHKGQSVISLDLYTCBLDNLNLLFSVSISSVLF 853
QY 641 --VVAIVAFLI-----YHFYFHLIIAGCKKYSRGSIDAFVYSSONE---DWVRNL 690
DB 854 LMVWMTTSHLFPWDMWYIYFWKAKIKGYOHLQSMESCDAFIYDTKASAVTEWLOEL 913
QY 691 VNLEEGVPR---FOLCLHYRDFIPGVAIAANIIQEGFHKSRYIVVSRHFIOGRWCIF 747
DB 914 VAKLED--PREKHFNLCLEERDMLPGQPVLENLSQ--SIQSKTYVFWMTQKAKTESFPM 970
QY 748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLRQO--VELYRLLSRNTYLEMEDNALGRHIFW 806
DB 971 AFYLSHQ--RLDEKVDVILILF--LEKPLQSKSFQRLRRLCRSSVLEWPAHPQHPYFW 1027
QY 807 RLKRLAL 813
DB 1028 QCLKNAL 1034

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Search completed: March 12, 2005, 20:27:59
Job time : 80.8956 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds
(without alignments)
3722.074 Million cell updates/sec

Title: US-09-396-985b-6

Perfect score: 4335
Sequence: 1 NMPLHLAHLTLMALFLSCL.....GKALNPDETSEBQATVLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597.5	13.8	661	2 I56258	RP105 - mouse
2	465.5	10.7	786	2 T06664	Toll protein-like
3	397	9.2	1097	2 A29943	gene wheeler prote
4	374	8.6	1389	2 T13852	clt protein - fru
5	371	8.6	1385	2 T13857	chaoptin precursor
6	320.5	7.4	1134	1 A29944	hypothetical prote
7	303	7.0	1066	2 T15864	insulin-like growt
8	301.5	7.0	603	2 JC6128	insulin-like growt
9	300.5	6.9	605	2 JC5339	insulin-like growt
10	290.5	6.7	603	2 JC1282	insulin-like growt
11	287.5	6.6	1112	2 T10504	disease resistance
12	285.5	6.6	1051	2 T13174	gpi50 protein - fr
13	281.5	6.5	605	2 A41915	insulin-like growt
14	279	6.4	1469	2 B36655	slit protein 2 pre
15	279	6.4	1480	2 A36665	slit protein 1 pre
16	274	6.3	1692	2 A33988	adenylate cyclase
17	270.5	6.2	1143	2 T10636	hypothetical prote
18	270	6.2	907	2 JG0193	G protein-coupled
19	266.5	6.1	1523	2 T13953	MEGF5 protein - ra
20	266	6.1	1531	2 T42218	slit-1 protein hom
21	265.5	6.1	1016	2 T30553	disease resistance
22	264.5	6.1	1027	2 B85089	receptor protein k
23	261	6.0	1232	2 T05322	hypothetical prote
24	259	6.0	910	2 G84648	probable disease r
25	256	5.9	560	2 A60166	platelet membrane
26	253	5.8	907	2 JB0176	orphan G protein-c
27	252	5.8	1120	2 B86479	hypothetical prote
28	250	5.8	1068	2 H96769	hypothetical prote
29	249	5.7	662	2 S42799	garp precursor - h

30	249	5.7	855	2 T17460	disease resistance
31	247.5	5.7	1778	2 AF1116	internein protein
32	247	5.7	890	2 T00800	disease resistance
33	246.5	5.7	853	2 T17461	disease resistance
34	246.5	5.7	910	2 B96770	hypothetical prote
35	243.5	5.6	738	2 T19938	hypothetical prote
36	243	5.6	1091	2 A58532	glial cell membran
37	243	5.6	1784	2 C96615	hypothetical prote
38	242.5	5.6	603	2 T24315	hypothetical prote
39	242.5	5.6	800	2 H84740	hypothetical prote
40	242.5	5.6	951	2 A96770	hypothetical prote
41	239	5.5	855	2 T07015	Cf-4A protein - co
42	237	5.5	994	2 H96510	probable disease r
43	236.5	5.5	622	2 JC7973	synleutin - human
44	235.5	5.4	983	2 G84524	probable disease r
45	235.5	5.4	2026	1 OYBY	adenylate cyclase

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A/Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: I56258; MUID:95204928; PMID:7897216
A/Accession: I56258
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:062192; GB:D37797; NID:G761711; PIM:BA07043.1; PID:G761712

Query Match 13.8%; Score 597.5; DB 2; Length 661;
Best Local Similarity 27.9%; Pred. No. 1.8e-29;
Matches 187; Conservative 125; Mismatches 314; Indels 45; Gaps 15;

QY	12	IMALFLSCLR--PGSLNPCEIVLPNTTQCMDQNTSKIPHDIPYTKNLDLSPNPKIKR	69
DB	10	LVALFLASCRATTSDDCKIEKVKYKNCENIGLNIPTLPNSIECFEFNVLPITQ	69
QY	70	SYSFTNPSQLQWLDLSRCIEITIEDKAMHGQNLSTIVLTGNPIKSPSPSGSLTNLEN	129
DB	70	NTTFERLINLTPDLTRCQYWIHEDTFQSGHRDPLVLTANPLIFMAETALSGPKALRG	129
QY	130	LVAVETKMTSLBGFHIGQLISLKLNVANLHSEFKLDEYFENLTLNLEHVDLSYNYTQT	189
DB	130	LEFIQTGSSIDFIFLHNQKTLBSLYLGSNHSIKLPRGFT-ELKLYLDQNNANLHVL	188
QY	190	SVKDIQFIRENDQVNLSDLSNPIDSIQAQFQGIIRHELTLSRNFSNVLKQCLQNM	249
DB	189	SKEDMSLQQ--ATNLINLNGNDIAGIEPGAFAVFSGL---NFGQTMVLVFEKL	242
QY	250	TEGHAHRLILGSEKERNLSEFDRSVMEGLCNVSIDEFPLTYINHFSDIYNVLNCANIS	309
DB	243	KNSTQSLMLGTFE-DMDEDISPAVFGLCMASVESINLQKHYFPNINSNTPHCFSGIQ	301
QY	310	AMSFVGVIKIHAD-----VPRHFKWQSIITRCHLKP--FPKLSLPLFKSWTL	356
DB	302	EIDLRAHLSLPSGLVGLSTLKKVLNANKRENT---CQISANFPELTHLSIKG---	354
QY	357	TNNREDISFGQLA-IPSLRYLDLSRNAMSFRCCGYSDFGTNNLKYLDSENGVT-LNSA	414
DB	355	NTRKRELGTGCLENENLRELDISHDDIETSDCCNLORNLSHOSLNSYNRPLSKTE	414
QY	415	NMGLEBELEYLDFQSTLKKVTEFSPVLSLEKLVLDISYNTKIDPQIFGLISLNTL	474
DB	415	AKKECPQELDLAFTRLKVKDAQSPFOVHLKLVNLHSLDLSISSEQLFDGLPALQHL	474

Db 606 TFEVROIER-----QTLICPLDPSDDPREKCPRGCHV-----TYDKALVIN 649
Qy 414 ANFMGLEELEYIDFQHSITLKVTEFSVPLEKLYLDISYNTKIDFGIPLGLISINT 473
Db 650 CHSGNLTVPRLPNLHKNNQLM-----LHLENNTLRLPSANTP-----GYESVTS 696
Qy 474 LKAGNSFQDNTLSNVFTTNTLTPDLDSKQLEQISRGVPTVRLQLLNNSHNNLFL 533
Db 697 LHLAGNNL-----TSIDVDQLPTMLTDLDIS-----WNLLQMLN----- 730
Qy 534 DSHVKQYLSTRLTDCSPRIETSKGILQHPKSLAVFNLINNVAICIEYQNFQWMD 593
Db 731 -----ATVGLFRLRTMKMSV-KLSGPNMCDCTAPFLFLFTD 768
Qy 594 QMFLVNEQMKASPIDMKASLYLDFTNSTCYIKTI-ISVSV-----SVLVAATAVFLI 649
Db 769 NFERIGDRNEMCVN-AEMPTRMVELSTNDICPAKGVFIALAVIALGLAGFAALY 827
Qy 650 YHF-----YFH-LILAGCKKYSRGESYDAFVYSSQNEQWVRELKYLEGVR 700
Db 828 YKQTEIKIMLYAHNLLMFVTEEDLDKDKPDAPFISYSHKQSPFIEDVLPOLBHPQK 887
Qy 701 FOLCHYRDFIPGVAIAANIIOEGFHSKRVIVVSRHPIQSRMCIFFEYIAQTWQFLSS 760
Db 888 FOLCHYRDMVLVGHIPENIMR-SVADSRTIIVLSQNFISKEMARLEFRAAHRGALNEG 946
Qy 761 RSGIIFIV-----LEKVEKSLRQOVELYRLLSRNTYLEMEDNALGRHIFWRRLKAL 813
Db 947 RSRIVITVYSIDIGDEKDE-----ELKAVLKNNTYIKW-----GDPWFMDKLRFL 993

RESULT 4

gene wheeler protein - fruit fly (Drosophila melanogaster)
T13852
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13852
R.Eldon, E.; Kooyer, S.; D'avey, D.; Duman, M.; Lawinger, P.; Botae, J.; Belien, H.
Development 120, 885-899, 1994
A.Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A.Reference number: Z17796; MUID:95324375; PMID:7600965
A.Accession: T13852
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1389 <EID>
A.Cross-references: UNIPROT:Q24591; EMBL:I23171; NID:g915682; PID:g1019104; PIDN:AAA7920
C.Genetics:
A.Gene: wheeler
A.Cross-references: FlyBase:FBgn0004364

Query Match 8.6%; Score 374; DB 2; Length 1389;
Best Local Similarity 21.2%; Pred. No. 3.7e-15;
Matches 230; Conservative 159; Mismatches 327; Indels 366; Gaps 48;

Qy 41 DONLSKIRHDIPTSTKNDLSFNPLKTIISYSFTNF-----SQIQ 80
Db 154 DNNIRQLPEGWCMSPSLQLNLTONIRSAFLFSEKLCAGSALSNANGAVSGSGSEIQ 213
Qy 81 WLDISRCIEITIEDKAMHG--LNOLSTLVLTGNPTKSPSGSGQLTNLENLVAVETKMT 138
Db 214 TLDSVFNELRSLPD-AMGASRLRLQTLSTLQHNNTISTLAPNALAGLSSLRVLTINISYHHV 272
Qy 139 SLEGFHIGQLISLKLVAHNLHSPKLE-----YFS 171
Db 273 SLPSFAFGNKEIRLHQLGNDL--YELPKGLHRLLEQLVLDLSGNQLTSHHVNSIFA 330
Qy 172 NLTNLEHVDLSYNTIQT---SVKLOLQRENPQVNLSDLSLNPDISIQAFQGI-RL 227
Db 331 GLIRIVLNTSNALTRIGSKFKELYPLO-----LIDMNNNSIGHIEGAFPLVYL 383
Qy 228 HELTLRSN-----FNSSNVL-KMCLQNMNTGLHVRHLIGE-FKXERNLESFDRS-- 274
Db 384 HTLNLAEKRLHTLDNRINGLVLYLTKLTLLN---NLVSIVESQAFRNCSDLKEIDLSSN 439

Qy 275 -----VMEGLCNVS-----IDFRLTYINHSDIYNLNCIANISAMS--FTGVH 317
Db 440 QLTVEPAVQDLSMLKTLIDIGENQISEFR-----NNTFRILNQLTGLRLIDNRIGNIT 492
Qy 318 IKHIDVPRHFQWQSLISIRCHLKPPKLSL-PFLKSWTLTNRDISF-----GOLA-L 370
Db 493 VQMFQDLPR-----LSVLNLAKNRIQSIERGAFKNTIEIARLDKNTLTDINGIFATL 546
Qy 371 PSLRYLDSIRNAMSFRGCCSYSDPGNNLKLYLDLSFNGVILMSANPMLEE--LEYLDF 427
Db 547 ASLMLNLSNNLVM---FDYA-FIPLSKMLDIGNYIEAL-GNYIKLQSEIRVTTLDA 601
Qy 428 QHSITKATYFESVPLSEKLYLDIS-----YNT-----KIDFDGIFGLISINTL 474
Db 602 SNRRTIETIGAMSVPSIE-LIFINNIIIGQIQANFVDKTRIALRDLVAVNLSKISLNL 660
Qy 475 KMA-----GNSFKDNTLSNVFTNTNLT-----FLDKR----- 503
Db 661 RVAPVSAKPVDEFYLGPNFECDSMELORINNLTTRQHPHVVDLGNIECLMPHSRA 720
Qy 504 -----COLBO----- 508
Db 721 PLRPLASASDFVCKYESHCPPTCHCEYEQCEVEICPGNCSFHDATATNIVDCR 780
Qy 509 -----ISRGVDTLY-----RLQLLNMGHNNLLFLDPHSHQOL 541
Db 781 QDLALPFRIPQDVSD-LYLDGNNMPELEVHLTGRNRLRALYLNASNNMTLQNGSLAQ 839
Qy 542 YSLRTLDCSFNRIETSKG-----ILOHFK-----SLAVNLTNNS 577
Db 840 VNLRYLHLENNCLTALBEGFERSGLRLRELYLNNMLTHTISNATEPVLSEVLRLDNR 899
Qy 578 V-----ACIC-BYONFLQWVDQKFLVNEQMKCA-SPIDMK 613
Db 900 LSSLPHLYRISLQSLTIGRNAMSCRCQOLKRLAOFSDNANVVDADHDYLDLGIKE 959
Qy 614 ASLVLDFTNST-----CYIKTIISVSVSVLVAATAVFLI 649
Db 960 LELIGNLNGPDCSDDLDAASNNISSQDLGAGICPCMPAYL---VILFVVLVLIIVPV 1016
Qy 650 YHFYHLLILAG-----CK-KYSGESYDAFVYSSQNEQWVRELKYLEGVRPQOL 703
Db 1017 PRESVRMMLFPHYGRVCEPRFEDAGKYDAIILHSEKDYERVCNIAAELEHGRPPFL 1076
Qy 704 CLHYRDFIPGVAIAANIIO-EGFHSKRVIVVSRHPIQSRMCIFFEYIAQTWQFLSR 761
Db 1077 CLQQRDLPP-----QASHQLVEGARSKTIILVLRNLATFWMRIEPRNA---FHESL 1128
Qy 762 SGII--FVLEK-----VEKSLRQOVELYRLLSRNTYLEMEDNALGRHIFWRRL 809
Db 1129 RGLAQKVIETISVASAEVDAELSPYKSVPSRLLTCORY-----FWERL 1176
Qy 810 KKAL 813
Db 1177 RYAI 1180

RESULT 5

tlr protein - fruit fly (Drosophila melanogaster)
T13887
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13887
R.Chang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A.Title: Expression of a novel Toll-like gene spans the parasegment boundary and contri
A.Reference number: Z17805; MUID:95151581; PMID:7848870
A.Accession: T13887
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1385 <CHI>
A.Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AA833383

F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #atctus atypical <LR
 F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.4%; Score 320.5; DB 1; Length 1133;

Best Local Similarity 22.0%; Pred. No. 3,9e-12; Mismatches 165; Conservative 111; Mismatches 236; Indels 237; Gaps 29;

42 QNLKIPHDIPYSTKNDLSFNPFLKIRSYFTNF-SQOMDLISRCETIEDKAMGL 100
 148 RHLOLRH-----LDGYNHITHICHSFRGLSDLSQTLILKENCISQMSHSFSL 199
 QY 101 NQSLTVLTGNPKSPSGF-SGLTNLENVAVETKMTSLGPHIGQLISLKLNVAN 159
 Db 200 LILETLDSGNLFEIDPVFVDGMPRLRLTLTNNILSEIPYDALGPKSLRTLDISHN 259
 QY 160 LIHSKLEBYF-----SNTLNLEHVDLSYNYIQTISVKQLFIRENPQVWLSLDSLNP 215
 Db 260 VYMSLSGNETYKIKASTKLNLDNLEVNHIEVLPPNSEKYP--DYVNRTP-FDGNPLH 315
 QY 216 STQAOAFOGIRLHELTNR-----SNFSSNVLKMCLOMGTGLVHRL----- 257
 Db 316 TUREDAFAPARIRELYMYKGLTNISPAVFDLSVLSQILDLSGNNTLKLH-HKLPNNPD 374
 QY 258 IL-----GEFKERNLESFDRSYMEGLCNVSIDEFRLTYINHSDDIYNLCANISA 310
 Db 375 VLKVISMDNKKIKQKPTETFN-AVHYTLKLKDLSDR-----NDPTNLQTLRMNR 425
 QY 311 M-SFGVAKHIAVD---PRHK-----WQSLSTRC-----HKPKPKSLPF 350
 Db 426 MNMMSLSLSRSGSSVGEDEKDFGVELEDQITRASLSGIQSHAFKVRGLKRLDF-- 483
 QY 351 LKSWTLTTRNEDISFGQL-----ALP-----SLRYLDSRRAMSPR 386
 Db 484 --SENGISISINDAHEIGHSLISLMSHGYSGLPAEPPLAHLTSLQELDSNNHISM 541
 QY 387 GCCSYSDF-----GT-----NNLKYLDLSPGVILMSAN----- 415
 Db 542 SPTSHPLKNLLELHONRIQVAKGTQGDHSLKEISLRFNHLTISQHTPEDLEA 601
 QY 416 -----PGLBELRYLDPOHSTLKKTVESVPLSEK----- 447
 Db 602 LRKLHLDNKKIDIERRAFNNLDELEYLSLRGNKINNLADES-FOVLPRLTETLDNAFNL 660
 QY 448 -----LY-----LDISYTNK 458
 Db 661 PNFNFDPQVGTLSNLNVNVSNOIRQLMYNSSGNEHGMHNSIKIILDSNNNS 720
 QY 459 IDPFGIFL-GLISLNTLKKMAKSPKONTLSNVFTNTNLTFLDLSKQLEQISRGVFDLT 517
 Db 721 IHPGFRFAEISLTHLHGYSIM-NTRDVFQGNPHIQWLDLSNWHHEIDPAFKMT 779
 QY 518 YRLQILNNSHNLFLDPESHYKQYSLRTLDCSPN-----RIETSKGL 561
 Db 780 KQLOLVFPGHNYLSIDIPODIFKPVQGLRIVDFSHNLRGLPDLNLYNGMEKLDVSHNM 839
 QY 562 QHPKPS-----LAVNLTNNSVACI 581
 Db 840 LKIPSSSLSSLAALTLCBLHLSNNFISTI 868

RESULT 7
 T15864
 hypothetical protein C56E.6 - Caenorhabditis elegans
 CSpecies: Caenorhabditis elegans
 CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 CAccession: T15864

R:Fullon, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C56E6.
 A:Reference number: 569019
 A:Accession: T15864
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1066 <FOL>
 A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
 C:Genetics:
 A:Gene: C56E.6
 A:Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 882/3; 9

Query Match 7.0%; Score 303; DB 2; Length 1066;

Best Local Similarity 22.8%; Pred. No. 6.6e-11; Mismatches 145; Conservative 110; Mismatches 260; Indels 120; Gaps 23;

34 NITVOCQNLKIPHDIPYSTKNDLSFNPFLKIRSYFTNFSGQLWDLISRCETIE 93
 Db 131 NITH-IMDTNEVTESEMKVILRN-----NKVRLDKHSFSGFKIRLIDISYNOITVE 184
 QY 94 DKAMHGLNQSLTVLTGNPKSPSGSGLTNLENVAVETKMTSLGPHIGQLISLKL 153
 Db 185 DSSEFTVGHMOSLDSYRIAYLRGM-----LKNPAK-----TLKT 221
 QY 154 LNVANHLHSFKLPEYFENLTNLEHVDLSYNYIQTISVKQLFIRENPQVWLSLDSLNP 213
 Db 222 LKLAENMHA--TPPALDLNRLTHLNLNGKLNRI--DGDVLKGTDTLVELFLANNY 276
 QY 214 IDSIOAQPQGR-LHEHTLSNFSNVKLCLOMGT-----HYRLL--GE 261
 Db 277 LEHIFPGVLSGKQLEHNDISK-----KIMSLKPPSLISTKEETSTYARMLIAGNR 330
 QY 262 FKNERNLESFDRSYMEGLCNVSIDEFRLTYINHSDDIYNLCANISAMSPGVAKH 321
 Db 331 INNSDYILFEMFLTYVDVSFNRIETSRVEX-----LKNLSLPLQNNQLAHF 383
 QY 322 ADVPRHFKWQSLSTRCHLKEPKKLS--LPFLKSWTLTTRNEDI-----SFGQLALPSIR 374
 Db 384 PSLPRLDLKRLHMLDNNOIQKIDNFSIADLPQLQHLSLAGNQLDITTEMFGSSSSSELK 443
 QY 375 YLDSRRNMSFRGCCSYSDFGTNNILKYLDSPGV-ILMSANFGLBELRYLDPOHSTLK 433
 Db 444 SLNLANKHHSISRSFSDL--DNLQQLRLSHNNRITTSFTSMRLMYRLIDLSHNRIT 501
 QY 434 KYTERSVF-LSLEKLYLDISYTNKIDPFGIFLGLISLNTLKKMAKSPK----- 482
 Db 502 KILPSALYQLPALDVLHLDHNNLN-EIDRDA-FRSFSDLOSLKLSHNAFRSPCEPLGSI 559
 QY 483 -----DNTLS--NVFTVTTNLTFLDLSKQLEQISRGVFDLTLYRLQILNNSHNL 531
 Db 560 SQVHOLDSSNQINIDIFCLARGIRKSLASNSVEKINRKLQDQATBELTISIDSHNGII 619
 QY 532 FLDPESHYKQYSLRTLDCSPFRKETSIGILOHFPKSLAVFNLTNNNSVACICEYONFLOW 591
 Db 620 DVDSAPCECRKLSHIKSHYIR-----MLMKGTAVCI-----PWI 656
 QY 592 KDQKMFV-----NVQOMKASPIDMKASIVLDFTN 622
 Db 657 SHLTTFCEFTKEHLERTISFSYIIVDSQSLTSFEN 691

RESULT 8
 JG6128
 insulin-like growth factor binding complex acid labile chain - mouse
 CSpecies: Mus musculus (house mouse)
 CDate: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 CAccession: JG6128
 R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
 Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
 A>Title: Organization and chromosomal localization of the gene encoding the mouse acid I
 A:Reference number: JG6128; MUID:96413591; PMID:8816745
 A:Accession: JG6128

A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; GB:U66900; NID:91621612; PID:AA17270.1; PID:916216
C:Comment: This protein is a serum protein and it is of the ternary complex in the phys
C:Genetics:
A:Gene: als
A:Map position: 17

Query Match 7.0%; Score 301.5; DB 2; Length 603;
Best Local Similarity 24.9%; Pred. No. 3.8e-11;
Matches 160; Conservative 87; Mismatches 240; Indels 155; Gaps 25;

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QY 39 CMDQNLSTKIPHDIPYSTKNDLSFNPPLKILRSYSTNSQQLMDLDSCELETIEDKXMH 98
DB 60 CSSRNLTPDPGIPVSTALMDGNLSSIPSAFQNLSSIDPFLMDQSGWLRSPQALL 119
QY 99 GLNQLSTVLTLGNPDKSPSGFSGLTNLENVAVETMTSLBGFHIGQLSLKKNLVAAH 158
DB 120 GLENLCHLHRLNRLSLAAGLFRTPPSLASISLGNLIGRLBGLFPGLSHMDNLGW 179
QY 159 NLHSFKLPE-YPSNLTNLEHVDLSYN--YIQITSVKDLQFLRENPQVNLSDLSNPI 214
DB 180 NSL--VVLPTVFGQGLNHLVLAGNKLTYLQPLALGGLGLRE-----LDLSRYAL 230
QY 215 DSIQAQAQGI-RHLELTLSNPNSSNVLMKCLQMTGVAHRLILGEPKNERNLSEFDR 273
DB 231 RSVKANVPHLPRLQKLYL-----RNLTVAVAPRAVLG-----264
QY 274 SVMELGNVSIDEFRLTYINHFSDIYNLNCIANISAMSF--TGVHKKIAD-----V 324
DB 265 --MKAL-----RMLDSH-----NRVAGLEETFPGLGLAHVRLAHNAITSLR 306
QY 325 PRHFQKQSLIIRCHLKPPLKSLPFLKSWTLTTNREDISFGQL-----ALPSLRVLDL 378
DB 307 PRTEK-----DLHFLELQGHNR-----IRQGEKTFEGGLQGLVLT 345
QY 379 SRNMSFRGCCSYSPFTNNLKYLDLSPNGVILMSAN-FMGLBELLEYDPQSHTKKYTE 437
DB 346 NDNOHEVKGAFF-FGLFNVAVMNLSGNCLRSLEHFGGIGRLSHLHESLGLRRL 403
QY 438 FSVFLSEKLYLDISYNTKIDFGDIFLAGLSLNTLMAGNSFKDNTLSNV---FTNT 493
DB 404 HT-----FAGLSGLRLTL-----RDNSSISIEBQSLAGL 433
QY 494 TNLFLDLISKQLEQISRGVFDLYRQLQLMNSHNNLLFLDPSHYKQYLSRTLDSPNR 553
DB 434 SELLELDLTANQLFTLPRQLFGQLGQLELYLLSNQLTMSBDVGLQRAFMWLDLSNR 493
QY 554 IET-SKGLQHPKSLAVFNLTNSVACISYQNFQWQKQKFLVNEQMKCASPIDM 612
DB 494 LETPAEGLFSSLGR-LRYLNLRRNSL-----QTFVPPQGLERLWL-DANPMDSCPLKA 545
QY 613 KASLVLD-----FTNSTC-----YIKTIISVSVS 639
DB 546 LRDPALQNPVPRFVQIVCEGDDCQPYVTYNNITCAGPANY 587
```

RESULT 9
JC5239
Insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: JC5239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 6.9%; Score 300.5; DB 2; Length 605;
Best Local Similarity 23.9%; Pred. No. 4.4e-11;
Matches 155; Conservative 81; Mismatches 238; Indels 175; Gaps 20;

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QY 39 CMDQNLSTKIPHDIPYSTKNDLSFNPPLKILRSYSTNSQQLMDLDSCELETIEDKXMH 98
DB 60 CSSRNLTPDPGIPVSTALMDGNLSSIPSAFQNLSSIDPFLMDQSGWLRSPQALL 119
QY 99 GLNQLSTVLTLGNPDKSPSGFSGLTNLENVAVETMTSLBGFHIGQLSLKKNLVAAH 158
DB 120 GLENLCHLHRLNRLSLAAGLFRTPPSLASISLGNLIGRLBGLFPGLSHMDNLGW 179
QY 159 NLHSFKLPE-YPSNLTNLEHVDLSYN--YIQITSVKDLQFLRENPQVNLSDLSNPI 214
DB 180 NSL--AVLPDAAFRGLGGLRELVLAGRLAVLQPLPSGLALELRE-----LDLSRYAL 230
QY 215 DSIQAQAQGI-RHLELTLSNPNSSNVLMKCLQMTGVAHRLILGEPKNERNLSEFDR 273
DB 231 RAIKAVFAQLPRLQKLYL-----DRNL-----253
QY 274 SVMELGNVSIDEFRLTYINHFSDIYNLNCIANISAMSFQVHKKIADVPRHFKQSL 333
DB 254 -----IAAVAQAPLGL-----KALRWLDL 273
QY 334 SIIRCHLKPPLKSLPFLKSWTLTTNR-----EDISFGQLALPSLRVLDLSRNMSFRGC 388
DB 274 S-----HNRVAGLEETFPGLL-----GLRVLRISHNAIASLRP 307
QY 389 CSYSPFTNNLKYLDLSPNGVILMSANFMGLBELLEYDPQSHTKKYTEVSFLSEKL 447
DB 308 RTFEDL--HFLELTQGLHNRRLQLAERSFEGGLQGLVLTLDHNLQEV-KVGAFLGLTNV 364
QY 448 LYLDISYNTKIDFGDIFLAGLSLNTLMAGNS-----FNDNTLSN 488
DB 365 AVNMLSGNCLRNLPDQVFRGGLKSHLHESGCLGRIRPHTFAGLSGLRRLFLKDNGLVG 424
QY 489 V-----FTNTTNLFTLDISKQLEQISRGVFDLYRQLQLMNSHNNLLFLDPSHYKQYLS 544
DB 425 IEBQSLWGLAELELDLTSTNQLFTLPHQLFGQLKLEYLLSHRLAELEPDALGPIQRA 484
QY 545 RTLDSPNRIRTSKGLQHPKSLAVFNLTNSVACISYQNFQ--WVDQKMFVNV 602
DB 485 FMDVSHNRLEALPGLSLASLGRRLYLNLRNSLRTFTPOPGLERLMBG-----N 536
QY 603 QMKCASPID-----MKASLVLDFTNSTC-----YIKTIISVS 635
DB 537 PWDSCPLKALRDPALQNPASVPRFQAICBGDDCQPYVTYNNITCAS 585
```

RESULT 10
JC1282

Insulin-like growth factor-binding protein acid labile chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1282

R:Del, J.; Baxter, R.C.

Biochem. Biophys. Res. Commun. 188, 304-309, 1992

A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac

A:Accession: JC1282

A:Molecule type: mRNA

A:Residues: 1-603 <DAI>

A:Cross-references: UNIPROT:P35859; GB:S46785; NID:9258002; PID:AA23770.2; PID:9570593

A:Experimental source: liver

A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status I

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.7%; Score 290.5; DB 2; Length 603;
Best Local Similarity 22.4%; Pred. No. 1.8e-10;
Matches 152; Conservative 99; Mismatches 204; Indels 223; Gaps 26;

QY 39 CMDONLSKIPHDIPYSTKULDISFNPPLKILRSYFTNFSQOLMDLSRCEIETIEDKAMH 98
 Db 60 CSSKULTHLPDIPVSTRALMDGNLSSIPSAQONSSLDLFINLQSGWLSLEPQALL 119
 QY 99 GINQSTVLTVGNPKSPSPGSPS----- 122
 Db 120 GLONLVYHLEERNRLNLAVALGFTHTPSLASLSLSSNLLGRLEBGLFQGLSHLMDLNGW 179
 QY 123 -----GLTNLENLVAVERKMTSLBGFHIGQLSLKKLVANHLHSFKLPEYF 170
 Db 180 NSLVLPDTPVFOGLQNLHLEVLQAGNKLTYLPALFCGLSELBLELDSRNALSVK-ANVF 238
 QY 171 SNLTNLEHVDLSYNYIQTIS-----VKDLOFLRENPNVNLSDLSLNFIDSIQAOAFQ 224
 Db 239 VHLPLQKLYLDRNLITANAPGAFGLMKLRW-----LDLSHNNVAGLMEDTFFG 288
 QY 225 -IRHLETLRSNFSNSNVLKMCLOQNTGHL-VHRLIGEFK---NERNLESFDRSVMEG 278
 Db 289 ILGLHVLRLAHN---AIASLRPRFKDLHFLLEQLGHNRIRQLGEFTFEGIGOLEVLT 344
 QY 279 LCNVSLDEPRL-TYINHEPDDIYNL--NCLANISMSFTGVHKKHIAADVPRHFKQSLI 335
 Db 345 LINDNQTTEVRVGAFGSLFVAVANNLSGNCRLPERVFOGLDKLH---SLHESCLGH 400
 QY 336 IRCHLKPFPKLS---LPFLKSWTLTTNREDISFGQALPSLYLIDLSRNAMS-----FR 386
 Db 401 VRLH--TFAGLSGLRLFLRDSISSIEQSLAG---LSBLELDITTRLTLPRQLP 455
 QY 387 GCCSYSDFGTNNLKYLDSFNGVILMSANFMGLEBLEYLDPOHSTLKKVTFESVFLSEK 446
 Db 456 -----GLGHLEVLLSYNQLTTLAEVLG-----PLOR 483
 QY 447 LLYLDISTYNTKIDPGCIFGLISLNTLKMAGNSFKDNTLSNVFTTNLTFLDLSKOL 506
 Db 484 AFWLIDISHNH-----L 494
 QY 507 EOLSRGVPTLYRLQLLNMSHNL-----LFLDPHYKQLYSLRTLDCSFNRIB 555
 Db 495 ETLAELFSSLSGLKVRILSLRNNSLOTFSPQGLERMLDANPW-----DCS----- 540
 QY 556 TSKGILQHPK-KSLAVENLTNNSVACICEYONFLQWVKD---QKMFVNVEQMKCASPI 610
 Db 541 -----CPLKALRDFALONPGVV-----PRFVQYVCBGDDQCPVYTVN--NITCAGRA 585
 QY 611 DMKASLVLDFTNSTCTIY 628
 Db 586 NV-SGLDLRDVSETHFVH 602

RESULT 11

T10504
 disease resistance protein Cf-2.1 - current tomato
 C/Species: Lycopersicon pimpinellifolium (current tomato)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T10504; T10515
 R/Titan, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
 Cell 84, 451-459, 1996
 A/Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
 A/Reference number: Z17062; MUID:96190812; PMID:8608599
 A/Accession: T10504
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1112 <DI>
 A/References: UNIPROT:Q41397; EMBL:U42444; NID:G1184074; PIDN:AACT5779.1; PID:G118
 A/Experimental source: cultivar Cf 2
 A/Accession: T10515
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1066, 'I', 1068-1085, 'E', 1087-1110, 'R', 1112 <DI>
 A/References: EMBL:U42445; NID:G1184076; PIDN:AACT5780.1; PID:G1184077
 A/Experimental source: cultivar Cf 2

Query Match

6.6%; Score 287.5; DB 2; Length 1112;

Best Local Similarity 23.5%, Pred. No. 6.4e-10;
 Matches 158; Conservative 93; Mismatches 243; Indels 179; Gaps 26;
 QY 23 GSNPCIVLPNIT--YQCMDONLSKIPHDIPY--STKULDISFNPPLKILRSYFTNFSQ 78
 Db 337 GSIPASLGNLNLSTLYLYNNQSSIPBEIGYLSLTYLDDSNNSINGFIASFGNMS 456
 QY 79 LQWLDLSRCEIETIEDKAMHGINQSTVLTVGNPKSPSPGSGULTNLENVAVETKMT 138
 Db 457 LAFLELYENQASSVPEEIGYLRSLNVLDSERNALNGSIPASFGNINLSRLNLVNNQSS 516
 QY 139 SLEGFHIGQLISKLQNLVNLHLSFKLPEVSNLTNLEHVDLSYNYIQTISVKLOFLR 198
 Db 517 GSIPBEIGYLRSLNVLDSERNALNG-SIPASFGNINLSRLNLVNNQSSIPBEIGYLR 575
 QY 199 ENPOVNL-----LDLSNPI 214
 Db 576 SLNDLGLSEBNALNGSIPASLGNLNLSTLYLYNNQSSIPBEIGYLSLTYLSSGNNSL 635
 QY 215 DSIOQAQAFQIR-LHELTFRS-----NFSNNVLM-----CLQNT 250
 Db 636 NGLIPASFGNINLQALLNDNNLIGELPSVVCNLTSLEVLYMPRNLLKGVPCIGNIS 695
 QY 251 GLAVERLLIGERKX-----RLES-----PDSVMEGL---C-NVSLDERLTYYNHF 295
 Db 636 NLOVLSMSNSPSGELPSGISNLTSLQILDFFGRNLEGAIPQCFGNISLSEVFMQNNPL 755
 QY 296 SDDI---VNLCLANISMSFTGVHKKHIAADVPRH---KQSSIIIRCHLK-PPPKL- 346
 Db 756 SGTLPNNSIGC--SLISNLHGNLELD--ELPRSLDNCKLQVLDLGNQNDPFWML 811
 QY 347 -SLPFLKSWTLTTNRED---ISFGQALPSLYLIDLSRNAMSFGCCSYSPGNTNKKY 401
 Db 812 GTLPBLRYLRSLNKLHGRIRSSRAIIMPDLRIIDLNRNAPS-----QDLPSLTFH 864
 QY 402 LPLSFNGVILMSANFMGLEBLEYLDPOHSTLKKVTFESVFLSEKLYLDISTYNTKIDP 461
 Db 865 L-----KQMTVDKT---MEPSYESYDDSVVAVTK----- 893
 QY 462 DGIFGLISLNTLKMAGNSFKDNTLSNVFTTNLTFLDLSKQLEQISRGVDTLYRLQ 521
 Db 894 -GLEIETVILSL-----YVIDLSNKKFEGHLPVYGLDLAIR 931
 QY 522 LTNMSHNLFLDPHYKQLYSLRTLDCSFNRILETSKILQHPKSLA-----VENLTN 575
 Db 932 IANVSHMLQGYIPSSLSLISLSDLSFNQLS-----GEIPQGLASITFLFPLNLSH 985
 QY 576 NSV-ACTICEYONF 587
 Db 986 NYLQGCIPQGPQF 998

RESULT 12

T11374
 gp150 protein - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C/Accession: T11374
 R/Titan, S.S.; Zinn, K.
 J. Biol. Chem. 269, 28478-28486, 1994
 A/Title: An adhesion molecule-like protein that interacts with and is a substrate for
 A/Reference number: Z17630; MUID:95050638; PMID:7961789
 A/Accession: T11374
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1051 <TIA>
 A/References: UNIPROT:Q24007; EMBL:U15220; NID:G595859; PID:G595860; PIDN:AAA617
 A/Experimental source: strain Oregon R
 C/Genetics:
 A/Cross-references: FlyBase:FBgn0013272
 A/Map position: 2

Query Match

6.6%; Score 285.5; DB 2; Length 1051;

Best Local Similarity 24.0%; Pred. No. 7.9e-10;
Matches 155; Conservative 114; Mismatches 211; Indels 167; Gaps 34;

QY 82 LDRSCEIETIEDKAMGMLNOLSTLVITGMPISFGSGSGLTNENLVAVETKMTSLE 141
D 297 IKRANCTLEVLAAAFGLNELVAVNLTDGLAIINDPTFVGKKKRLMLTISNDLSVMS 356
QY 142 GFH-IGQLISLKLAVANHLHSPKPEYPSNLTNLEHVDLSYNYIQTTSVKOLQPLREN 200
D 357 SIHYLKSSSIEELDPSRRNNLMELN-PKAFSHLSNVVYIINLSQNSKKKPEKAFE----- 410
QY 201 PQVNL-SLDSLNPIDSIQAQAFQGRIRHELTLSN-----FNSNVTKKCLQMTMG 251
D 411 -KVTLLEEDLSYNSLTLEPDIPIFNGTTLSLHLKNTNRGDLHFGTKLOQDUSFNSI 469
QY 252 LHVHRLIIGFKNERNLESPDRSVMEGLQVST-----DEFRLTYINHFSDDIYN 301
D 470 VQVNH-----SWFDK-MPGLTNLMKNGIKKIQPDSP-LTLKRLRHIDL-S 513
QY 302 INCLANISAMFTGVHKKIADVPKFKQSLSIRCHLKPPKLS-LP---FLKSWTLT 357
D 514 INDLQISGMLF-----FKNSELDVAR-LMDNPRLSOLPTDGF-L-SYS-- 554
QY 358 TNREDISFGQALPELRVLDLSRNAMSPFGCCSYSDPFGT-NNLKXVLDLSPNGVILMSANF 416
D 555 -----GEF--TVVYLDISNCAI---GPIGHKAFSTMRHLTKLAMNT-----NH 595
QY 417 MGLEELEYLDPOHSTLKKVTERSVLSLEKLYLDISTY-NTKIDPDIPLGLISANTLK 475
D 596 LPRE-----IFPTGHLKLIIDLISNNLITRMD-DLIFDNDNELTGLS 635
QY 476 MAGNSFKDNTLS-NVFTNTNLTPLDLSKQLEQISKRVPTLVRLQLANSHNNLLFLD 534
D 636 LAGNPI--SRLSVAVLPLRLHQLRCLDVADECETTL-----LSDDDL----- 674
QY 535 PSNKKOYLSRTLDSCSNRI-ETSKGILQHPKSLAVENLTNNSVACICEQNOLQWVKD 593
D 675 GAGYKIDPSLRSPNASNLIKKISSBDVKSF-KYLRSLDITNNPLKCTPPDQETISY--- 730
QY 594 OKMFLVNEQMKKASPIDMKASLYLDFTNSTCYIKTISVSVSVLVAVTVAFLIYHFY 653
D 731 -----VTLQOMTPPKRLPYLANLEDAT-----IYQLETLAQAGSSSL 768
QY 654 FHLILAGCKKYSRGESIVDAFYIYSSQNEQWVRELKRLSEGVPR 700
D 769 AHEV-----CKHAEGSLD-----EKKADSAEAKLEKRLKESVYK 804

Db 769 AHEV-----CKHAEGSLD-----EKKADSAEAKLEKRLKESVYK 804

RESULT 13

A41915

Insulin-like growth factor-binding complex acid-labile chain precursor - human

N:Alternate names: Acid-labile Subunit (ALS)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A41915

R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A:Title: Structure and functional expression of the acid-labile subunit of the insulin-1

A:Reference number: A41915; MUID:92357025; PMID:1379671

A:Accession: A41915

A:Status: Preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-605 <LEO>

A:Cross-references: UNIPROT:P35658; GB:M86826; NID:9184807; PIDN:AAA36047.1; PID:9184806

A:Note: sequence extracted from NCBI backbone (NCBI:P110171)

F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>

F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match

Best Local Similarity 6.5%; Score 281.5; DB 2; Length 605;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;

QY 39 CMDQNLSTKIPDIPSTKNLDSFVPLKILASYSSTNSQLOWLDLSRCEIETEDKAMH 98
D 60 CSSRNLTLDPGVREGTQALWLDGNNLSVPPAFQONLSIGFINTLQGGQSGISLEPQALL 119
QY 99 GLNDLSTLVITGNPIKSPSPSGFGLTNYLVAVETKMTSEGFHIGQLISLKLAVANH 158
D 120 GLENLCHLHERNQLRSLAGTFAHTPALASGLSNRSLSLDEGLGELGSLMDLNGW 179
QY 159 NLHSFKLPE-YESNLTNLEHVDISYN---YIQTTSVKDLOFLRENQVNLDSLNP 214
D 180 NSL--AVLPAAAFGLSLSRELVLAGNRLAVLQALPSGLAELE-----LDSLNAL 230
QY 215 DSIQAQAF-QGIRHELTLSNTRNSNVVLKCLQMTGHLVHRLIIGFKNERNLESPDR 273
D 231 RAIKANVFDVLPRLQKYL-----DNL----- 253
QY 274 SVMEGLQVNSIDFRLTYINHFSDDIYNLCLANISAMFTGVHKKIADVPKFKQS 333
D 254 -----IAVAPGAFGL-----FALRWLDL 273
QY 334 SIIRCHLKPPKLSLPLKSWTLTNR-----EDISFGQALPELRVLDLSRNAMSPFGC 368
D 274 S-----HNRVAGLEDTPGGL--GLAVLNSHNAISLSP 307
QY 389 CSYSPFGTNLKYLDLSPFNGV--ILMSANFMELELEYLDPOHSTLKKVTERSVLSLEK 447
D 308 RFPKDL--HFLBELQGHNRIRQLAERSFEGQLEVLTLDHNOQEV-KAGAFGLGLTNY 364
QY 448 LYLDISTYNTKIDPDIPLGLISLNTLKAGNS-----FKONTLSN 488
D 365 AVMNLSGNCLRNLPGVFRGLKHSLSHESGLRIRPHPTTGSLGRRLFLKONGLVG 424
QY 489 V-----FTYTNLTPLDLSKQLEQISKRVFTLVRLQLANSHNNLLFLDPSHYQQLYS 544
D 425 IEEQSLGWLAELELDLTSNQLTLPHRLPQGLTGLVLLSRNLALPADALGPLORA 484
QY 545 RTDSCFRIETSKGILQHPKSLAVENLTNNSVACICEYQNFLO--WKQOKMFLVAV 602
D 465 FWLDVSHRLEAPNSGLAPLGRRLYSLRNNSRTPTPPGGERLWLEG-----N 536
QY 603 QMKKASPID-----MKASLYLDFTNSTC-----YIKTIISSVSVYL 640
D 537 FWDGCGPLKALRDPAQNPSAVPRFVQALCEGDCCQCPAYTYNNITCASPEV 590

Db 537 FWDGCGPLKALRDPAQNPSAVPRFVQALCEGDCCQCPAYTYNNITCASPEV 590

RESULT 14

B3665

alt protein 2 precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C:Accession: B3665

R:Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

Genes Dev. 4, 2169-2187, 1990

A:Title: alt: an extracellular protein necessary for development of midline glia and con

A:Reference number: A3665; MUID:91099665; PMID:2176636

A:Accession: B3665

F:115-1148/Domain: EGF homology <EGF1>

Query Match

Best Local Similarity 6.4%; Score 279; DB 2; Length 1480;
Matches 151; Conservative 85; Mismatches 238; Indels 224; Gaps 21;

```

QY 39 CMDQNLGKIPHDIDYSTKNDLDFNPLKILRSYSFTNSQLQWLDLRCETIETEDKAMH 98
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 308 CREKSLTSVPVTLPPDDTVDVRLBNFTTELPPKSFSSFRRLRIDLSNNNISRIADALS 367
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 99 GLNQLSTLVLTGNPDISFSPGSGSLTNLENLVAETKMTSLGEGHIGQLISLKVAVAH 158
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 368 GLKQLITLVLYGKNIKDLPSGVFKGLSLRLLLNANEISCIRKDAFRDLHSLSLSLYD 427
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 159 NLHSGFKLPEYFESNLTNLEHVDLSYNYIQIISVKDIQFLRENPQVNLSDLSNPIDSIG 218
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 428 NNIOSL-ANGTFDAKMSKMTVHLAKN-PFICDCLRWLADY-----LKNPLETSG 476
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 219 AQAFQGIHLHETLNS---NPNSSNVLMKCLQNNMTGLVHRLILGEFNERNLESFDRS 274
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 477 ARCESPKKWHRRRISLREEKFKS-----WGEL-----RM 507
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 275 VMEGLCNVSIDEFRLTYINHSDDIYNINCLANISAMSGFTGVHKKI-ADVPKPKWQSL 333
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 508 KLSGECRMDSD-----CPAMCHCEGTVDCTGRILKEIIPDIPLH----- 547
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 334 SIIRCHLKPPPKSLPFLKSWTLTNREDIS-----FQGLAPSLRYLDLSRNAMSPR 386
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 548 -----TELLLNDENLGRISSDGLFGR-LPHLVKLELKNQULT-- 584
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 387 GCCSYSDFGTNNLKYLDLSPNGVILMSAN-FMGLLELEYLDPOHSTLKKVTEFSVFLSLE 445
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 585 -----GI---EPNAFEGASHIQBLQGENKIKEISN-KMFLGLH 619
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 446 KLLYLDISYNTKIDPDGIFLGILSLNTLKMGNSF----- 481
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 620 QLKTINLYDNQISCVPGSFEHLNLSLTSLNLSNPENCNCHLAWFAECVRKKSILNGAAR 679
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 482 -----KD----- 489
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 680 CGAPSKVDVOIKDLPHSEFKCSSENSGCLGDGYCPSPCTCTGTVAACSRNQLKEIPRG 739
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 490 -----FTNTNLTFLDLSCQLBOISRGVFDLYRLQLNMSH 527
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 740 IPATSELYESNEIEQIHYERIRHRLSLTDLSSNQITILSNYTFANLTKLSTLISY 799
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 528 NNLLFLDPSSHVKQLYSRTIDCSFNRIE-TSGGILQHFPKSLAVFNLTNNSVACICEYQN 586
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 800 NKLQCLQRIHALSGLNLRVSLHGNRISMLPEGSEFDL-KSLTHIALGSNPLYCDGGLKW 858
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 587 FLQWYDQKRMFLVNVQMKCASPIDMKASLYLDFTNST 624
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 859 FSDWI---KLDYVEPGIARCAEPQMKDILISTPSS 893
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Search completed: March 12, 2005, 19:57:06
Job time : 27.5445 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds

(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-98

Perfect score: 4355

Sequence: 1 MMSASRLAGTILPMAFLISC.....SNDEGTGVCNNQEAITSI 839

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*
2: geneseqp1980s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4355	100.0	839	ABU04773	ABU04773 Human exp
2	4355	100.0	839	ABU04774	ABU04774 Human exp
3	4355	100.0	839	ABU04775	ABU04775 Human exp
4	4355	100.0	839	ADC78785	ADC78785 Human PRO
5	4355	100.0	839	ADD48826	ADD48826 Human PRO
6	4335.5	99.6	837	AAW86361	AAW86361 Human DNA
7	4335.5	99.6	837	AAE16102	AAE16102 Human DNA
8	4335.5	99.6	837	ABU04776	ABU04776 Human exp
9	4328.5	99.4	837	AAE16116	AAE16116 Human DNA
10	4178	95.9	808	ADOS57782	ADOS57782 Chimpanze
11	4167	95.7	808	ADOS57785	ADOS57785 Gorilla t
12	4164	95.6	808	ADOS57803	ADOS57803 Chimpanze
13	4141	95.1	799	AAW86352	AAW86352 Human DNA
14	4141	95.1	799	AAE16093	AAE16093 Human DNA
15	4141	95.1	799	ABE83162	ABE83162 Human Tol
16	4141	95.1	799	ABR42963	ABR42963 Human Tol
17	4141	95.1	799	ADB39121	ADB39121 Human Tol
18	4141	95.1	799	ADP56656	ADP56656 Human Tol
19	4141	95.1	799	ADP48597	ADP48597 Human Tol
20	4040	92.8	801	ADOS57788	ADOS57788 Gibbon to
21	3918	90.0	795	ADOS57791	ADOS57791 Rhesus mo
22	3892	89.4	795	ADOS57800	ADOS57800 Hamadryas
23	3819	87.7	801	ADOS57797	ADOS57797 Squirrel
24	3683.5	84.6	738	ADP29455	ADP29455 Human sec
25	3501	80.4	745	ADOS57794	ADOS57794 White-fac

26	1090	25.0	208	3	AAV88059	AAV88059 Human Tol
27	919	21.1	178	8	ADN12270	ADN12270 IL-IR/TLR
28	785	18.0	179	7	ADC42707	ADC42707 Murine To
29	629.5	14.5	661	2	AAW28510	AAW28510 Product o
30	629.5	14.5	661	2	AAW87556	AAW87556 B cell su
31	629.5	14.5	661	7	ADC36552	ADC36552 Human sec
32	629.5	14.5	661	7	ADP69098	ADP69098 Human MP5
33	628.5	14.4	650	3	AAV82527	AAV82527 Human RPI
34	615.5	14.1	661	2	AAW47274	AAW47274 Human B-C
35	603.5	13.9	784	2	AAW86350	AAW86350 Human DNA
36	603.5	13.9	784	5	AAE16091	AAE16091 Human DNA
37	603.5	13.9	784	5	ABE83161	ABE83161 Human Tol
38	603.5	13.9	784	8	ADN02005	ADN02005 Human inf
39	602.5	13.8	784	2	AAV05869	AAV05869 Human Tol
40	602.5	13.8	784	6	ABU61956	ABU61956 Human Tol
41	602.5	13.8	784	7	ADL15005	ADL15005 Human Tol
42	602.5	13.8	784	8	ADP56652	ADP56652 Human Tol
43	602.5	13.8	784	8	ADP48593	ADP48593 Human Tol
44	602.5	13.8	784	8	ADP23787	ADP23787 PRO Polyp
45	602.5	13.8	784	8	ADQ39727	ADQ39727 Human myo

ALIGNMENTS

RESULT 1
ABU04773
ID ABU04773 standard; protein; 839 AA.

XX AC ABU04773;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1439.

mammal an immunogenic response directed against any of the purified CC polypeptide. The purified polypeptide, or the antibody that binds to this CC polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed CC class I or class II MHC-binding polypeptide. The polypeptides and CC polynucleotides are particularly useful for treating or preventing CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, CC lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational CC profiling. Note: This sequence does not appear in the printed CC specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MMSASRLAGTLIPAMAFISCVRPSWPCVAVVNNITTCQMEINFYKIPDNLPSTKND 60
1 MMSASRLAGTLIPAMAFISCVRPSWPCVAVVNNITTCQMEINFYKIPDNLPSTKND 60
1 LSFNPLRHLSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSTLLTGNPISIALG 120
61 LSFNPLRHLSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSTLLTGNPISIALG 120
61 LSFNPLRHLSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSTLLTGNPISIALG 120
121 AFGSLSLQKLVAVETNLASLENPPIGHILKTLKLANANHLIOGFKIPYPSNLTNLEHL 180
121 AFGSLSLQKLVAVETNLASLENPPIGHILKTLKLANANHLIOGFKIPYPSNLTNLEHL 180
121 AFGSLSLQKLVAVETNLASLENPPIGHILKTLKLANANHLIOGFKIPYPSNLTNLEHL 180
181 DLSNKLQSIYCTDRLVHQWPLNLTSLDLSINPMNFIOGAFKIRLHKLTLLNNPDSL 240
181 DLSNKLQSIYCTDRLVHQWPLNLTSLDLSINPMNFIOGAFKIRLHKLTLLNNPDSL 240
181 DLSNKLQSIYCTDRLVHQWPLNLTSLDLSINPMNFIOGAFKIRLHKLTLLNNPDSL 240
241 NNMKTCTIOGLAGLEVHRLVIGEFNENLEKPKSALLEGICNLTIEEPRLAYDYDDI 300
241 NNMKTCTIOGLAGLEVHRLVIGEFNENLEKPKSALLEGICNLTIEEPRLAYDYDDI 300
241 NNMKTCTIOGLAGLEVHRLVIGEFNENLEKPKSALLEGICNLTIEEPRLAYDYDDI 300
301 IDLFNCLTNVSSPELVVTLERVKDPFVYNGWQHLVNCQFQGPPLTKLSRLNPTS 360
301 IDLFNCLTNVSSPELVVTLERVKDPFVYNGWQHLVNCQFQGPPLTKLSRLNPTS 360
301 IDLFNCLTNVSSPELVVTLERVKDPFVYNGWQHLVNCQFQGPPLTKLSRLNPTS 360
361 NKGNASEVDLPSELEFLDSRNGLSFGKCCSQSDFGTTSKLYDLSFNGVITMSSNPLG 420
361 NKGNASEVDLPSELEFLDSRNGLSFGKCCSQSDFGTTSKLYDLSFNGVITMSSNPLG 420
361 NKGNASEVDLPSELEFLDSRNGLSFGKCCSQSDFGTTSKLYDLSFNGVITMSSNPLG 420
421 LEQLEHLDPQHSNKKOMSEFVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKMG 480
421 LEQLEHLDPQHSNKKOMSEFVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKMG 480
421 LEQLEHLDPQHSNKKOMSEFVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKMG 480
481 NSFPENLPDIFTELRNLTFDLISQCCLEQSLSPAFNSLSLOYLNNSHNPFSDTPPY 540
481 NSFPENLPDIFTELRNLTFDLISQCCLEQSLSPAFNSLSLOYLNNSHNPFSDTPPY 540
481 NSFPENLPDIFTELRNLTFDLISQCCLEQSLSPAFNSLSLOYLNNSHNPFSDTPPY 540
541 KCLNSLOYLDSLNIHIMTSKKOELOHFPSSLAFLNTQNDPACCEHOSFLOMKDROL 600
541 KCLNSLOYLDSLNIHIMTSKKOELOHFPSSLAFLNTQNDPACCEHOSFLOMKDROL 600
541 KCLNSLOYLDSLNIHIMTSKKOELOHFPSSLAFLNTQNDPACCEHOSFLOMKDROL 600
601 LVEVERMECATPSDKQMPVLISNITCQMNKTIIGVSVLSLVVSVVAVLVKPFHML 660
601 LVEVERMECATPSDKQMPVLISNITCQMNKTIIGVSVLSLVVSVVAVLVKPFHML 660
601 LVEVERMECATPSDKQMPVLISNITCQMNKTIIGVSVLSLVVSVVAVLVKPFHML 660
661 LAGCIKYGRENITDAFYSSQDBDWARNELVKNLEGVPPDCLAHYRPIGVAA 720
661 LAGCIKYGRENITDAFYSSQDBDWARNELVKNLEGVPPDCLAHYRPIGVAA 720
661 LAGCIKYGRENITDAFYSSQDBDWARNELVKNLEGVPPDCLAHYRPIGVAA 720
721 NIIEGFHKSRLVIVVSOHFIOSRWCIFFEYIAQTQFSLSSRAIGIIVLVQKYEKTLR 780
721 NIIEGFHKSRLVIVVSOHFIOSRWCIFFEYIAQTQFSLSSRAIGIIVLVQKYEKTLR 780
721 NIIEGFHKSRLVIVVSOHFIOSRWCIFFEYIAQTQFSLSSRAIGIIVLVQKYEKTLR 780
781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGTVGTGNCWQBATSI 839

781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGTVGTGNCWQBATSI 839

RESULT 2
ID ABU04774 standard; protein; 839 AA.
ABU04774;
29-JAN-2003 (first entry)
Human expressed protein tag (EPT) #1440.
Translational profiling; expressed protein tag; EPT; kinases; phosphatase;
protease; protease inhibitor; transporter; cytoskeletal protein;
receptor; transcription factor; cancer; MHC;
major histocompatibility complex; myeloma; colon cancer; gastric cancer;
adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
Homo sapiens.
WO200278524-A2.
10-OCT-2002.
28-MAR-2002; 2002WO-US009671.
28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
(ZYCO-) ZYCO INC.
Chicz RM, Tomlinson AJ, Urban RG;
WPI; 2003-040607/03.
New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukaemia.
Example 2; SEQ ID NO 1440; 134pp; English.
The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukaemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MMSASRLAGTLIPAMAFISCVRPSWPCVAVVNNITTCQMEINFYKIPDNLPSTKND 60

```

Db      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVENVNITYQCMELNPFYKIPDNLPESTKXLD 60
Qy      61 LSFNPLRLHLSGSYSFSPFPELQVLDLSRCEIQTEBGAQOSLSHLSLTLITGNPIQSALG 120
Db      61 LSFNPLRLHLSGSYSFSPFPELQVLDLSRCEIQTEBGAQOSLSHLSLTLITGNPIQSALG 120
Qy      121 AFSGLSSIQKLVAVETNLASLENPPIGHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Db      121 AFSGLSSIQKLVAVETNLASLENPPIGHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Qy      181 DLSNKTIOSTICTDLRVLHQMPPLNLSLDLSLNPNNFIOPGAFKIRLHKTLRNPPSL 240
Db      181 DLSNKTIOSTICTDLRVLHQMPPLNLSLDLSLNPNNFIOPGAFKIRLHKTLRNPPSL 240
Qy      241 NMKTCIOGLAGLEVHRLVGEFNRNEGNELEKFDKSALEGLCNLTIEBRRLAYLDYLDI 300
Db      241 NMKTCIOGLAGLEVHRLVGEFNRNEGNELEKFDKSALEGLCNLTIEBRRLAYLDYLDI 300
Qy      301 IDLFNCLTNVSSFSLSVYTIERVKDPSYNGMOHLELVNCKRGOPPTLKSLKRLPTS 360
Db      301 IDLFNCLTNVSSFSLSVYTIERVKDPSYNGMOHLELVNCKRGOPPTLKSLKRLPTS 360
Qy      361 NKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDPFTSLKYLDLSFNGVITWSSNPLG 420
Db      361 NKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDPFTSLKYLDLSFNGVITWSSNPLG 420
Qy      421 LEQLEHLDFOHSNLKOMESEFVSFLSRNLITYLDISHTRVAFNGIFNGLSLEVLKXAG 480
Db      421 LEQLEHLDFOHSNLKOMESEFVSFLSRNLITYLDISHTRVAFNGIFNGLSLEVLKXAG 480
Qy      481 NSFOENFLPDIETELRNLTPLDLSQCOLEQSPFASNSLSISQVLNMSHNNFSLDTPPY 540
Db      481 NSFOENFLPDIETELRNLTPLDLSQCOLEQSPFASNSLSISQVLNMSHNNFSLDTPPY 540
Qy      541 KCLNSLOVLDYSLNHTMTSKQEOLOHPFSSSLAFNLTLQNDPACTEHOSEFLQWIDQOL 600
Db      541 KCLNSLOVLDYSLNHTMTSKQEOLOHPFSSSLAFNLTLQNDPACTEHOSEFLQWIDQOL 600
Qy      601 LVEVERMECATPSPDQKQMPVLSLNTTCOMNKTIIISVLSVYVAVLVVYKFEFHLML 660
Db      601 LVEVERMECATPSPDQKQMPVLSLNTTCOMNKTIIISVLSVYVAVLVVYKFEFHLML 660
Qy      661 LAGCCKYGRGENIYDAFVIYSSODEDWVNLVKNLEBQVPEFQCLHYRDPITPGVAIAA 720
Db      661 LAGCCKYGRGENIYDAFVIYSSODEDWVNLVKNLEBQVPEFQCLHYRDPITPGVAIAA 720
Qy      721 NIIEGFHFKSRKVIYVVSQHPIQSRWCIFEFYELIAQTWQPLSSRAGITIVLOKVEKTLR 780
Db      721 NIIEGFHFKSRKVIYVVSQHPIQSRWCIFEFYELIAQTWQPLSSRAGITIVLOKVEKTLR 780
Qy      781 QOVELYRLSRNTYLEMEDSVLGRHIFWRRLKALLDDKSNMPEGTGTCNMOWATSI 839
Db      781 QOVELYRLSRNTYLEMEDSVLGRHIFWRRLKALLDDKSNMPEGTGTCNMOWATSI 839

```

RESULT 3
ABU04775
ID ABU04775 standard; protein; 839 AA.

AC ABU04775;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1441.

KW Translational profiling; expressed protein tag; EPT; kinase, phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

```

XX      XX      WO200278524-A2.
PN      XX      10-OCT-2002.
XX      PD      28-MAR-2002; 2002WO-US009671.
XX      PF      28-MAR-2001; 2001US-0279495P.
XX      PR      21-MAY-2001; 2001US-0292544P.
XX      PR      08-AUG-2001; 2001US-0310801P.
XX      PR      01-OCT-2001; 2001US-0326370P.
XX      PR      04-DEC-2001; 2001US-0336780P.
XX      PR      20-FEB-2002; 2002US-0358985P.
XX      PA      (ZYCO-) ZYCOS INC.
XX      PI      Chicx RM, Tomlinson AJ, Urban RG;
XX      DR      WPI; 2003-040607/03.
XX      PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT      cytoskeletal proteins, receptors or transcription factors), useful for  
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT      leukemia.
XX      PS      Example 2; SEQ ID NO 1441; 134pp; English.
XX      XX      The invention describes a purified polypeptide, which comprises a  
CC      fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC      transporter, cytoskeletal protein, receptor or transcription factor. The  
CC      polypeptide is useful as an immunogenic composition for eliciting in a  
CC      mammal an immunogenic response directed against any of the purified  
CC      polypeptide. The purified polypeptide, or the antibody that binds to this  
CC      polypeptide, is useful for treating cancer. The polypeptide is also  
CC      useful for identifying compounds that binds to a naturally processed  
CC      class I or class II MHC-binding polypeptide. The polypeptides and  
CC      polynucleotides are particularly useful for treating or preventing  
CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC      lymphoma or leukemia. These are also useful for screening agents for  
CC      treating the above mentioned diseases. This sequence represents an  
CC      expressed protein tag (EPT) isolated from human tissue for translational  
CC      profiling. Note: This sequence does not appear in the printed  
CC      specification and was obtained in electronic format directly from WIPO at  
CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 839 AA:

```

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVENVNITYQCMELNPFYKIPDNLPESTKXLD 60
Db      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVENVNITYQCMELNPFYKIPDNLPESTKXLD 60
Qy      61 LSFNPLRLHLSGSYSFSPFPELQVLDLSRCEIQTEBGAQOSLSHLSLTLITGNPIQSALG 120
Db      61 LSFNPLRLHLSGSYSFSPFPELQVLDLSRCEIQTEBGAQOSLSHLSLTLITGNPIQSALG 120
Qy      121 AFSGLSSIQKLVAVETNLASLENPPIGHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Db      121 AFSGLSSIQKLVAVETNLASLENPPIGHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Qy      181 DLSNKTIOSTICTDLRVLHQMPPLNLSLDLSLNPNNFIOPGAFKIRLHKTLRNPPSL 240
Db      181 DLSNKTIOSTICTDLRVLHQMPPLNLSLDLSLNPNNFIOPGAFKIRLHKTLRNPPSL 240
Qy      241 NMKTCIOGLAGLEVHRLVGEFNRNEGNELEKFDKSALEGLCNLTIEBRRLAYLDYLDI 300
Db      241 NMKTCIOGLAGLEVHRLVGEFNRNEGNELEKFDKSALEGLCNLTIEBRRLAYLDYLDI 300
Qy      301 IDLFNCLTNVSSFSLSVYTIERVKDPSYNGMOHLELVNCKRGOPPTLKSLKRLPTS 360

```

Db 301 IDLFNCLTNVSSFLSVVTERVYKDFSNFGWQHLELVNCKFGQFPPTLKLSKRLTFTS 360
Qy 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDPGTTSLKYLDLSENGVITMSSNFLG 420
361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDPGTTSLKYLDLSENGVITMSSNFLG 420
Qy 421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
Db 421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
Qy 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
Db 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
Qy 601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
Db 601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
Qy 661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
Db 661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
Db 721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839
781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839

RESULT 4
ADCT8785
ID ADCT8785 standard; protein; 839 AA.
AC ADCT8785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GERTH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADCT8784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA:
Query Match 100.0%; Score 4355; DB 7; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSASRLAGTILPAMAFICVBPRESMEPCVAVPNITTCQMEINFYKIPNNLPSTGNLD 60
1 MMSASRLAGTILPAMAFICVBPRESMEPCVAVPNITTCQMEINFYKIPNNLPSTGNLD 60
Db 1 MMSASRLAGTILPAMAFICVBPRESMEPCVAVPNITTCQMEINFYKIPNNLPSTGNLD 60
Qy 61 LSFNPRLHLSYSFSPFPELQVLDLSKCEIQTTEDEGAYOSLSHLSTLITGNPIQSALG 120
61 LSFNPRLHLSYSFSPFPELQVLDLSKCEIQTTEDEGAYOSLSHLSTLITGNPIQSALG 120
Db 61 LSFNPRLHLSYSFSPFPELQVLDLSKCEIQTTEDEGAYOSLSHLSTLITGNPIQSALG 120
Qy 121 AFGSLSLQKLVAVETNLASLENFPICHLKTLKELVAVANLISFKLPEYFSNLTNLEHL 180
121 AFGSLSLQKLVAVETNLASLENFPICHLKTLKELVAVANLISFKLPEYFSNLTNLEHL 180
Db 121 AFGSLSLQKLVAVETNLASLENFPICHLKTLKELVAVANLISFKLPEYFSNLTNLEHL 180
Qy 181 DLSNKTQSIYCTDLRYLHQMPILNLSLISLPMNFIQGAPEIRLHLTLRNPDLSL 240
181 DLSNKTQSIYCTDLRYLHQMPILNLSLISLPMNFIQGAPEIRLHLTLRNPDLSL 240
Db 181 DLSNKTQSIYCTDLRYLHQMPILNLSLISLPMNFIQGAPEIRLHLTLRNPDLSL 240
Qy 241 NVMKTCIQGLAGLEVHRLVGEFFRNENLEKFPKSALEGLCNTLIEEFLAYLDYLDI 300
241 NVMKTCIQGLAGLEVHRLVGEFFRNENLEKFPKSALEGLCNTLIEEFLAYLDYLDI 300
Db 241 NVMKTCIQGLAGLEVHRLVGEFFRNENLEKFPKSALEGLCNTLIEEFLAYLDYLDI 300
Qy 301 IDLFNCLTNVSSFLSVVTERVYKDFSNFGWQHLELVNCKFGQFPPTLKLSKRLTFTS 360
301 IDLFNCLTNVSSFLSVVTERVYKDFSNFGWQHLELVNCKFGQFPPTLKLSKRLTFTS 360
Db 301 IDLFNCLTNVSSFLSVVTERVYKDFSNFGWQHLELVNCKFGQFPPTLKLSKRLTFTS 360
Qy 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDPGTTSLKYLDLSENGVITMSSNFLG 420
361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDPGTTSLKYLDLSENGVITMSSNFLG 420
Db 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDPGTTSLKYLDLSENGVITMSSNFLG 420
Qy 421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
Db 421 LEQLEHLDFOHNSLKQSESEVFLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
Qy 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNMSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
Db 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDQROL 600
Qy 601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
Db 601 LVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFPHLM 660
Qy 661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
Db 661 LAGCIKTGREGNIYDAFVIYSSQDEDMVRNLELVNLEEGVPPQCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
Db 721 NIHEGFHRSKRVLVVVSQHFIQSRWCIFEYEIAQTMQFLSSRAGIIFIVLQKYEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839
781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTCNMQEARSI 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
AC ADD48826;
XX
XX

DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
DE Human Protein AAF05316, SEQ ID NO 14536.
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
OS Homo sapiens.
OS unidentified.
XX MO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (PARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; AAF05316.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (described in Table 3
XX of the specification) which is differentially expressed during pain.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 839 AA;
XX
XX Query Match 100.0%; Score 4355; DB 7; Length 839;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MMSASRLAGTLIPAAAFICVRPESBPCVAVPITQCKELNFKYKIPDNLPESTKLD 60
XX 1 MMSASRLAGTLIPAAAFICVRPESBPCVAVPITQCKELNFKYKIPDNLPESTKLD 60

QY 61 LSFNPLRLHLSGYSFFSPPELQVLDLSRCEIQTIDGAYQSIHSLSTLITLNPPIQSIALG 120
DB 61 LSFNPLRLHLSGYSFFSPPELQVLDLSRCEIQTIDGAYQSIHSLSTLITLNPPIQSIALG 120
QY 121 AFGSLSSLOKLVAVETNLASLENPPIGHILKTLKELAVAHNLIOGPKLPEYPSNLTNLEHL 180
DB 121 AFGSLSSLOKLVAVETNLASLENPPIGHILKTLKELAVAHNLIOGPKLPEYPSNLTNLEHL 180
QY 181 DLSNKKIQSICYTDLRLVHQMPPLNLSLDSLNPMNFIOGAFKFIKRLKTLRNPDSTL 240
DB 181 DLSNKKIQSICYTDLRLVHQMPPLNLSLDSLNPMNFIOGAFKFIKRLKTLRNPDSTL 240
QY 241 NMKTCIOGLAGLVHRLVIGEPNBNGLKFKDASALEGICNLITIEFRILAYLDYDDI 300
DB 241 NMKTCIOGLAGLVHRLVIGEPNBNGLKFKDASALEGICNLITIEFRILAYLDYDDI 300
QY 301 IDLFNCLTNVSSFSVSVTLERVKDFSTFGMHLVNCRFQGPPIKLKSLKRLKLTFS 360
DB 301 IDLFNCLTNVSSFSVSVTLERVKDFSTFGMHLVNCRFQGPPIKLKSLKRLKLTFS 360
QY 361 NKGNAFSEVDLPLEFLDLSRNLSPKGCSSQSDFGTSLKLYDLSPNGVITWSSNPLG 420
DB 361 NKGNAFSEVDLPLEFLDLSRNLSPKGCSSQSDFGTSLKLYDLSPNGVITWSSNPLG 420
QY 421 LEQLEHLDPQHSNLIKQSEFSVPLSLNRLIYLDISHTTRVAFNGIFNGLSLBYLKAAG 480
DB 421 LEQLEHLDPQHSNLIKQSEFSVPLSLNRLIYLDISHTTRVAFNGIFNGLSLBYLKAAG 480
QY 481 NSPOENFLPOLFTFLRLNLTPLDLSQCOLEQSLPFAFNSLSQVLMNSHNNFSLDTPPY 540
DB 481 NSPOENFLPOLFTFLRLNLTPLDLSQCOLEQSLPFAFNSLSQVLMNSHNNFSLDTPPY 540
QY 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSIAFNLITQNDPACTCEHOSFLQWIKDQROL 600
DB 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSIAFNLITQNDPACTCEHOSFLQWIKDQROL 600
QY 601 LVEVERNECATPSDKQGMPLVSLNITQNMNTIIGSVLSVAVVAVLYKTFEHLML 660
DB 601 LVEVERNECATPSDKQGMPLVSLNITQNMNTIIGSVLSVAVVAVLYKTFEHLML 660
QY 661 LAGCITKRGENTYDAFVYSSQDEDMVRNVLNLEBGGVPPOLCLHYRDFIGVATAA 720
DB 661 LAGCITKRGENTYDAFVYSSQDEDMVRNVLNLEBGGVPPOLCLHYRDFIGVATAA 720
QY 721 NIIEGFHKSRYVWVSOHPFIOGRWCIFEYIAQTQFLSSRAGIIFIVLOKYEKTLR 780
DB 721 NIIEGFHKSRYVWVSOHPFIOGRWCIFEYIAQTQFLSSRAGIIFIVLOKYEKTLR 780
QY 781 QQVELYRLLSRNTYLEWEDSVLGHIFWRRLRKALDQKSWNPBGTVGTGCMQDEATSI 839
DB 781 QQVELYRLLSRNTYLEWEDSVLGHIFWRRLRKALDQKSWNPBGTVGTGCMQDEATSI 839
RESULT 6
AAW86361
ID AAW86361 standard; protein; 837 AA.
XX
XX AAW86361;
XX
XX 15-MAR-1999 (first entry)
XX
XX Human DNAK toll-like receptor DTLR4.
XX
XX DNAK toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
XX Homo sapiens.
XX
XX W09850547-A2.
XX
XX 12-NOV-1998.
PD

XX 07-MAY-1998; 98WO-US008979.
XX
XX 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX WPI: 1999-059670/05.
DR N-PSDB; AAV80675.
XX
PT Human DNX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Claim 3; Page 147-149; 171pp; English.
XX
XX The present invention specifically describes human DNX toll-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 837 AA:
Query Match 99.6%; Score 4335.5; DB 2; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 MSASRLAGTLIPAAAFISCVRPESMPCVEVVPVNTYQCMELNPKYKIPDNLPSTKNL 61
Db 1 MSASRLAGTLIPAAAFISCVRPESMPCVE-VPNTTYQCMELNPKYKIPDNLPSTKNL 59
QY 62 SFNPLRLHGSYSFSPPELQVLDLSRCEIQTIEDGAYQSLHSTLITGNPISLALGA 121
Db 60 SFNPLRLHGSYSFSPPELQVLDLSRCEIQTIEDGAYQSLHSTLITGNPISLALGA 119
QY 122 FSGLSLQKLVAVETNLTASLENFPIGHLKTKELNVAHNLQSFRLPEYFSNLTNLEHLD 181
Db 120 FSGLSLQKLVAVETNLTASLENFPIGHLKTKELNVAHNLQSFRLPEYFSNLTNLEHLD 179
QY 182 LSSNKISQICTDPAFVHOMPLNLSLDLSLNPNFTOPGAFKEIRLHKLTLRNPNLSLN 241
Db 180 LSSNKISQICTDPAFVHOMPLNLSLDLSLNPNFTOPGAFKEIRLHKLTLRNPNLSLN 239
QY 242 VMKTCIOGLAGLEVHRLVLSGFNNEGMLKEFKDSALBGLCNLTIEEFLAVLDYLDII 301
Db 240 VMKTCIOGLAGLEVHRLVLSGFNNEGMLKEFKDSALBGLCNLTIEEFLAVLDYLDII 299
QY 302 DLFNCLTNVSSFSFVSTIERVVDPSYKPFQMOHLEVNCKRGOPPTLTKSLKLTFTSN 361
Db 300 DLFNCLTNVSSFSFVSTIERVVDPSYKPFQMOHLEVNCKRGOPPTLTKSLKLTFTSN 359
QY 362 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGFTSLKYLDLSPFNGVITMSNFG 421
Db 360 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGFTSLKYLDLSPFNGVITMSNFG 419
QY 422 EQLEHLDPOHSNLTQMSSEFVLSLRNLIYLDISHTHTRVAFNGIPLNGSLSEVLKMG 481
Db 420 EQLEHLDPOHSNLTQMSSEFVLSLRNLIYLDISHTHTRVAFNGIPLNGSLSEVLKMG 479
QY 482 SFQENFLPDIETELRNLTFLDLSQCLEQLSPFAPNSLSLQVLNMSHNNFSLDTFPYK 541

Db 480 SFQENFLPDIETELRNLTFLDLSQCLEQLSPFAPNSLSLQVLNMSHNNFSLDTFPYK 539
QY 542 CLNSIQVLDYSLNHNIMTSKQELQHPSSLAFTNLQNDPACCEHQSFLQWIKDQRL 601
Db 540 CLNSIQVLDYSLNHNIMTSKQELQHPSSLAFTNLQNDPACCEHQSFLQWIKDQRL 599
QY 602 VEVERMECAPSPDKQMPVLSLNTCOMKTTIIGSVLSVLSVVAVALYKFEFHLML 661
Db 600 VEVERMECAPSPDKQMPVLSLNTCOMKTTIIGSVLSVLSVVAVALYKFEFHLML 659
QY 662 AGCTKRGENTIDAFYVSSODEDWARNLVNLEBGPVPPOLCHYRDFIGVALAAN 721
Db 660 AGCTKRGENTIDAFYVSSODEDWARNLVNLEBGPVPPOLCHYRDFIGVALAAN 719
QY 722 IIEHGFHRSKRVIVVWSQHFIQSRWCIFEXEIAQWQFLSSRAGIIFIVLQKEKTLRQ 781
Db 720 IIEHGFHRSKRVIVVWSQHFIQSRWCIFEXEIAQWQFLSSRAGIIFIVLQKEKTLRQ 779
QY 782 QVEIYRLISNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGTVGTGCMQEAISI 839
Db 780 QVEIYRLISNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGTVGTGCMQEAISI 837
RESULT 7
ID AAE16102 standard; protein; 837 AA.
XX AAE16102;
AC AAE16102;
XX 26-MAR-2002 (first entry)
DT Human DNX Toll like receptor (DTLR) 4 #2.
XX
DE Human DNX Toll like receptor (DTLR) 4 #2.
XX
KM Human; DNX Toll like receptor; DTLR; therapy; immunological disorder;
KM interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX Homo sapiens.
OS Homo sapiens.
XX WO200190151-A2.
PN 29-NOV-2001.
PD 23-MAY-2001; 2001WO-US016766.
XX 25-MAY-2000; 2000US-0207558P.
PR (SCHE) SCHERING CORP.
PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX WPI: 2002-083085/11.
DR N-PSDB; AAD26292.
XX
PT New DNX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 3; Page 41; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAE16116). However these sequences differ
 CC at several locations

XX
 XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 5; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAMAFISCVRPESWPCVEVPNTTYQCEMLNFKYKIDNLPSTKNDL 61
 DB 1 MSASRLAGTLIPAMAFISCVRPESWPCVE-VPNITTYQCEMLNFKYKIDNLPSTKNDL 59
 QY 62 SFNPLRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 DB 60 SFNPLRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 119
 QY 122 FSGSLSLQKLVAVENINLASLENFPIGHLKTLKELVAVANILQSFLPEYFSMLTNLEHLD 181
 DB 120 FSGSLSLQKLVAVENINLASLENFPIGHLKTLKELVAVANILQSFLPEYFSMLTNLEHLD 179
 QY 182 LSSNKIOSIYCTDLRLVHQMPLNLSDLSLNPNNFIOPGAFKEIRLKLTLRNNPDSLN 241
 DB 180 LSSNKIOSIYCTDLRLVHQMPLNLSDLSLNPNNFIOPGAFKEIRLKLTLRNNPDSLN 239
 QY 242 VMKTCIQGLAGLEVRLVYGEFRNNGNLEKFDKSLBGLCNLTIEPRILAYLDYLDII 301
 DB 240 VMKTCIQGLAGLEVRLVYGEFRNNGNLEKFDKSLBGLCNLTIEPRILAYLDYLDII 299
 QY 302 DLFNCLTNVSSFSIVSVTIERKDSYNFGMOHLELVNCKRGQPTLKLKSLKRLTFTSN 361
 DB 300 DLFNCLTNVSSFSIVSVTIERKDSYNFGMOHLELVNCKRGQPTLKLKSLKRLTFTSN 359
 QY 362 KGNNAFSEVDLPSELEFLDLSRNGLSFKGCCSDGFTSLKLYDLSFNGVITMSNFTGL 421
 DB 360 KGNNAFSEVDLPSELEFLDLSRNGLSFKGCCSDGFTSLKLYDLSFNGVITMSNFTGL 419
 QY 422 EOLEHLDFQHSNLSKOMSEFSVFLSRNLIIYLDISHTHTRVAFNGIFNGLSLEVLKMGAN 481
 DB 420 EOLEHLDFQHSNLSKOMSEFSVFLSRNLIIYLDISHTHTRVAFNGIFNGLSLEVLKMGAN 479
 QY 482 SFQENFLPDIETELRNLTFLDLSQQLSPTAENSLSLOYLMSNNPFSLDTPFYK 541
 DB 480 SFQENFLPDIETELRNLTFLDLSQQLSPTAENSLSLOYLMSNNPFSLDTPFYK 539
 QY 542 CLNSIQVLDVSLNHNMTSKQELQHPFSSLAFLNLTQNDFACTCHQSFLOWIKDQRL 601
 DB 540 CLNSIQVLDVSLNHNMTSKQELQHPFSSLAFLNLTQNDFACTCHQSFLOWIKDQRL 599
 QY 602 VEVEBMECATPSDKQGMFVLSLNTIQNNKTIIGVSVLSVIVSVVAVLVYKFFHMLL 661
 DB 600 VEVEBMECATPSDKQGMFVLSLNTIQNNKTIIGVSVLSVIVSVVAVLVYKFFHMLL 659
 QY 662 AGCTIKYGGENIYDAFVYSSODEWVWVNNELVKNLEBVPPOCLAHRPDIPGVAIAN 721
 DB 660 AGCTIKYGGENIYDAFVYSSODEWVWVNNELVKNLEBVPPOCLAHRPDIPGVAIAN 719
 QY 722 IHHGFFHSRKVIYVVSQHFIOSRWCIFEYELIAQTMQFLSSAGIIFIVLOKVEKTLRQ 781
 DB 720 IHHGFFHSRKVIYVVSQHFIOSRWCIFEYELIAQTMQFLSSAGIIFIVLOKVEKTLRQ 779
 QY 782 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNDEGTGTCNQWQATSI 839
 DB 780 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNDEGTGTCNQWQATSI 837

RESULT 8
 ABU04776

ID ABU04776 standard; protein; 837 AA.

XX AC ABU04776;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1442.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 XX protease; protease inhibitor; transporter; cytoskeletal protein;

XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0232544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AU, Urban RG;

XX WPI, 2003-040607/03.

XX Example 2; SEQ ID NO 1442; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

XX fragment of a kinase, phosphatase, protease, protease inhibitor,

XX transporter, cytoskeletal protein, receptor or transcription factor. The

XX polypeptide is useful as an immunogenic composition for eliciting in a

XX mammal an immunogenic response directed against any of the purified

XX polypeptide. The purified polypeptide, or the antibody that binds to this

XX polypeptide, is useful for treating cancer. The polypeptide is also

XX useful for identifying compounds that binds to a naturally processed

XX class I or class II MHC-binding polypeptide. The polypeptides and

XX polynucleotides are particularly useful for treating or preventing

XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

XX lymphoma or leukaemia. These are also useful for screening agents for

XX treating the above mentioned diseases. This sequence represents an

XX expressed protein tag (EPT) isolated from human tissue for translational

XX profiling. Note: This sequence does not appear in the printed

XX specification but was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 6; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAMAFISCVRPESWPCVEVPNTTYQCEMLNFKYKIDNLPSTKNDL 61
 DB 1 MSASRLAGTLIPAMAFISCVRPESWPCVE-VPNITTYQCEMLNFKYKIDNLPSTKNDL 59
 QY 62 SFNPLRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 DB 60 SFNPLRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 119

QY 122 FSGLSLQKLVAVETNLASLENPPIGHLKTLKELVANHLIQSEFKLPEYFSNLTNLHL 181
DB 120 FSGLSLQKLVAVETNLASLENPPIGHLKTLKELVANHLIQSEFKLPEYFSNLTNLHL 179
QY 182 LSSNKIOSICTDRLVHOMPLNLSDLSINPNMFIOPGAFAKEIRLHKLTLRNPFSLN 241
DB 180 LSSNKIOSICTDRLVHOMPLNLSDLSINPNMFIOPGAFAKEIRLHKLTLRNPFSLN 239
QY 242 VMKTCIOGLAGLEVHRLVLFGEFRNENKEDKALBGLCNLTIEBRFLATLDYLDII 301
DB 240 VMKTCIOGLAGLEVHRLVLFGEFRNENKEDKALBGLCNLTIEBRFLATLDYLDII 299
QY 302 DLFNCLTNVSSFSLSVSTIERVKDFSYNFGQHLVNCCKFGQPTLKLSIKRLTFTSN 361
DB 300 DLFNCLTNVSSFSLSVSTIERVKDFSYNFGQHLVNCCKFGQPTLKLSIKRLTFTSN 359
QY 362 KGNAPSEVDLPSEFLDLSPNGLSFKGCCSQSDFGTTSKLYLDLSENGVITMSSNPLGL 421
DB 360 KGNAPSEVDLPSEFLDLSPNGLSFKGCCSQSDFGTTSKLYLDLSENGVITMSSNPLGL 419
QY 422 EQLHLDPQHSNLSKQMSSEVFLSRNLIVLDISHTRVAFNGIFNGLSLEVLKXAGN 481
DB 420 EQLHLDPQHSNLSKQMSSEVFLSRNLIVLDISHTRVAFNGIFNGLSLEVLKXAGN 479
QY 482 SFQENFLPDITELRLNLTFLDLSOCQLEQLSPTAFNSLSQVLMNSHNNFSDTPPYK 541
DB 480 SFQENFLPDITELRLNLTFLDLSOCQLEQLSPTAFNSLSQVLMNSHNNFSDTPPYK 539
QY 542 CLNSIQVLDYSNLNMTSKKQELQHPSSLAFLNLTQNDPACTGCHOSFLOWIKDQRL 601
DB 540 CLNSIQVLDYSNLNMTSKKQELQHPSSLAFLNLTQNDPACTGCHOSFLOWIKDQRL 599
QY 602 VEVRMECATPSDKQGMVLSLNTICQNNKTIIGVSVSVVAVVAVVYKFFPHMLL 661
DB 600 VEVRMECATPSDKQGMVLSLNTICQNNKTIIGVSVSVVAVVAVVYKFFPHMLL 659
QY 662 AGCIKYGGENIYDAFVIYSSQDEBDMVNELVKNLEBGPVPPOLCLHYRDEIPGVALAN 721
DB 660 AGCIKYGGENIYDAFVIYSSQDEBDMVNELVKNLEBGPVPPOLCLHYRDEIPGVALAN 719
QY 722 IHHGFKSRKVIYVVSQHPFIQSRWCIFREYIAQTWQFLSSRAGIIFVLQKVEKTLRQ 781
DB 720 IHHGFKSRKVIYVVSQHPFIQSRWCIFREYIAQTWQFLSSRAGIIFVLQKVEKTLRQ 779
QY 782 QVELYRLISRTYLEWEDSVLGRHFMARLRKALLDGSMNPEGTVGTCMMQEATSI 839
DB 780 QVELYRLISRTYLEWEDSVLGRHFMARLRKALLDGSMNPEGTVGTCMMQEATSI 837

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX AAE16116;
AC AAE16116;
DT 26-MAR-2002 (first entry)
DE Human DNAX Toll like receptor (DTR) 4 #2, alternative version.
XX Human; DNAX Toll like receptor; DTR; therapy; immunological disorder;
KW interleukin 1, IL-1; screening; immunomodulator; chromosome 9q32-33.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 211
FT /label= Unknown
FT /note= "Encoded by AAY"
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.

XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DB N-PSDB; AAD2630C.
XX
PT New DNAX Toll like receptor (DTR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.

Claim 3; Page 240-243; 297pp; English.

CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTR) protein and their corresponding
CC nucleic acids. The DTR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTR or its various fragments. The
CC purified DTR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTR or cells that express it. The present sequence is
CC human DTR4 protein, alternative version. The DTR4 gene is located on
CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC be similar to the sequence shown in page 41 (AAE16102). However these
CC sequences differ at several locations

Sequence 837 AA:

Query Match 99.4%; Score 4328.5; DB 5; Length 837;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

DB 2 MSASRLAGTILIPAMAFSCVRPESBECVAVENITYQCEMLNYYKIPDMLPSTKMLDL 61
1 MSASRLAGTILIPAMAFSCVRPESBECVAVENITYQCEMLNYYKIPDMLPSTKMLDL 59
QY 62 SFNPLRHLSGYSFSPPELOVLDLSRCEIQTIBDGAQSLSHLSTLLITGNPIQSLALGA 121
DB 60 SFNPLRHLSGYSFSPPELOVLDLSRCEIQTIBDGAQSLSHLSTLLITGNPIQSLALGA 119
QY 122 FSGLSLQKLVAVETNLASLENPPIGHLKTLKELVANHLIQSEFKLPEYFSNLTNLHL 181
DB 120 FSGLSLQKLVAVETNLASLENPPIGHLKTLKELVANHLIQSEFKLPEYFSNLTNLHL 179
QY 182 LSSNKIOSICTDRLVHOMPLNLSDLSINPNMFIOPGAFAKEIRLHKLTLRNPFSLN 241
DB 180 LSSNKIOSICTDRLVHOMPLNLSDLSINPNMFIOPGAFAKEIRLHKLTLRNPFSLN 239
QY 242 VMKTCIOGLAGLEVHRLVLFGEFRNENKEDKALBGLCNLTIEBRFLATLDYLDII 301
DB 240 VMKTCIOGLAGLEVHRLVLFGEFRNENKEDKALBGLCNLTIEBRFLATLDYLDII 299
QY 302 DLFNCLTNVSSFSLSVSTIERVKDFSYNFGQHLVNCCKFGQPTLKLSIKRLTFTSN 361
DB 300 DLFNCLTNVSSFSLSVSTIERVKDFSYNFGQHLVNCCKFGQPTLKLSIKRLTFTSN 359
QY 362 KGNAPSEVDLPSEFLDLSPNGLSFKGCCSQSDFGTTSKLYLDLSENGVITMSSNPLGL 421
DB 360 KGNAPSEVDLPSEFLDLSPNGLSFKGCCSQSDFGTTSKLYLDLSENGVITMSSNPLGL 419

QY 422 EOLEHLDFQHSNLTQKMSSESVFLSRNLIIYLDISTHTRVANGIFNGLSLEVLKMGN 481
Db 420 EOLEHLDFQHSNLTQKMSSESVFLSRNLIIYLDISTHTRVANGIFNGLSLEVLKMGN 479
QY 482 SFOENFLDFIDFELNLTFLDLSDQCOLBOLSPTAFNLSLSLOVLMNSHNNFSLDTPPK 541
Db 480 SFOENFLDFIDFELNLTFLDLSDQCOLBOLSPTAFNLSLSLOVLMNSHNNFSLDTPPK 539
QY 542 CLNSLOVLDSYSLNHTMSKQELQHPSPSLAFNLTONDFACTCHOSFLQWIKDORQL 601
Db 540 CLNSLOVLDSYSLNHTMSKQELQHPSPSLAFNLTONDFACTCHOSFLQWIKDORQL 599
QY 602 VBEVMECATPSDKQKMPVLSLNTTCQANKTIGVSLSVSVVAVLVYKFFHYHML 661
Db 600 VBEVMECATPSDKQKMPVLSLNTTCQANKTIGVSLSVSVVAVLVYKFFHYHML 659
QY 662 AGCIYRGENTYDAFVLYSSODEDMVNEVLKMLEEGVPPQCLAHYRDFIPGVAIAN 721
Db 660 AGCIYRGENTYDAFVLYSSODEDMVNEVLKMLEEGVPPQCLAHYRDFIPGVAIAN 719
QY 722 IIHGFHRSRKVIIVVSOHFIQSRWCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLARQ 781
Db 720 IIHGFHRSRKVIIVVSOHFIQSRWCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLARQ 779
QY 782 QVELYRLISRTYILEWEDSVLGRHIFWRRLRKALLDGKSWNEBGTGTCNMQEATSI 839
Db 780 QVELYRLISRTYILEWEDSVLGRHIFWRRLRKALLDGKSWNEBGTGTCNMQEATSI 837

RESULT 10

ID ADO57782 standard; protein; 808 AA.

AC ADO57782;

DT 12-AUG-2004 (first entry)

DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.

KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
sepsis; severe sepsis; septic shock; asthma; chimpanzee.

OS Pan troglodytes.

PN WO2004042365-A2.

XX 21-MAY-2004.

XX 03-NOV-2003; 2003WO-US036247.

XX 01-NOV-2002; 2002US-0423113P.

XX (EVOLO-) EVOLUTIONARY GENOMICS LLC.

XX Meesier W;

XX MPI; 2004-400726/37.

XX N-PSDB; ADO57780, ADO57781.

XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
in treating sepsis and asthma, by comparing the TLR4 polynucleotide
sequence of the Old World monkey with that of a human.

XX Example 1; SEQ ID NO 3; 111pp; English.

XX The invention relates to a novel method for identifying a nucleotide
change in a TLR4 polynucleotide sequence of an old world monkey
comparing the TLR4 polynucleotide sequence of the Old World
monkey with corresponding TLR4 polynucleotide sequence of a human. The
method of the invention has antibacterial, immunosuppressive, and
antiasthmatic activity. The method is useful in identifying a nucleotide
change in a TLR4 polynucleotide sequence of an Old World monkey where the

CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.

SQ Sequence 808 AA;

Query Match 95.9%; Score 4178; DB 8; Length 808;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 805; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 32 VVPNTTYCMLNFKIKIDNPFTSKNLDSPNPRHIGSYFSPPELOVLDLSRCRQ 91
Db 1 VVPNTTYCMLNFKIKIDNPFTSKNLDSPNPRHIGSYFSPPELOVLDLSRCRQ 60
QY 92 TIEDGAYOSLSHLSTLITGNPIOSIALGASGSLSKLVAVENTLASLENFPIGHKT 151
Db 61 TIEDGAYOSLSHLSTLITGNPIOSIALGASGSLSKLVAVENTLASLENFPIGHKT 120
QY 152 LKELNVAANLLQSPFLPEYFNSLNTLEHLDLSSNKIQSIYCTDLRVLHQMPNLNLSLDLS 211
Db 121 LKELNVAANLLQSPFLPEYFNSLNTLEHLDLSSNKIQSIYCTDLRVLHQMPNLNLSLDLS 180
QY 212 LNPWFIOPGAFAKEIRLKLTLRNNFDSLANWKTCTOGLAGIEVHRVLYGERRNANLXK 271
Db 181 LNPWFIOPGAFAKEIRLKLTLRNNFDSLANWKTCTOGLAGIEVHRVLYGERRNANLXK 240
QY 272 FDKSALBGLCNLTTEEPRLAYLDYLDIIDLPLNCLTNVSSPSLVSVTIERKQDSYNG 331
Db 241 FDKSALBGLCNLTTEEPRLAYLDYLDIIDLPLNCLTNVSSPSLVSVTIERKQDSYNG 300
QY 332 WQHELNVCKFGQPTTLKLSLKLTLTSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 391
Db 301 WQHELNVCKFGQPTTLKLSLKLTLTSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 360
QY 392 SOSDFGTTSLKYLDLSFNGVITMGSNFIQLEHLEHLDQHSNLTQKMSSESVFLSRNLII 451
Db 361 SOSDFGTTSLKYLDLSFNGVITMGSNFIQLEHLEHLDQHSNLTQKMSSESVFLSRNLII 420
QY 452 LDISHTRVAVNGIFNGLSLEVLKMGNSFOENFLDITFELNLTFLDLSDQCOLBOL 511
Db 421 LDISHTRVAVNGIFNGLSLEVLKMGNSFOENFLDITFELNLTFLDLSDQCOLBOL 480
QY 512 SPTAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDYSLNHTMSKQELQHPSPSL 571
Db 481 SPTAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDYSLNHTMSKQELQHPSPSL 540
QY 572 AFLNLTONDFACTCHOSFLOWIKDORQLVEVERMECATPSDKQKMPVLSLNTTCQANK 631
Db 541 AFLNLTONDFACTCHOSFLOWIKDORQLVEVERMECATPSDKQKMPVLSLNTTCQANK 600
QY 632 TIIGVSVLSVSVVAVLVYKFFHYHMLTAGCTKYGGENIYDAFVLYSSODEDMVNE 691
Db 601 TIIGVSVLSVSVVAVLVYKFFHYHMLTAGCTKYGGENIYDAFVLYSSODEDMVNE 660
QY 692 LVKNLEBGPFPQCLAHYRDFIPGVAIAANIIHGFHRSRKVIIVVSOHFIQSRWCIFEY 751
Db 661 LVKNLEBGPFPQCLAHYRDFIPGVAIAANIIHGFHRSRKVIIVVSOHFIQSRWCIFEY 720
QY 752 EIAQTWQFLSPRAGIIFIVLOKVEKTLRQVELYRLISRTYILEWEDSVLGRHIFWRRL 811
Db 721 EIAQTWQFLSPRAGIIFIVLOKVEKTLRQVELYRLISRTYILEWEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSWNEBGTGTCNMQEATSI 839
Db 781 RKALLDGKSWNEBGTGTCNMQEATSI 808

RESULT 11

ID ADO57785 standard; protein; 808 AA.

AC ADO57785;

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XX 12-AUG-2004 (first entry)
DT
XX
XX Gorilla toll-like receptor 4 SEQ ID NO:6.
DE
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
OS
XX Gorilla gorilla.
PN
XX MO2004042365-A2.
PD
XX 21-MAY-2004.
PF
XX 03-NOV-2003; 2003WO-US036247.
PR
XX 01-NOV-2002; 2002US-0423113P.
PA
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
PI
XX MPI: 2004-400726/37.
DR
XX N-PSDB; ADO57783; ADO57784.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Example 1; SEQ ID NO 6; 11bp; English.
PS
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
XX Sequence 808 AA;
SQ
Query Match 95.7%; Score 4167; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 32 VVPNITTYOCMEINFYKIPDNLPFSTKNLDLSPNPLRHLSYSPFSPPELQVLDLSRCEIQ 91
DB 1 VVPNITTYOCMEINFYKIPDNLPFSTKNLDLSPNPLRHLSYSPFSPPELQVLDLSRCEIQ 60
QY 92 TIEDAYOSLSLSTLITGNPIQSLAGAFSGSLSLQKLVAVENTLASLEPFPIGHKT 151
DB 61 TIEDAYOSLSLSTLITGNPIQSLAGAFSGSLSLQKLVAVENTLASLEPFPIGHKT 120
QY 152 LKEILVANHLIOSFKLPEYFSNLTLNLEHLDSNNKIOSIYCTDLVHLHOMPLNLSLDS 211
DB 121 LKEILVANHLIOSFKLPEYFSNLTLNLEHLDSNNKIOSIYCTDLVHLHOMPLNLSLDS 180
QY 212 LNPNNFIQPGAFKEIRLHKLTLRNNFDSLNWKTICIOGLAGLEVRLVYGERFNGNLEK 271
DB 181 LNPNNFIQPGAFKEIRLHKLTLRNNFDSLNWKTICIOGLAGLEVRLVYGERFNGNLEK 240
QY 272 FDKSLBEGICNLTIEFRLAYIDYLDIIDLFNCLTNVSSGLSVTIERKYDPSYNG 331
DB 241 FDKSLBEGICNLTIEFRLAYIDYLDIIDLFNCLTNVSSGLSVTIERKYDPSYNG 300
QY 332 MOHLELVNCKRGQFPTLKLKSLKRLTPTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCC 391
DB 301 MOHLELVNCKRGQFPTLKLKSLKRLTPTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCC 360

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QY 392 SOSDFGTTSLKYLDLSFNGVITMSSNFLGLEOLEHLDFOHSNLIKOMSEFSVFLSLRNILY 451
DB 361 SOSDFGTTSLKYLDLSFNGVITMSSNFLGLEOLEHLDFOHSNLIKOMSEFSVFLSLRNILY 420
QY 452 LDIHTHTRAVFNFIIFNGLSLETVLKMAGNSFQNFPLPDIPTTELRLNLTFFDLSGCCOLEQ 511
DB 421 LDIHTHTRAVFNFIIFNGLSLETVLKMAGNSFQNFPLPDIPTTELRLNLTFFDLSGCCOLEQ 480
QY 512 SPTAFNSLSLSQVLMNHNHNFSSLDTEPPYKCLNSLQVLDYSLNHNMTSSKKOELQHPSSL 571
DB 481 SPTAFNSLSLSQVLMNHNHNFSSLDTEPPYKCLNSLRLVDSLHNHNMTSSKKOELQHPSSL 540
QY 572 AFLNLTONDFACITCEHOSFIQWIKDQROLVVERMFCATPDSKQMPVLSLNTTCQMNK 631
DB 541 AFLNLTONDFACITCEHOSFIQWIKDQROLVVERMFCATPDSKQMPVLSLNTTCQMNK 600
QY 632 TITGVSVLSVTVVSVVAVLVYKFFHMLLAGCTIKYRGENVYAPFIYSSQDSDWRNE 691
DB 601 TITGVSVLSVTVVSVVAVLVYKFFHMLLAGCTIKYRGENVYAPFIYSSQDSDWRNE 660
QY 692 LVKNLEBGPFPOLCHYRDFIPGVAIAANIHHGFHKSRYIVVVSQHFQSRMCIFEX 751
DB 661 LVKNLEBGPFPOLCHYRDFIPGVAIAANIHHGFHKSRYIVVVSQHFQSRMCIFEX 720
QY 752 EIAQTWQPLSSRAGIIFIVLQKVEKTLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
DB 721 EIAQTWQPLSSRAGIIFIVLQKVEKTLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNMPEGTGTGCMWQCATSI 839
DB 781 RKALLDGKSNMPEGTGTGCMWQCATSI 808
RESULT 12
ID ADO57803 standard; protein; 808 AA.
XX
XX ADO57803;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Chimpanzee toll-like receptor 4 SEQ ID NO:24.
DE
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
XX Pan troglodytes.
OS
XX
XX MO2004042365-A2.
PN
XX
XX 21-MAY-2004.
PD
XX
XX 03-NOV-2003; 2003WO-US036247.
PF
XX
XX 01-NOV-2002; 2002US-0423113P.
PR
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
PA
XX
XX Messier W;
PI
XX
XX MPI: 2004-400726/37.
DR
XX N-PSDB; ADO57801, ADO57802.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 24; 11bp; English.
PS
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey

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comprising comparing the TLR4 polynucleotide sequence of the Old World monkey with corresponding TLR4 polynucleotide sequence of a human. The method of the invention has antibacterial, immunosuppressive, and antiaesthetic activity. The method is useful in identifying a nucleotide change in a TLR4 polynucleotide sequence of an Old World monkey where the change may be associated with reduced sensitivity to Gram-negative bacterial infection. The methods, agents and composition are useful in treating sepsis, severe sepsis or septic shock and asthma. The present sequence represents chimpanzee TLR4.

Sequence 808 AA;

Query Match 95.6%; Score 4164; DB 8; Length 808;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 803; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 32 VVPNTTYOCMEINFKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLSRCEIQ 91
DB 1 VVPNTTYOCMEINFKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLSRCEIQ 60
QY 92 TIEDGAYOSLSHSLITLTGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHUKT 151
DB 61 TIEDGAYOSLSHSLITLTGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHUKT 120
QY 152 LKEILNVAHNLIQSFYKPEYFSNLTNLEHLDLSSNKIQSYCTDRLVHQPMLNLSLDS 211
DB 121 LKEILNVAHNLIQSFYKPEYFSNLTNLEHLDLSSNKIQSYCTDRLVHQPMLNLSLDS 180
QY 212 LNPMPFIOPGAFKEIRLHKLTIRNPNDSLNVMKTCIOGLAGLEVHRLVGEFRNENLEK 271
DB 181 LNPMPFIOPGAFKEIRLHKLTIRNPNDSLNVMKTCIOGLAGLEVHRLVGEFRNENLEK 240
QY 272 FDKSALBEGLCNLTIEFRFLAYDYLDIIDLFNCLTNVSSPSLVTERKYDESYNFG 331
DB 241 FDKSALBEGLCNLTIEFRFLAYDYLDIIDLFNCLTNVSSPSLVTERKYDESYNFG 300
QY 332 WQHELVNCKFGQFPPLTKLSIKRLTFTSNKGNAPSEVDLPLEFLDLSRNGLSFKGCC 391
DB 301 WQHELVNCKFGQFPPLTKLSIKRLTFTSNKGNAPSEVDLPLEFLDLSRNGLSFKGCC 360
QY 392 SOSDGTTSIKYLDLSPNCGVITMSSNFGLEQLEHLDPOHSLKQMSSESVLSLRNLY 451
DB 361 SOSDGTTSIKYLDLSPNCGVITMSSNFGLEQLEHLDPOHSLKQMSSESVLSLRNLY 420
QY 452 LDISHTHTRVAFNGIFNGLSLEVLMAGNSFOENFLPDIFELRNLTFLDLSQOCLEOL 511
DB 421 LDISHTHTRVAFNGIFNGLSLEVLMAGNSFOENFLPDIFELRNLTFLDLSQOCLEOL 480
QY 512 SEPTAENSLSLQVLNMSHNNPFLDTPPYKCLNSLQVLDYSLNHIMTSKKQELQHPSSL 571
DB 481 SEPTAENSLSLQVLNMSHNNPFLDTPPYKCLNSLQVLDYSLNHIMTSKKQELQHPSSL 540
QY 572 AFLNLTQNDFACTCHQSFLOWIKQORQLLVEVERNECTPBDKQMPVLSNITTCQNMK 631
DB 541 AFLNLTQNDFACTCHQSFLOWIKQORQLLVEVERNECTPBDKQMPVLSNITTCQNMK 600
QY 632 TIGGSVSVLVVAVVAVVYKFFPHMLLAGICIKYRGENTYDAFAVYSSODEBVRNE 691
DB 601 TIGGSVSVLVVAVVAVVYKFFPHMLLAGICIKYRGENTYDAFAVYSSODEBVRNE 660
QY 692 LVKNLEBGPFPOLCLHVRDPIPGVAIAANIIEGHFHSRKVIIVVSGHFISQRMCIPEY 751
DB 661 LVKNLEBGPFPOLCLHVRDPIPGVAIAANIIEGHFHSRKVIIVVSGHFISQRMCIPEY 720
QY 752 ELAQWQPLSSRAGIIFIVLQVVEKTLRQOVELRRLSRNLYLEBEDSVLGRHIFWRRL 811
DB 721 ELAQWQPLSSRAGIIFIVLQVVEKTLRQOVELRRLSRNLYLEBEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNPEGTGTCNMQOATS 839
DB 781 RKALLDGKSNPEGTGTCNMQOATS 808

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RESULT 13

AAW86352 standard; protein; 799 AA.

AAW86352;

15-MAR-1999 (first entry)

Human DNAX toll-like receptor DTLR4.

DNAX toll-like receptor; DTLR4; Drosophila toll receptor; IL-1 receptor; interleukin 1 receptor; phosphate metabolism; innate immunity response;

modulate inflammatory function; morphological effect;

immunological disorder.

Homo sapiens.

MO9850547-A2.

12-NOV-1998.

07-MAY-1998; 98WO-US008979.

07-MAY-1997; 97US-0044293P.

22-JAN-1998; 98US-0072212P.

05-MAR-1998; 98US-0076947P.

(SCHE) SCHERING CORP.

Hardiman GT, Rock FL, Bazan JF, Kastelein RA;

WPI, 1999-059670/05.

N-PsDB; AAV80666.

Human DNAX toll-like receptor, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate immunity response.

Example; Page 115-117; 171pp; English.

The present invention specifically describes human DNAX toll-like receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate immunity responses or morphological effects. The DTLR proteins can be used in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. These abnormalities are typically manifested by immunological disorders

Sequence 799 AA;

Query Match 95.1%; Score 4141; DB 2; Length 799;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 41 MELNFKYKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLSRCEIQTEDGAYOS 100
DB 1 MELNFKYKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLSRCEIQTEDGAYOS 60
QY 101 LSHSLTLLTGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHUKTKEILNVAH 160
DB 61 LSHSLTLLTGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHUKTKEILNVAH 120
QY 161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSYCTDRLVHQPMLNLSLDSINPMPFIOP 220
DB 121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSYCTDRLVHQPMLNLSLDSINPMPFIOP 180
QY 221 GAFKEIRLHKLTIRNPNDSLNVMKTCIOGLAGLEVHRLVGEFRNENLEKFDKALBGL 280

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Db 181 GAFKEIRLHKLTLRNNFDSLVNWKTCIOGLAGLEVHRLVJGEPFRNEGULEKFDKSALEGL 240
Qy 281 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 340
Db 241 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 300
Qy 341 KFGQFPTLKLSKRLTFTSNKGNAGFSEVDLPSEFLDLSRNGLSFKGCCOSDPGTT 400
Db 301 KFGQFPTLKLSKRLTFTSNKGNAGFSEVDLPSEFLDLSRNGLSFKGCCOSDPGTT 360
Qy 401 LKYLDLSFNGVITWSSNFIJGLEHLDFOHNSNKQSESVFSLRNLIYLDISHTTR 460
Db 361 LKYLDLSFNGVITWSSNFIJGLEHLDFOHNSNKQSESVFSLRNLIYLDISHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCLEOLSPFAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCLEOLSPFAFNLS 480
Qy 521 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNLTQND 580
Db 481 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNLTQND 540
Qy 581 FACTCEHOSFLOWIKDQROLVVEVERMECATPSPDKQMPVLSNITCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWIKDQROLVVEVERMECATPSPDKQMPVLSNITCOMNKTIIIGSVLS 600
Qy 641 VLAVSVAVLVYKFFHMLLAGCICKYRGENIYDAFIYSSQEDWVRNLELVNLEEGV 700
Db 601 VLAVSVAVLVYKFFHMLLAGCICKYRGENIYDAFIYSSQEDWVRNLELVNLEEGV 660
Qy 701 PPFOCLAHYRDPFIPGVALAANIIEHGFHKSRRVIVVVSQHFIOGRWCIFEYELAQWQFL 760
Db 661 PPFOCLAHYRDPFIPGVALAANIIEHGFHKSRRVIVVVSQHFIOGRWCIFEYELAQWQFL 720
Qy 761 SSRGIIIFIVYQXVEKTLRQOVELYRLSNTYLEWEDSVLGRHIFRRRLKALLDQKS 820
Db 721 SSRGIIIFIVYQXVEKTLRQOVELYRLSNTYLEWEDSVLGRHIFRRRLKALLDQKS 780
Qy 821 WNPGETVGTGCMQOATS 839
Db 781 WNPGETVGTGCMQOATS 799

RESULT 14
AAE16093
ID AAE16093 standard; protein; 799 AA.
XX
AC AAE16093;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTRLR) 4 #1.
XX
KW Human; DNAX Toll like receptor; DTRLR; therapy; immunological disorder;
XX
OS Interleukin 1; Il-1; screening; immunomodulator; chromosome 9q32-33.
XX
XX Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DR N-PSDB; AAD26283.
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XX New DNAX Toll like receptor (DTRLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 1; Page 35; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTRLR) protein and their corresponding
CC nucleic acids. The DTRLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTRLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTRLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTRLR or its various fragments. The
CC purified DTRLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTRLR or cells that express it. The present sequence is
CC human DTRLR4 protein. The DTRLR4 gene is located on chromosome 9q32-33
CC
XX
SQ Sequence 799 AA;
Query Match 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 MELNFYKIPNLPSTKNDLSFNPRLHLSYSFSPPELOVLDLSRCEIQTIEDGAYOS 100
Db 1 MELNFYKIPNLPSTKNDLSFNPRLHLSYSFSPPELOVLDLSRCEIQTIEDGAYOS 60
Qy 101 LSHSTLILGNPQISALAFSGLSLQCLVAVETMLASLENPFIHKLTKELNVAHN 160
Db 61 LSHSTLILGNPQISALAFSGLSLQCLVAVETMLASLENPFIHKLTKELNVAHN 120
Qy 161 LIOSFKLPEYFSNNTNLEHDLSENKIOSIYCTDRLYLHQMPLNLTSLDLSLNPMTIOP 220
Db 121 LIOSFKLPEYFSNNTNLEHDLSENKIOSIYCTDRLYLHQMPLNLTSLDLSLNPMTIOP 180
Qy 221 GAFKEIRLHKLTLRNNFDSLVNWKTCIOGLAGLEVHRLVJGEPFRNEGULEKFDKSALEGL 280
Db 181 GAFKEIRLHKLTLRNNFDSLVNWKTCIOGLAGLEVHRLVJGEPFRNEGULEKFDKSALEGL 240
Qy 281 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 340
Db 241 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 300
Qy 341 KFGQFPTLKLSKRLTFTSNKGNAGFSEVDLPSEFLDLSRNGLSFKGCCOSDPGTT 400
Db 301 KFGQFPTLKLSKRLTFTSNKGNAGFSEVDLPSEFLDLSRNGLSFKGCCOSDPGTT 360
Qy 401 LKYLDLSFNGVITWSSNFIJGLEHLDFOHNSNKQSESVFSLRNLIYLDISHTTR 460
Db 361 LKYLDLSFNGVITWSSNFIJGLEHLDFOHNSNKQSESVFSLRNLIYLDISHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCLEOLSPFAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCLEOLSPFAFNLS 480
Qy 521 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNLTQND 580
Db 481 SLOVLANSHNNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSLAFLNLTQND 540
Qy 581 FACTCEHOSFLOWIKDQROLVVEVERMECATPSPDKQMPVLSNITCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWIKDQROLVVEVERMECATPSPDKQMPVLSNITCOMNKTIIIGSVLS 600
Qy 641 VLAVSVAVLVYKFFHMLLAGCICKYRGENIYDAFIYSSQEDWVRNLELVNLEEGV 700
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Db 601 VLVVSVAVLVYKFFHMLLAGCIKYGGENITYAPFVYSQDEDMWRNELVKNLEBKV 660
Qy 701 PPOLCLHYRDFIPGVAIAANIIEGPHKSRKVIIVVSQHFIOSRWCIFEYEIAQTWQFL 760
Db 661 PPOLCLHYRDFIPGVAIAANIIEGPHKSRKVIIVVSQHFIOSRWCIFEYEIAQTWQFL 720
Qy 761 SSRAGIIFIVYQKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFRRRLKALLDGS 820
Db 721 SSRAGIIFIVYQKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFRRRLKALLDGS 780
Qy 821 WNPBGVGTGCMQOATSI 839
Db 781 WNPBGVGTGCMQOATSI 799
RESULT 15
ABB83162
ID ABB83162 standard; protein; 799 AA.
AC ABB83162;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human Toll-like receptor-4, Tlr4.
XX
KW Human; vitucide; antibacterial; fungicide; parasiticide; receptor;
KW cytosolic; immunostimulatory; scavenger receptor; Toll receptor;
KW respiratory tract infection; Toll-like receptor; Tlr4.
XX
OS Homo sapiens.
XX
PN WO200235236-A1.
XX
PD 02-MAY-2002.
XX
PE 26-OCT-2001; 2001WO-FR003352.
XX
PR 27-OCT-2000; 2000FR-00013883.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Jeanm P, Magistrel J G, Herbault N, Bonnefoy J;
XX
DR WPI; 2002-383586/41.
DR N-PSDB; AEN83318.
XX
PT Identifying agent that binds to scavenger receptors and signals through a
PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
PT cytotoxic T cell response.
XX
PS Disclosure; Page 58-60; 71pp; French.
XX
CC The present invention relates to a method for identifying new therapeutic
CC compounds (I) by selecting molecules that bind to scavenger receptors and
CC signal through a Toll receptor. The present sequence is the protein
CC sequence for human Toll-like receptor-4, Tlr4, which was used to
CC illustrate the method of the invention. (I) are useful as carriers and/or
CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC tumour cell, especially a pathogen that causes respiratory tract
CC infection, also more generally for inducing an immune response. (I) can
CC also be used for specific targeting of active agents (antigens etc.) to
CC antigen-presenting cells (especially immature dendritic cells), for
CC subsequent internalisation by these cells
XX
SQ Sequence 799 AA;
Query Match 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MELNPKIPDNL PSTKLDLSFNPDLRLGSGSPFPELOVLDLSRCEIOTIEDGAVOS 60
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Db 61 LSHSTLLITGNPDIOSLALGAFSGLSLOKLVAVETNLASLENPFIHKLTKELVANHN 120
Qy 161 LIOSFKLPEYNSNLTNLEHDLSSNKIOSICTDILRVLHQPPLNLSDLSINPMNFIOP 220
Db 121 LIOSFKLPEYNSNLTNLEHDLSSNKIOSICTDILRVLHQPPLNLSDLSINPMNFIOP 180
Qy 221 GAFKEIRLHKLTNNPESLVMKTCIOGLAGVHRVTLGEPFREGLEKPKALGL 280
Db 181 GAFKEIRLHKLTNNPESLVMKTCIOGLAGVHRVTLGEPFREGLEKPKALGL 240
Qy 281 CNLTIEEPRLAYLDYDDIDILFNCLTNVSSFSIVSTIRVDFSNFGHLELVNC 340
Db 241 CNLTIEEPRLAYLDYDDIDILFNCLTNVSSFSIVSTIRVDFSNFGHLELVNC 300
Qy 341 KFGQPTLKLSLRLETNSKGNAPSEVDLPSEFLDLSRNGISFGCCSQSDPGTTS 400
Db 301 KFGQPTLKLSLRLETNSKGNAPSEVDLPSEFLDLSRNGISFGCCSQSDPGTTS 360
Qy 401 LKYLDLSFNGVITWSSNPLGLEOLEHDPQHSNKKQSEFVSFLRNLIVLDSHTTR 460
Db 361 LKYLDLSFNGVITWSSNPLGLEOLEHDPQHSNKKQSEFVSFLRNLIVLDSHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSPOENFLPDIETELRNLTFFDLSCQLEQSPFAFNSLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSPOENFLPDIETELRNLTFFDLSCQLEQSPFAFNSLS 480
Qy 521 SLOVLNMSHNNPESLDTFPYKCLNSLOVLDYSLNHNMTSKQOELQHPSSIAFLNLTOND 580
Db 481 SLOVLNMSHNNPESLDTFPYKCLNSLOVLDYSLNHNMTSKQOELQHPSSIAFLNLTOND 540
Qy 581 FACTCEHOSFLOWKDORQLVEVERMECAPSPDQGPVJSLNTCOMNKTIIISVATLS 640
Db 541 FACTCEHOSFLOWKDORQLVEVERMECAPSPDQGPVJSLNTCOMNKTIIISVATLS 600
Qy 641 VLVVSVAVLVYKFFHMLLAGCIKYGGENITYAPFVYSQDEDMWRNELVKNLEBKV 700
Db 601 VLVVSVAVLVYKFFHMLLAGCIKYGGENITYAPFVYSQDEDMWRNELVKNLEBKV 660
Qy 701 PPOLCLHYRDFIPGVAIAANIIEGPHKSRKVIIVVSQHFIOSRWCIFEYEIAQTWQFL 760
Db 661 PPOLCLHYRDFIPGVAIAANIIEGPHKSRKVIIVVSQHFIOSRWCIFEYEIAQTWQFL 720
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Qy 821 WNPBGVGTGCMQOATSI 839
Db 781 WNPBGVGTGCMQOATSI 799

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Job time : 90.4 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds

(without alignment)
2715.523 Million cell updates/sec

Title: US-09-396-985B-98

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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	629.5	14.5	661	1	Sequence 4, Appli
3	629.5	14.5	661	1	Sequence 4, Appli
4	599.5	13.8	784	4	Sequence 23, Appli
5	539	12.4	775	4	Sequence 8799, Ap
6	316	7.3	605	3	Sequence 5, Appli
7	305	7.0	605	3	Sequence 10995, A
8	303	7.0	605	3	Sequence 49, Appli
9	303	7.0	605	3	Sequence 49, Appli
10	303	7.0	605	3	Sequence 49, Appli
11	303	7.0	605	3	Sequence 49, Appli
12	303	7.0	605	3	Sequence 49, Appli
13	299.5	6.9	662	4	Sequence 1355, Ap
14	299.5	6.9	662	4	Sequence 6619, Ap
15	299.5	6.9	662	4	Sequence 10710, A
16	299	6.9	662	4	Sequence 10710, A
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21	296	6.8	603	1	Sequence 2, Appli
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23	292.5	6.7	907	4	Sequence 50, Appli
24	292.5	6.7	907	4	Sequence 50, Appli
25	289.5	6.6	1112	3	Sequence 264, App
26	289	6.6	1529	3	Sequence 278, App
27	286	6.6	1112	3	Sequence 396, App

28	285	6.5	1523	3	US-09-182-024A-2	Sequence 2, Appli
29	283.5	6.5	1166	4	US-10-101-464A-900	Sequence 900, App
30	281	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
31	278	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
32	275	6.3	620	4	US-09-907-794A-73	Sequence 73, Appli
33	275	6.3	620	4	US-09-905-125A-73	Sequence 73, Appli
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45	271	6.2	1139	4	US-09-513-505-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1	US-09-949-016-9438	Sequence 9438, Application US/09949016	Patent No. 6812339
GENERAL INFORMATION:	APPLICANT: VENTER, J. Craig et al.	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/237,768	PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768	PRIOR FILING DATE: 2000-10-03	PRIOR APPLICATION NUMBER: 60/231,498	PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012	SOFTWARE: FASTSEQ for Windows Version 4.0	SEQ ID NO 9438	LENGTH: 844
TYPE: PRT	ORGANISM: Human	US-09-949-016-9438	Query Match
Best Local Similarity 100.0%; Pred. No. 0;	Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Score 4197; DB 4; Length 844;	96.4%;
31 EVVNITTYQCEMLNFKYIPDNLPSTKNLDSFNPRLHLSGSPFPELOVLSRCEI 90	=====	=====	=====
36 EVVNITTYQCEMLNFKYIPDNLPSTKNLDSFNPRLHLSGSPFPELOVLSRCEI 95	=====	=====	=====
91 QTIDGAYQSLSTLILGNPIQSLALGAFSGLSLQKVAAYETNLSLENPIGHLK 150	=====	=====	=====
96 QTIDGAYQSLSTLILGNPIQSLALGAFSGLSLQKVAAYETNLSLENPIGHLK 155	=====	=====	=====
151 TLKEINVAHNLIOGFKPEYPSNLTNLEHLDSSNKLQSIYCTDLRVLHQMPLNLSIDL 210	=====	=====	=====
156 TLKEINVAHNLIOGFKPEYPSNLTNLEHLDSSNKLQSIYCTDLRVLHQMPLNLSIDL 215	=====	=====	=====
211 SLNPMNFIQGAPEIRLHKITLNNPDSLVNMTCTIQGLAGLEVHRLVIGEPNENGL 270	=====	=====	=====
216 SLNPMNFIQGAPEIRLHKITLNNPDSLVNMTCTIQGLAGLEVHRLVIGEPNENGL 275	=====	=====	=====
271 KFDSSALEGCLNLTIEFRILAYLDYDDIILFNCLTNVSSPSLVSTIERVDFSYNF 330	=====	=====	=====
276 KFDSSALEGCLNLTIEFRILAYLDYDDIILFNCLTNVSSPSLVSTIERVDFSYNF 335	=====	=====	=====
331 GWOHLIELVNCCKFGPPTLKLSLRLTFTSNKGNNAFSEVDLPSELEFLDSRNGLSPKXG 390	=====	=====	=====

DB 336 GCHQHELVNCKRQGFPTLKLKSLKRLTFTSNKGNKAFSEVDLPSEFLDLSTRNGLSFKGC 395
QY 391 CSQSDFGTTSKLYLDSFNGVITMSSNPLGEBOLHLDPOHSLTKOMSESVLSLRNLI 450
DB 396 CSQSDFGTTSKLYLDSFNGVITMSSNPLGEBOLHLDPOHSLTKOMSESVLSLRNLI 455
QY 451 YLDSHTHTRVAVNGIFNGLSLEVLKMGNSFOENPLPIFTELNLTLFLDLSQCOLBQ 510
DB 456 YLDSHTHTRVAVNGIFNGLSLEVLKMGNSFOENPLPIFTELNLTLFLDLSQCOLBQ 515
QY 511 LSPFTANSLSSLOVLMNSHNPFSLDTFPYKCLNSLOVDLSLNHIMTSKKQELQHPPSS 570
DB 516 LSPFTANSLSSLOVLMNSHNPFSLDTFPYKCLNSLOVDLSLNHIMTSKKQELQHPPSS 575
QY 571 LAFNLNTONDFACTCEHOSFLQWIKQOROLLVEVERMECATPSDKQMPVLSLNTICQMN 630
DB 576 LAFNLNTONDFACTCEHOSFLQWIKQOROLLVEVERMECATPSDKQMPVLSLNTICQMN 635
QY 631 KTIIGSVLSVAVSVAVLVYKFFPHMLLAGCIKRGENTYDAFVYSODEDVPVRN 690
DB 636 KTIIGSVLSVAVSVAVLVYKFFPHMLLAGCIKRGENTYDAFVYSODEDVPVRN 695
QY 691 ELVKNLEEGVPFQOLCHYRDFIPGVAIAANIIEGPHKSRKVIIVVSOHFISRWCFE 750
DB 696 ELVKNLEEGVPFQOLCHYRDFIPGVAIAANIIEGPHKSRKVIIVVSOHFISRWCFE 755
QY 751 YELAQWQPLSSRAGIIFIVLOKVEKTLRQOVELYLLSRNTYLEMDEVSLGRHITWR 810
DB 756 YELAQWQPLSSRAGIIFIVLOKVEKTLRQOVELYLLSRNTYLEMDEVSLGRHITWR 815
QY 811 LKRALDGSKNPEGTGTCNMQOATS1 839
DB 816 LKRALDGSKNPEGTGTCNMQOATS1 844

RESULT 2

US-08-514-014-4
Sequence 4, Application US/08514014
Patent No. 5707829
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-014-4

Query Match 14.5%; Score 629.5; DB 1; Length 661;
Best Local Similarity 29.7%; Pred. No. 5,3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

QY 25 SNEP-CVEVVPNTTQOCMELNPKYKIDPNLPSTKNULDSFNLBRHGSVSFPPELOVY 83
DB 23 SMDWCIEKBAKTYNCENLGLSELPDTPNTELEFSFNLPPIHNTFSRLANUTL 82
QY 84 DLSRCEIQTIEDGAYOSLSLSTLITGNPIOSLALGAFSGLSLOKLAVALNETNASLEN 143
DB 83 DLTRQIMNHEDTPSHHQOLSTLVLTGNPLIFMETSINGRPSLHGLFLIGISNLER 142
QY 144 FPIGHLKTIKEINVAHNLIQSEKLPYFESNLTNLEHLDSNKLQSIYCTDLRVLHOMPL 203
DB 143 IPVHNLENLESYLGSNHSISIKFPDPF-ARNLKVLDFQNNAIHYSISREDMKSLBO-A 199
QY 204 LNLSDLSLNPKNFIPQCAFKELRLHKLTLRNNPDSLVNWKTCIOGLAGLEVRLVYGEF 263
DB 200 INLSLNFNGNNAVIGILGADSTVFOSL---NFGGPNLSVIFNGLONSTTOSLMLGT 255
QY 264 RNEGNLEKEDKALIEGLCNLTIEFRLAYLDYLDIID-LFNCLTNVSSFSLSVATIER 322
DB 256 EDIDD-EDISSANLKLCEMSVESLMLQ--EHRFSDISSSTFFQCFPOLELDLTATHLKG 312
QY 323 VKDFSNFGQHLIELVN-----CKF--GQFPLT-----KLSLRLLPFTSN 361
DB 313 LPS-----GWKGLNLKLVLSVNHFDOLCOLSAANFPSTLHLYIRGNVKKHLGVGLE 367
QY 362 KGNNAFSEVDLPSEFLDLSTRNGLSFKGCQSDFGTTSKLYLDSFNGVITMSSN-FLG 420
DB 368 KLGN-----LQTLDSHNDIEASDCCSLQKLSHQTLNLSINEPLGLQSQAFKE 418
QY 421 LEQLEHLDFQ-----HSNLKOMSEFS--VPLSLNRLY--LDISHTHTRVAVNGIFNGLS 472
DB 419 CPQLEHLDLAFTLHINAPQ-SFPQNLHFLQVNLTFYCFDTSNOH-----LAGLAPV 470
QY 473 LEVLRKAGNSFOENPL--PDIFTELNLTLFLDLSQCOLBOLSPAFNLSLSLOVLMNSH 530
DB 471 LRHLNKGNHFOGTITKTMLQTVGSLLEVLISSCOLSIDOAFSLKMSHVDLSH 530
QY 531 NFP--SLDTPPY-----KCLNSLOVLDLSLNHIMTSKKQELQHPPSLAFNLNTONDF 581
DB 531 SLTCDSTDSLHKLGIYLNLAANSINITSPRLPIL-----SQOSTNLSHNPL 579
QY 582 ACTCEHOSFLOWIKQOROLLVEVERMECATPSDKQMPVLSLNTICQMNKTIIGSVLSV 641
DB 580 DCTCSNHLFTWKENHLKRGSEETTCANPRLRGVGLDVKLSGCI--TAIGIFPLIV 637
QY 642 LVSVAVLVY 652
DB 638 FIL-LIALLLF 647

RESULT 3

US-08-833-823-4
Sequence 4, Application US/08833823
Patent No. 5969093
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 14.5%; Score 629.5; DB 2; Length 661;
Best Local Similarity 29.7%; Pred. No. 5.3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CVEVVPNTYQCEMELNFYKIPDNLPRSTKNLDSFNPRLHLSYSFSPPELOVL 83
23 SWDMCIEKEANKTYNCENLGLSEIPDLPTTEFLERFEPFLTIHNRTPSRMLNLTFL 82
84 DLSRCEIQTIEDGAYQSLSHSTLILTGNPISLALGAFSGSLSLQVLAVETNLASLEN 143
83 DLTRCQNMWIEDTFQSHHQLSTVLVTGNPLIFMAETSLNPKSLKHLFIQTGISNLEF 142
144 FPIGLKTLKELNVAHNLIOFVKLPEYFSNLTNLEHDLSSNKISQIYCTDLRYLHQMPL 203
143 IPIVNNLENTSLVYGSNHSISIKRPPRP-ARNLKVLDPQNNALHYISREMBLEQ-A 199
204 LNLSDLSLNPWFIOGAFKEIRLHLKLTNNPDSLNVMKTCIOGLAGLEVHRLVIGEF 263
200 INLSLNFNGNNAKIEIGAFDSVTFQSL---NFGTNPNLSEVINGLQNSTTQSLMIGTF 255
264 RNEGNLEKFKSALLEGICNLTEEFRLAYLDYDDIID-LFNLCLTVSSSLVSITIER 322
256 EDIDDD-EDISSAMKGLCEMSVESLNQ--EHRPSDISSTTFQCFIQLQELDLATYHKG 312
323 VKDFSVNFGQHLLELVN-----CKF--GPFPTL-----KLKSLKLTFTSN 361
313 LPS-----GKGLNLKLKVLVSVNHPDLCQISANPSPSLHLYIRGNVKKLHGVGCL 367
362 KGNNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDFGTSLKYDLSPNGVITMSSN-FLG 420
368 KLGK-----LQTLDSLHNDIEASDCSLQKLNLSHLQTLNLSHNEPLGLQSAFKE 418
421 LEOLEHDPQ-----HSLMKQMSERS--VFLSLRLIY--LDISTHTRVAFNGIFNGLS 472
419 CPQLEHLDLAFRLHINAPQ--SPQNIHFQVLNLTVCFLDTSNQ-----LLAGLPV 470
473 LEVLKMAAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLSEOLSPAFNLSLSIQLVANN 530
471 LRHLNKGNNHQQDGTIKTNLQVGSLEVLILSSCGSLSDQGAHFSLSGMSHVDLSHN 530
531 NFF--SLDTIPPY-----KCLNSLQVLDVSLNHNMTSKOELQHPSPSLAFLNLTONDF 581

531 SLTCDSDISLSHLKGIYLNIAANSINITISPRLLPIL-----SQOSTNLNSHPL 579
582 ACTCEHOSFLOWIKDQRLVVEVERMECAPSPDQKMPVLSTNTQNNKIIIGSVLSV 641
580 DCTCSNIHFLTWYENHAKLEGSEBETTCANPPIRGVLSVYKLSGCI--TAIGIFLIV 637
642 LVSVVAVLVY 652
638 FLT-LTALILF 647

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Iundell, Daniel
APPLICANT: Iunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavodny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: JB0601QC
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 13.8%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 4.1e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPRSTKNLDSFNPRLHLSYSFSPPELOVLDSRCEIQTIEDGAYQSLSHSTL 107
46 IPSGLEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSGINTFIEDSFSSLSLEHL 105
108 ILTGNPISLALGAFSGSLSLQVL-----VAVETNLASLENPPIGLKLT----- 151
106 DLSVNTSLNLSGMSFKLSLTLPLNLGNYKTLGERSLSLHLTKQDLIRGNNDITPKI 165
152 -----LKELVANHLIOFVKLPEYFSNLTNLEHDLSSNK-----IQSI 190
166 QKQDFAGLTLELEIDASDLQSYE--PKSLKIQNVSHLILHMKQHLILEIFVDTVSSV 224
191 YCTDLRYLHQMPLNLSDLSLNPWF--IQGAFKEIRLHLKLTNR--NFDL-NVMK 244
225 ECLLELR-----DIDLDTFHFSELSSTGTSNL-IKKTFRVNKTDESDFQVMK 271
245 TC--IQGLAGLEVHRLV-----GEFRNNGNLEKFKSALLEGICNLTEEFRLA--YLDYVL 297
272 LNLGISGLLELEPDDCTLNGVGNFRASDNRRVIDPGKVE--TLTIRRHIPRYLVY-- 326
298 DDIIDLFNCLTNVSSRSLSVTTIERVQDFSYNFGQHLLELVNCKFGQFPYLKLSLRKT 357
327 -DLSTLYSLTERVK-----RITVNSKVF-----LVPCLLSQ----- 357
358 FTSNKGNAFSEVDLPSEFLDLSRNL-----GLSPKCCSQSDFGTSLKYDLSPNGVI 412
358 -----HLNSLETLDSLENLMAVEYLNKNSAC-----EDAWPSTQTLILIRON--- 397

QY 93 IEDAYOSLSHSLTILITGNPIQSIALGAFS-----GLSSL 128
DB 113 LEPOLAGLENI,CHLHRLNOLRSI,AVGTFAITPALALL,IGLSNNRLSRLDEGLFEGISLNL 172
QY 129 OKUAVETNLASLENPIGHLKTKELVANHL,IOSFLPEYFSNLTNLEHDLSSNKIQ 188
DB 173 WDLNIGNSLAVLPAAFRGLGGLRELVLAGNRL-AYIQALFSGLAELRELDLSRNALR 231
QY 189 SIYCTDLRVLHQPMLNLSLDSLNPMNFIOGAFKEIR-LHKLTLRNNFDSLNVKTCI 247
DB 232 AI-----KANVFAQLPRLQ-KLYIDRLN,IAVAPGATLGKALRWLDLSHN-RVAGLLEDTF 286
QY 248 OGAGLEVRHVLGFEFRNEGNLEKFDKALBGLCNLTIEFRFLAYLDYIDLDIENCL 307
DB 287 PGLGLRRLRL-----SHNAIASLRPFEDL-----HFLEEL----- 319
QY 308 TNVSFSLVSTIEVKDPSYNGWQHLELVNCKFGQFPLTKLSIKRLTFTS--NKGN 365
DB 320 -----QLGHNRIROLAERSFE-GLGQLEVLTLDNQLOEVKVGFLGLTNVAVNLSGN 372
QY 366 AFSEVDLPSEFLDLSR-NGLSFKGCC-----SOSDFGTSIKYDLSFNGVITWSSNPL 419
DB 373 CLR--NLPEQVFRGLKLSHLBSSCLGRIRPHFTAGLSGLRRLFLKDNGLVGEBSL 430
QY 420 -GLEOLEHLDPOHSNKKOMSEPSVFLSLRLIYLDISHTTRVAFNGIFNGLSLEVLKM 478
DB 431 WGLLELLELDLTSNOL-----THLP--HQLFOGLKLEYLL 465
QY 479 AGNSFOENFLP-DIFTELRLNLFELDLSOCOLBOLSPFAFNSLSLOVNMSSNNFSLDT 537
DB 466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEALPGLSLASGRIRYLNLRN--SLRT 520
QY 538 PPKYCLNSLOVLDYSLNHTMSKKOELHFPSSLAFLNLTONDFACTCEHOS----- 589
DB 521 FTPO-----PGLERLWLEGNPMWCSCPLALRDPALON 554
QY 590 -----FLQWT--XDRQLVEVERMECATPSDKQMPVLST 623
DB 555 PSAVPRFVOALCEGDDCQPPVYTYNNITCASPEEVAAGLDRLD 597

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Query Match 7.0%; Score 305; DB 4; Length 623;
Best Local Similarity 24.3%; Pred. No. 4.4e-19;
Matches 171; Conservative 96; Mismatches 260; Indels 178; Gaps 28;

QY 4 ASRLA---GTLIPMAFLSCVR--PESME-----PCV-----EVVPVIT 37
DB 16 ACRWALRKGLALAILLISLWVALGRPSLEGADPGTGGABEGPACPAACVCSYDDADELS 75

QY 38 YQCELNLFYKIPDNLPESTKNLDSFNELRHLSYSPFSPELOVLDSRCEIQTIEDGA 97
DB 76 VFCSSRNLTLPDGVPGGTQALMTLDGNNLSVPPAAFAFNLSLGLFNIGGQGLSLEPOA 135
QY 98 YQSLSHSLTILITGNPIQSIALGAFS-----GLSSIQKVA 133
DB 136 LIGLENLCHLHRLNOLRSI,AVGTFAITPALALL,IGLSNNRLSRLDEGLFEGISLMDLNL 195
QY 134 VETNLASLENPIGHLKTKELVANHL,IOSFLPEYFSNLTNLEHDLSSNKIQSIYCT 193
DB 196 GNSLAVLPDAAPRGLSRLVLVLAGNRL-AYIQALFSGLAELRELDLSRNALRAI--- 251
QY 194 DLRYLHQPMLNLSLDSLNPMNFIOGAFKEIR-LHKLTLRNNFDSLNVKTCIQIAG 252
DB 252 KANVFAQLPRLQ-KLYIDRLN,IAVAPGATLGKALRWLDLSHN-RVAGLLEDTFPGLLG 309
QY 253 LEVRHVLGFEFRNEGNLEKFDKALBGLCNLTIEFRFLAYLDYIDLDIENCLTNVSS 312
DB 310 LRVLR-----SHNAIASLRPFEDL-----HFLEEL----- 337
QY 313 FSLVSTIEVKDPSYNGWQHLELVNCKFGQFPLTKLSIKRLTFTS--NKGNAPSEV 370
DB 338 -QLGHNRIROLAERSFE-GLGQLEVLTLDNQLOEVKVGFLGLTNVAVNLSGNCLR-- 393
QY 371 DLPSEFLDLSR-NGLSFKGCC-----SOSDFGTSIKYDLSFNGVITWSSNPL-GLEQ 423
DB 394 NLPEQVFRGLKLSHLBSSCLGRIRPHFTAGLSGLRRLFLKDNGLVGEBSLGLAE 453
QY 424 LEHLDPOHSNKKOMSEPSVFLSLRLIYLDISHTTRVAFNGIFNGLSLEVLKMAAGSF 483
DB 454 LLELDLTSNOL-----THLP--HQLFOGLKLEYLLLSRRL 488
QY 484 QENFLP-DIFTELRLNLFELDLSOCOLBOLSPFAFNSLSLOVNMSSNNFSLDTFPYKC 542
DB 489 AE--LPADALGPLQRAFWLDVSHNRLEALPGLSLASGRIRYLNLRN--SLRTFTQ- 542
QY 543 LNSLOVLDYSLNHTMSKKOELHFPSSLAFLNLTONDFACTCEHOSFLQWKD----- 596
DB 543 -----PGLERLWLEGNPMWCSCPLALRDPALON 573

QY 597 ---ORQLVEVERMECATPSDKQMPVLSTITOMAKTITIGSV 638
DB 574 SAVPRFVOALCEGDDCQPPVYTYNNITCASPEEVAAGLDRLD 612

RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; FILE REFERENCE: Thereof
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 265
; ADDRESS: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 7.0%; Score 303; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFKYKIDNLPSTKNDLSFNPRLHLSYSFSPPELQVLDLSRCEIQTEDGAYQ 99
DB 60 CSSRNLTRLDPGVGGTQALWLDGNLSSVPPAFAQNLSSGLFNLQGGQLSLEPQALL 119
QY 100 SLSHLSTLITGNPIQSIALGAFS-----GLSLQKLVAVE 135
DB 120 GLENLCHLHERNQRLSLAGTFAHTPALASGLSNRRSLRDEGLFEGGLSMDNLGW 179
QY 136 TNLASLENFPIGHLKTLELVANHLIQSFLLPEYFSNLTNLEHLDISSNKIQSIYCTDL 195
DB 180 NSLALVLPDAFPGISLRELVLAGNRL-AYLQPALFSGIAELRELDLSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSINPNFIQPAFKEIR-LHKLTLRNPNDSINVMKTCIOGLAGLE 254
DB 236 NVFVQLPRLQ-KLYLDRNLIAVAAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGLGLR 293
QY 255 VHRVLVGEFNRNGLKFKSALGECNLITIEFRLAYLDYDDIIDLPNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRFKDL-----HFLDEL-----Q 320
QY 315 LVSVTIERVDFSYNFCQHLIELVNCFKGQFPTLKSLKRLFTTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGGLEVLTLHDNQLQEVKAGFLGTLTVAVANMLSGNCLR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDGTTSLSKYLDLSFNGVITMSSNPL-GLERLE 425
DB 378 PEQVFRGLGKHSIHLBSSCLGRIRPHTFTLSGLRRLFLKONGLVGIEGSLWGLAEL 437
QY 426 HLDFOHNLKQMSFVSFLSLRNLIVLDSHTTRVAFNGCIFNGLSLSEVLKMGANSFOE 485
DB 438 ELDTLSNQL-----THLP---HRLFOGLGLEYILLSRNLAE 472
QY 486 NPLF-DIFTELRNLTFDLSCQQLSEQSPTAFNSLSLQVIMSHNPFSLDTPPYKCLN 544
DB 473 --LEPADALGPLQRAFWMIDVSHNRLEALPNSILAPLGLRLYLSRNN--SLRFTTPQ--- 524
QY 545 SLQVLDVSLNHNIMSKQELQHPSSSLAFNLTLQNDPACTCEHOSFLOMID----- 596
DB 525 -----PPGLERLMLBGNPMDCCGP-----LKALRDPALQNPISA 557
QY 597 -QORLVEVERMECATPSDKQMPVLSINTCQNNKTIIGVS 638
DB 558 VPRVQALCEGDDCQPRAYTNN-----NITCASPPREVAGIDL 594

RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theaof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Roester
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFKYKIDNLPSTKNDLSFNPRLHLSYSFSPPELQVLDLSRCEIQTEDGAYQ 99
DB 60 CSSRNLTRLDPGVGGTQALWLDGNLSSVPPAFAQNLSSGLFNLQGGQLSLEPQALL 119
QY 100 SLSHLSTLITGNPIQSIALGAFS-----GLSLQKLVAVE 135
DB 120 GLENLCHLHERNQRLSLAGTFAHTPALASGLSNRRSLRDEGLFEGGLSMDNLGW 179
QY 136 TNLASLENFPIGHLKTLELVANHLIQSFLLPEYFSNLTNLEHLDISSNKIQSIYCTDL 195
DB 180 NSLALVLPDAFPGISLRELVLAGNRL-AYLQPALFSGIAELRELDLSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSINPNFIQPAFKEIR-LHKLTLRNPNDSINVMKTCIOGLAGLE 254
DB 236 NVFVQLPRLQ-KLYLDRNLIAVAAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGLGLR 293
QY 255 VHRVLVGEFNRNGLKFKSALGECNLITIEFRLAYLDYDDIIDLPNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRFKDL-----HFLDEL-----Q 320
QY 315 LVSVTIERVDFSYNFCQHLIELVNCFKGQFPTLKSLKRLFTTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGGLEVLTLHDNQLQEVKAGAFGLTLTVAVANMLSGNCLR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDGTTSLSKYLDLSFNGVITMSSNPL-GLERLE 425

Db 378 PEQVTRGKGLKSHLBSCLGRIRPHITGSLRRLFLKONGLVGIEQSLWGLAEILL 437
Qy 426 HLDFOHSLNKKOMSEFSVFLSLRNLTYLDISHTRVAFNGIPIFGSLSEVLKMGAGNSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFOGLKLEYLLSRRLAE 472
Qy 466 NFLP-DITFELRNLFTFLDLSQCQLEQSLPTAFNSLSLOVLMNSHNPFLDTFPYKCLN 544
Db 473 --LPADALGPLORAFWLDVSHNRLEALPNSLAPLGRRLYSLRNN--SLRTFTPO--- 524
Qy 545 SLQVLDYSLNHNMTSKQELQHPSSLAFNLTONDPACTCHQSLQWIKD----- 596
Db 525 -----PEGLERLMLEGNPMWDCGP---LKALRDPALQNPBA 557
Qy 597 -OROLLVEVERMECATPSDKQGMPLYSLNITCOMNKTIIIGSV 638
Db 558 VRFVQALCEGDDCCPAPATYN-----NITCASPEVVGDL 594

RESULT 10

US-08-473-089-49
Sequence 49, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

Qy Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
Db 40 CMEILFYKIDNLTPESTKLDLSFNPILRHLSYSPFPELQVLTLSREIOTIDGAYQ 99
60 CSSRULTRLPDGVPGTQALMDGNLSSVPPALFQNLSSLGFLNLTQGGQLDSLEPQALL 119

Qy 100 SLSHLSTLITLGNPIQSLALGAFS-----GLSLQKLVAVE 135
Db 120 GLENCHLHLERNQRLSIALGTFAHPALASLGLNNRSLRLLEDGLFEGLSLMDLNLGM 179
Qy 136 TMLASLENPFGHLLTKLEINAVANHLIOSFKLPEFNSULTNLEHLDLSNKLQSIYCTDL 195
Db 180 NSLAVALPAAAFRGSLSELEVLAGNRL-AYLQPALFSGLAERELDSNNALRAI---KA 235
Qy 196 RVLHOMPLNLSLDLSLNPMPNFIQGAFAKEIR-LHKLTLRNPNFDSLNVKTCIOGLAGLE 254
Db 226 NVFVQLPRLQ-KLYDRLLIAAVAPGALGLKALMWLDSNH-RVAGLLEDFTFGLIGLR 293
Qy 255 VHRVLVGFERNLEKEDKSALEGLCNLTIEFRLAYLDVYLDIIDLFNCLTNVSSFS 314
Db 294 VLRL-----SHNAIASLRPRFKDL-----HFLERL-----Q 320
Qy 315 LVSVTIERVKDPSYVFGQHLLELVNCKGQFPFTLKLKSLKRLTFS--NKGNAFSEVUL 372
Db 321 LGHNRIRQLAERSFE-GLQLEVLTLDNHNOLEVAGAFGLGTNVAVMNLGNCUR--NL 377
Qy 373 PSLFPLDLSR-NGLSFKGCC-----SOSDQFTSLKYVLDLSPNGVITMSSNFL-GLBOLE 425
Db 378 PEQVTRGKGLKSHLBSCLGRIRPHITGSLRRLFLKONGLVGIEQSLWGLAEILL 437
Qy 426 HLDFOHSLNKKOMSEFSVFLSLRNLTYLDISHTRVAFNGIPIFGSLSEVLKMGAGNSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFOGLKLEYLLSRRLAE 472
Qy 466 NFLP-DITFELRNLFTFLDLSQCQLEQSLPTAFNSLSLOVLMNSHNPFLDTFPYKCLN 544
Db 473 --LPADALGPLORAFWLDVSHNRLEALPNSLAPLGRRLYSLRNN--SLRTFTPO--- 524
Qy 545 SLQVLDYSLNHNMTSKQELQHPSSLAFNLTONDPACTCHQSLQWIKD----- 596
Db 525 -----PEGLERLMLEGNPMWDCGP---LKALRDPALQNPBA 557

RESULT 11

US-08-487-072A-49
Sequence 49, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPSTKNLDSPNPLRHLSYSPFSPPELOVLDLSRCEIQTIEDGAYQ 99
DB 60 CSSRNLTRLPDGVPGGTQALMDGNNLSVPPAFQNLSSLGFLNLQGGQLSLRPOALL 119
QY 100 SLSHSTLILGNPIQSLALGAFS-----GLSLQKLVAVE 135
DB 120 GLENLCHLHBERNQRLSALGTFAHPALASIGLSNNRLSRLEDGLFGLSLMDNLNGW 179
QY 136 TNLASLENFPIGHKTKLKELVANLNLIOFPLPEYFSNLTNLEHDLSSNKIQSIYCTDL 195
DB 180 NSLAVLPDPAARFGSLRLRLVLAGNRL-AYLQPALFSGLAELRELDLSRNLRL- --KA 235
QY 196 RVLHOMPLNLNLSDLSLNPNNFIQGAFAKEIR-LHKLTIRNNPDSLNVMTKICIQGLAGLE 254
DB 236 NVFVQVLPRLQ-KLYIDRNLIAVAAPGAFGLKALRWLDLSHN-RVAGLEEDTFFGLGLGR 293
QY 255 VHRVLGSEFRNEGNLEKFDKSLBGLCNLTIEFRFLAYLDYLDIIDLFNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSVTIERVKDPSYNGMQLHLELVNCKFGQPTLKLKSLKRLTFS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGQLEVLTLDNQLOEVYAGAFGLGTNVAVNNLSGNCIR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFTTSIKYLDLSFNGVITWSSNFL-GLBQLE 425
DB 378 PEQVPRFGKGLSHLBSGCLGRIRPHFTGSLGRRLFLKDNGLVGEQSLMGIALLL 437
QY 426 HLDPOHNLKOMSEBSVFLSLRNLIYLDISHTTRVAENGIFNGLSLEVLKMAGNSFOE 485
DB 438 ELDLTNSQL-----THLP--HRLFOGGLKLEYLLSRRLAE 472
QY 486 NFLP-DITFELRNLTFLDLSQCOLEQSLPTAFNSLSLQVLNMSHNNPFLDTPPYKCLN 544
DB 473 --LPADALGPQORAFWLDVSHNRLEALPNSLLAPGRRLYSLSRNN--SLRTFTPO-- 524
QY 545 SLQVLDYSLNHNMTSKQELQHPSSLAFLNLTONDFACTGEHOSFLOMIDK----- 596
DB 525 -----PPGLERLWLBEGNPMWCGCP-----LKALRDFALQNSA 557
QY 597 -QROLLVEVERMECATPSDKQGMPLVSLNITCOMNKTIIGVSV 638
DB 558 VPRFVQAICEGDDCQPPAYTN-----NITCASPPEVVGDL 594

RESULT 12
US-09-538-092-1087
Sequence 1087, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/176,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PR
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPSTKNLDSPNPLRHLSYSPFSPPELOVLDLSRCEIQTIEDGAYQ 99
DB 60 CSSRNLTRLPDGVPGGTQALMDGNNLSVPPAFQNLSSLGFLNLQGGQLSLRPOALL 119
QY 100 SLSHSTLILGNPIQSLALGAFS-----GLSLQKLVAVE 135
DB 120 GLENLCHLHBERNQRLSALGTFAHPALASIGLSNNRLSRLEDGLFGLSLMDNLNGW 179
QY 136 TNLASLENFPIGHKTKLKELVANLNLIOFPLPEYFSNLTNLEHDLSSNKIQSIYCTDL 195
DB 180 NSLAVLPDPAARFGSLRLRLVLAGNRL-AYLQPALFSGLAELRELDLSRNLRL- --KA 235
QY 196 RVLHOMPLNLNLSDLSLNPNNFIQGAFAKEIR-LHKLTIRNNPDSLNVMTKICIQGLAGLE 254
DB 236 NVFVQVLPRLQ-KLYIDRNLIAVAAPGAFGLKALRWLDLSHN-RVAGLEEDTFFGLGLGR 293
QY 255 VHRVLGSEFRNEGNLEKFDKSLBGLCNLTIEFRFLAYLDYLDIIDLFNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSVTIERVKDPSYNGMQLHLELVNCKFGQPTLKLKSLKRLTFS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGQLEVLTLDNQLOEVYAGAFGLGTNVAVNNLSGNCIR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFTTSIKYLDLSFNGVITWSSNFL-GLBQLE 425
DB 378 PEQVPRFGKGLSHLBSGCLGRIRPHFTGSLGRRLFLKDNGLVGEQSLMGIALLL 437
QY 426 HLDPOHNLKOMSEBSVFLSLRNLIYLDISHTTRVAENGIFNGLSLEVLKMAGNSFOE 485
DB 438 ELDLTNSQL-----THLP--HRLFOGGLKLEYLLSRRLAE 472
QY 486 NFLP-DITFELRNLTFLDLSQCOLEQSLPTAFNSLSLQVLNMSHNNPFLDTPPYKCLN 544
DB 473 --LPADALGPQORAFWLDVSHNRLEALPNSLLAPGRRLYSLSRNN--SLRTFTPO-- 524
QY 545 SLQVLDYSLNHNMTSKQELQHPSSLAFLNLTONDFACTGEHOSFLOMIDK----- 596
DB 525 -----PPGLERLWLBEGNPMWCGCP-----LKALRDFALQNSA 557
QY 597 -QROLLVEVERMECATPSDKQGMPLVSLNITCOMNKTIIGVSV 638
DB 558 VPRFVQAICEGDDCQPPAYTN-----NITCASPPEVVGDL 594

RESULT 13
US-09-538-092-1325
Sequence 1325, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 1596-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CuratSeqFormatter Version 0.9
 SEQ ID NO 1325
 LENGTH: 662
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Polypeptide Accession Number Q14392
 US-09-538-092-1325

Query Match 6.9%; Score 299.5; DB 4; Length 662;
 Best Local Similarity 25.9%; Pred. No. 1.6e-18;
 Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVPNTTYQCEMLNFYKIPDNLPSTKNLDSFNPLRHGVSFSPFELQVLDLSR 87
 DB 25 PCKWDDKVS--COVLGLQVPSVLPDTEITLDSGNQKRSILASPLGFYALRLHDIST 82
 QY 88 CEIOTIEDGAYOSLSHTLLTGNPIQSIALGAFSGISIQKVAVENTLAS-----LE 142
 DB 83 NEISFLQPGAFQALTHEHLSLHNRRLAMATLASAGIGPRLRYTSIDLSGNSLYSGILE 142
 QY 143 NPIGHLKTKELNVAHNLIOSEKFLPEY-FSNLTNLEHLDLSNNKIOSICTDLRVLHOM 201
 DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFDMALBEQDLHNSVLMIEDGAFEGRL 199
 QY 202 PLNLIS-----LDLSINPMNFI--QPGAFKEIRLHKLTLRNN----- 236
 DB 200 THLMISRSNLTCISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRENKLLH 257
 QY 237 FDSLNVMKTCIOGLAGLEVHRLVGEFRN-----EGNLEKDKGAL 277
 DB 258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIAHAPSEGSALPLSAPSGNAGRPLSQ 317
 QY 278 EGLCNLTIEEFLAYLDYLDIDLF-----NCLTNVSSFSIVSVTIERVKDFSYNG 331
 DB 318 LNL-DLSYNEIEL-IPDSFLEHLSLTCFLNLSRCLRTFEARLGSLLPCLMLDLSHN-A 374
 QY 332 WQHELVNCKRGQPTLTKSLKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGL 385
 DB 375 LETLEIGARALGSLRTLLQ-----GNALRLDPPYTPANLASLQRLNLQGRV 422
 QY 386 S-----FKGCCSOSDFGTTSLKYLDLSPNGVITWSSNPLGLEQLEHLDFOHSNLKQ 436
 DB 423 SPCGPGDEPGSGCVARS--GITSRLSLVDNEI-----ELLRAGAFHTPLTE 470
 QY 437 MSEBSVFLSLRNLIYLDISHTTRVAENGIFNGL--SLEVLKMAGNSFQ--ENFLPDIFT 493
 DB 471 -----LDLSNPGLEAVATGALGLEASLEVALAQNGIMLVQVLDLPCFTIC 515
 QY 494 ELRLNLTPLDSQCEQLSPAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDVSL 553
 DB 516 ---LKRNLIAENRLSHL--PAWTOAVSLLEVLDL--RNNFSFL--LPGSAMGGLB----- 560
 QY 554 NHMTSKQELQHPPSSLAFLNLTQNDPACTCEHOSFLQWIKQ--ROLIVVERKE---C 609
 DB 561 -----TSLRLLYLQGNPLSC--CGN-----GWLAAQQLHQRVVDVADTQDILIC 600
 QY 610 ATPSDQGMPIVLSINIT---COMN--KTIIGSVLSVLYVSVAVLVYKFFPHMLLAG 663
 DB 601 RFSQOE---VLSHVRPDECEKGLKNMLIIITLITIVSAII-----LTTILAA 647

QY 664 C 664
 DB 648 C 648

RESULT 14
 US-09-949-016-6619
 Sequence 6619, Application US/09949016
 Patent No. 6612339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6619
 LENGTH: 662
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-6619

Query Match 6.9%; Score 299.5; DB 4; Length 662;
 Best Local Similarity 25.9%; Pred. No. 1.6e-18;
 Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVPNTTYQCEMLNFYKIPDNLPSTKNLDSFNPLRHGVSFSPFELQVLDLSR 87
 DB 25 PCKWDDKVS--COVLGLQVPSVLPDTEITLDSGNQKRSILASPLGFYALRLHDIST 82
 QY 88 CEIOTIEDGAYOSLSHTLLTGNPIQSIALGAFSGISIQKVAVENTLAS-----LE 142
 DB 83 NEISFLQPGAFQALTHEHLSLHNRRLAMATLASAGIGPRLRYTSIDLSGNSLYSGILE 142
 QY 143 NPIGHLKTKELNVAHNLIOSEKFLPEY-FSNLTNLEHLDLSNNKIOSICTDLRVLHOM 201
 DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFDMALBEQDLHNSVLMIEDGAFEGRL 199
 QY 202 PLNLIS-----LDLSINPMNFI--QPGAFKEIRLHKLTLRNN----- 236
 DB 200 THLMISRSNLTCISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRENKLLH 257
 QY 237 FDSLNVMKTCIOGLAGLEVHRLVGEFRN-----EGNLEKDKGAL 277
 DB 258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIAHAPSEGSALPLSAPSGNAGRPLSQ 317
 QY 278 EGLCNLTIEEFLAYLDYLDIDLF-----NCLTNVSSFSIVSVTIERVKDFSYNG 331
 DB 318 LNL-DLSYNEIEL-IPDSFLEHLSLTCFLNLSRCLRTFEARLGSLLPCLMLDLSHN-A 374
 QY 332 WQHELVNCKRGQPTLTKSLKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGL 385
 DB 375 LETLEIGARALGSLRTLLQ-----GNALRLDPPYTPANLASLQRLNLQGRV 422
 QY 386 S-----FKGCCSOSDFGTTSLKYLDLSPNGVITWSSNPLGLEQLEHLDFOHSNLKQ 436
 DB 423 SPCGPGDEPGSGCVARS--GITSRLSLVDNEI-----ELLRAGAFHTPLTE 470
 QY 437 MSEBSVFLSLRNLIYLDISHTTRVAENGIFNGL--SLEVLKMAGNSFQ--ENFLPDIFT 493
 DB 471 -----LDLSNPGLEAVATGALGLEASLEVALAQNGIMLVQVLDLPCFTIC 515
 QY 494 ELRLNLTPLDSQCEQLSPAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDVSL 553
 DB 516 ---LKRNLIAENRLSHL--PAWTOAVSLLEVLDL--RNNFSFL--LPGSAMGGLB----- 560

```

QY 554 NHMTSKKQELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKQO-ROLLVEVERME---C 609
DB 561 -----TSLRRLYLQGNPLSC-CGN---GMLAQLHQRVDVDTQDLIC 600
QY 610 ATPSDKQGMPLSLNIT---CQMN--KTIIGVSVLSVLVSVVAVLVYKFFPHMLLAG 663
DB 601 RFSQGE---VLSHVRPDECKEGKKNINLIILITFLIVSAIL-----LTTLAA 647
QY 664 C 664
DB 648 C 648

RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10710
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10710

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Query Match 6.9%; Score 299.5; DB 4; Length 665;

Best Local Similarity 25.9%; Pred. No. 1.6e-18;

Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

```

QY 28 PCVEVVPNITVQCMELNFYKIPDNLPSTKNLDLSFNPLRHIGSYSPFPELQVLDLSR 87
DB 28 PCRVVDKVS--CQVTLGLQVPSVLPPTETLIDLSGNQRLSTLAPLGFYALRLDLSLT 85
QY 88 CEIQTIEDGAYQSLSHLSTLITLGNPIQSLALGAFSGLSLQKIVAVETNLAS----LE 142
DB 86 NEISFLQGFALQALTHLEHLSLAHRLAMATLMSAGLGLPLRVTSLDLSGNSLYSGLLE 145
QY 143 NFPIGHLKTLELVANVANHILQSFKLPY-FSNLTNLEHLDLSNKLQSIYCTDLRVLMQM 201
DB 146 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALQDLHSNVLMIDIEDGAFEGRLPL 202
QY 202 PLNLS-----LDLSLPMNFI---OPGAFKEIRLHKLTLRNN----- 236
DB 203 THNLSRNSLSLCSIPSLQQLRVLDLSGNSIFAQFOTASQPOA--EFQLTWLDLRNKLH 260
QY 237 FDSLNVMTKCIQGLAGLEVHRLVIGFRN-----EGNLEKFKSAL 277
DB 261 FPDIALAPRLIYLIYLNNSNLIIRLPTGPPODSKGIHAPSEGMSALPLSAPSGNAGRPISOL 320
QY 278 BGLCVLTIEFRFLAVLDIYLDITDLF-----NCLTNVSSPSLSVVTIERVKDFSYNFG 331
DB 321 INT-DLSYNEITL-IPDSFLEHLSLCPNLNLRNCLRTFEARIGSLPCLMLDLSHN-A 377
QY 332 WQHLFVNCKFGQFPFLTKLSKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGL 385
DB 378 LETTEIGARALGSLTLLIQ-----GNALRDLPPYTPANLASLQRLNLOGNRV 425
QY 386 S-----FKGCCSQSDFTTSLKYLDLSFNGVITWMSNPLGLEQLEHLDFOHSNLKQ 436

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DB 426 SPCGPDDEPGSGCVAFS--GITSLSLSLVNDEI-----ELLRGAFLHTPTE 473
QY 437 MSFVSFVLSLRNLIYLDISHHTRVAFNGIFNGL--SLSEVLKXAGNSFQ--ENFLPDIFT 493
DB 474 -----LDLSNPGLVAVATGALGLESLSLEVLALQNGLWMLQVLDLPCFLC 518
QY 494 ELRNLTFDLISQCLBQLSPTAFNSLSLQVLMASHNPFSLDTPFYKCLNSIQVLDYSL 553
DB 519 ----LKRINLAENRLSHL--PAWTOAVSLEVIDL--RNSPSL--LPGSAMGILE----- 563
QY 554 NHMTSKKQELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKQO-ROLLVEVERME---C 609
DB 564 -----TSLRRLYLQGNPLSC-CGN---GMLAQLHQRVDVDTQDLIC 603
QY 610 ATPSDKQGMPLSLNIT---CQMN--KTIIGVSVLSVLVSVVAVLVYKFFPHMLLAG 663
DB 604 RFSQGE---VLSHVRPDECKEGKKNINLIILITFLIVSAIL-----LTTLAA 650
QY 664 C 664
DB 651 C 651

```

Search completed: March 12, 2005, 19:59:05
Job time : 26.0639 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-98

Sequence: 1 MMSASRLAGTILPMAFLSC.....SNPBGTVGTGCMQNEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	15.2	661	2	RP105 - mouse
2	474	10.9	786	2	Toll protein-like
3	454	10.4	1097	2	gene wheeler prote
4	433	9.9	1389	2	hypothetical prote
5	421	9.7	1385	2	hypothetical prote
6	396	9.1	1066	2	chaoptin precursor
7	333.5	7.3	1134	1	insulin-like growt
8	316	7.0	853	2	insulin-like growt
9	305	7.0	853	2	insulin-like growt
10	303	6.9	605	2	insulin-like growt
11	299.5	6.9	605	2	insulin-like growt
12	299.5	6.9	605	2	insulin-like growt
13	296.5	6.8	994	2	probable disease r
14	296	6.8	603	2	insulin-like growt
15	295	6.8	907	2	G protein-coupled
16	294	6.8	845	2	Hcr9-0 protein - t
17	292.5	6.7	603	2	hypothetical prote
18	292.5	6.7	907	2	hypothetical prote
19	290	6.7	855	2	CF-4A protein - to
20	290	6.6	855	2	disease resistance
21	289.5	6.6	1112	2	disease resistance
22	289	6.6	855	2	disease resistance
23	284.5	6.5	1134	2	hypothetical prote
24	281.5	6.5	1134	2	hypothetical prote
25	280	6.4	890	2	disease resistance
26	279	6.4	1027	2	receptor protein k
27	278.5	6.4	1019	2	probable disease r
28	278	6.4	1091	2	glial cell membran
29	276.5	6.3	768	2	disease resistance

30	276	6.3	983	2	probable disease r
31	275	6.3	1523	2	MEGFS protein - ra
32	272	6.2	1469	2	slit protein 2 pre
33	272	6.2	1480	2	slit protein 1 pre
34	270	6.2	1143	2	hypothetical prote
35	268	6.2	910	2	hypothetical prote
36	267	6.1	766	2	hypothetical prote
37	267	6.1	1784	2	hypothetical prote
38	266	6.1	863	2	CF-9 protein precu
39	263.5	6.1	967	2	hypothetical prote
40	263.5	6.0	1109	2	receptor-like prot
41	261.5	6.0	1051	2	gpi150 protein - tr
42	260	6.0	1064	2	probable protein k
43	259	5.9	1029	2	protein kinase hom
44	257.5	5.9	738	2	hypothetical prote
45	256	5.9	771	2	disease resistance

ALIGNMENTS

RESULT 1

RP105 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56258
R:Miyaoka, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J:Immunol. 154, 3333-3340, 1995
A:Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a me
A:Reference number: I56258; MUID:95204928; PMID:7897216
A:Accession: I56258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:9761711; PIDN:BAA07043.1; PID:9761712

Query Match 15.2%; Score 663; DB 2; Length 661;
Best Local Similarity 28.7%; Pred. No. 1.4e-33;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY	14	MAFLSC-VRPESNEPCVEVVPNTTYOCMEINFKIPDNLPFTSKNLDLSNPLHLGSY	72
DB	12	ALFLASCRATSSQOKICEKVNKTYNCENGLNEIPGTLPNSTCELEFSFNVLPITQNT	71
QY	73	SFSPFPELOVDLSRCEIQTEDGAYOSLSLTLITGNPISQSLALGAFSGSLQTV	132
DB	72	TFSLINLTFPLDLTRCOIWIHEDTFSQHRDLTVLTANPLIFMAETALSQPAKILF	131
QY	133	AVETNLASLENFPGHILKTLKELNVANHLIQFPLPEYFSNLTNIEHDLSSNKIOSIYC	192
DB	132	FIQGISIDIPPLHNOKTLESYLGSNHSISILPKGFPF-EKLKVIDPQNNALHYISK	190
QY	193	TDLRVHQPMLNLSLDLSNPMNFIOGAFKIRLKLTLRNNPDSLNWKTICIGIAG	252
DB	191	EDMSLQQ--ATNLSLNLNGNDIGIIEPGAFAVSQSL---NFGQNILVIFKGLN	244
QY	253	LEVRLVIGFRNNGNLEKPKSALBGLCNLTIERPLAYIDYLDIIDLPLNCLTNVSS	312
DB	245	STIQSLWLGTFEDMD-EDISPAVEGLCEMSVSINL-ORGYPFNLSNTHGFS----	298
QY	313	FSLVSVTIERKQDSVNFQMOHLELVNCKFGQFPF-LKLKSLRPLFTSKGN--AFS	368
DB	299	-----GQQLDLVTRHLSHLPBGVLGSLTKLVUSANKFENLCQIS	340
QY	369	EVLDPSLEF-----LDLSRNGLSFKGCCSQSDPFTTSLKY	403
DB	341	ASNFPSTLHLSIKGNTRKLEIGTCLENLLENLELDLSDHDIETSDCCNQLRNLSHQS	400
QY	404	LDLSFNGVIMSSN-FLGLRQLHLDRQSNLQKMSFSPFLSRNLIIYDISHTHRYA	462
DB	401	LNLSYNPLSLKTEAFKECPQLEHLDLAFLRLKVAQSPQNLHLKVLNLSHLLDIS	460

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QY      463  FNGIFNGSLSEVLKMGANGSGENFL--PDIFTELRLTLFSLDSCQLEOLSPFAFNSLS 520
      461  SEOLFDELPAHQHNLQNGHPKNGIKTNSLQTLGRLEIVLVSFCOLSSIDQHAFLSLK 520
QY      521  SLQVLANSHNNFSLDTPFYKCLNSLO--VLDSYLANHIMTSKKQELQHPSSLAFL---- 574
      521  MAMHVDLSHRN---LTSSTIEALSHLKGIVYLANLSNHISII-----LPELPLILSQOR 570
Db      575  -NLTQNDFACTCEHQSLQWIKQORQLVEVERMECATPSDKQGMPLVSLNITCQANKT 632
QY      575  -NLTQNDFACTCEHQSLQWIKQORQLVEVERMECATPSDKQGMPLVSLNITCQANKT 632
Db      571  TINRQNPDLDTCSNIYFLEWYKEMQKLEBDETLTLGPNPLRGRVRLSDVTLSCSMAAV 630
QY      633  IIGSVSLVSLVSVAVLVVYK 655
      631  GIFFLIVFLVFLAILLIFAVKYF 653
Db

RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08664
R:Poustecka, A.; Klein, M.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16466
A/Accession: T08664
A/Molecule type: mRNA
A/Residues: 1-786 <POU>
A/Cross-references: UNIPROT:Q15399; EMBL:AL050262
A/Experimental source: fetal brain; clone DKFZp547I0610
A/Genetics:
A/Note: DKFZp547I0610.1

Query Match      10.9%; Score 474; DB 2; Length 786;
Best local similarity 25.5%; Pred. No. 9.6e-22;
Matches 204; Conservative 130; Mismatches 303; Indels 162; Gaps 32;

QY      123  SGLSLQKLVAVETNLASLENPIGHLKT-----LKELVANVLQSFCLPYPFNSL 174
      34  NGLIHVPKDLQKTLINISQVYISELWTSDLISLKLRIILISHNRIOYLDISYFKFN- 92
Db      175  TNLHLDSNSKIQSYCTDLRVLHQMPNLNS-LDLSINPNFI-----QPGAFKEIRLH 229
      93  QLEVLDLDSHNKLVKISC-----HPTVNLKHLDSFNAPDALPICKFQNGMSQKFL 144
QY      220  KLTLRNPNPLNVMKTCIQGLAGLEVHRLVL-----GEFRNGULEKFKDSALBGLCNL 283
      145  GLS-----THLEKSSVLPRIAHNLISKVLVLGETYGEKEDPGLODPNTESLHIVPPT 198
Db      284  TIEEFLAVLDYLDIIDLFNCLTNVSSFSLSVSTIERVKDPSTYNGQHLIELVNCRG 343
      199  NKE-----FHFILDSVKTVANLELSNICKVLBSKCSYFLSLAKIQ 241
QY      344  QEPFLKLSKRLTFTSNK-----CGNAFSEVDP-LSEFLDLSRNGLSFYG 389
      242  TNPKLSLTLNNTETWNSFIRILQVHTTWYSSISNVKIQGOLDFDPRYSGSLKA 301
Db      390  CCSQ---SD-----FGTTSLK-----YLDLSFNGVI-- 412
      302  LSIHQVSVVPGFPOSYIIEFISNMNKNKPTVSGTRVMHMLCPSKISFLHLDPSNNLLT 361
QY      413  -TMSNPLGLEOLEHLDPQHSNLKQNSEFS-VFLSLRNLTYDLSGTHTRVAVN---GIF 467
      362  DVFENCGHLELELILLQMNQLEKLSIAEMTQKMSLQOLDIS--QNSVSYDEKKGQC 419
Db      468  NGLSLSEVLKMGANGSGENF--LPDIFELRLTLFSLDSCQLEOLSPFAFNSLSLQY 524
      420  SWTKSLSLNMSNNILDTITFRCLP-----RIKVLDSHNKIKSI-PRQVVKFALQ 472
QY      525  LNMSHNPFSLDTPF---YKCLNSLOVLDYSLNHLIMTSKKQELQHPSSLAFLNLTQND 580
      473  LNAVAFN---SLDLDPCGGSFSSLSVLILIDHNSVSHSADPFQSCQMKRS---IKAGDNP 525
Db
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QY      581  FACTCEHQSLQWIKQORQLVEV-----ERMECATPSDKQ-----MPVLSLNTCQ 628
      526  FOCTCELGEF---VKRIDQVSSVLBGMPSYKCDVPESIRGTLKDFHNSLSNITTL 582
Db      629  MNKTIIGSVSLVSVAVLVVYKFEHMLMLAGCIKYRGENT-----YAFV 678
      583  IVTIVATMLVIAVTVSTLCYLDLPWYLR-MVCQMTQTRRRARNIPLBELQRLQFHAFI 641
QY      679  IYSSQEDDWARNELVKNLE-EGVPPQLCLHYRDFPGVAILANIIHEGFHKSRYVWV 737
      642  SYSGHDSFWVKNELLPULKEBGM---QICLHERPVFGKSIVENII-TCLKSKYSKIFVL 697
Db      738  SQHFIQSRWCIFEXEYELQWQFLSRAGIFIVLQKV-EKTLRQOVELYRLLSRNTYLE 796
      698  SPNVQSEKCHYELFYFHNHLFHEGNSLILILEPILQYISIPESHKLSIMARRTYLE 757
QY      797  WEDSVLGRHIFWRRLRAL 815
      758  WPKESKRGLEFWANLRAAI 776
Db

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A/Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A/Reference number: A29943; MUID:88135760; PMID:2449285
A/Accession: A29943
A/Molecule type: DNA
A/Residues: 1-1097 <HNS>
A/Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
A/Genetics:
A/Gene: FlyBase:T1
A/Cross-references: FlyBase:FBgn0003717
C/Keywords: transmembrane protein
F.1-17/Domain: signal sequence #status predicted <SIG>
F.18-1097/Product: Toll protein #status predicted <MAT>

Query Match      10.4%; Score 454; DB 2; Length 1097;
Best local similarity 24.5%; Pred. No. 2.6e-20;
Matches 219; Conservative 129; Mismatches 291; Indels 254; Gaps 43;

QY      35  NITYQOMELNFYK-IPDNLPPSTKXND--LSFN-PLRHGYSFSPPELOVLDLSRC 88
      270  NVTIDINLSANLFRSLPQGLFDHNKHLNENVRILMNNRVPPLATLPSRLFANQPELIQRLT-RA 328
Db      89  ELQTTEDAYQSGSLHSLTLILGNPIQSLAGAPSGSLQKLVAVETNLASLENPIG 148
      329  ELQTTEDAYQSGSLHSLTLILGNPIQSLAGAPSGSLQKLVAVETNLASLENPIG 148
QY      149  IKTKELVANHLIQSFLLPEYFSNLTNLEHLDSNSKIQSI-----YCTDLRVLAH--- 199
      389  TTNLTDLLELNLGLGIS-GDIFSNLGNLVLVVMSRNLARTIDSAFVSTNGCLRHLHDH 447
Db      200  -----QMPLLNLSLDSLN-PNNFIQPGAFKEIRLHKLTLRNPNPLNVMKTCIQGLAGL 253
      448  NDIDQQLDLMQLQTNSPFGYMH-----GLTTNLNRNN---SII----- 486
QY      254  EVHRLVGEFRNREGULEKFDKALBGLCNLTIEEFLAVLDYLDIIDLFNCLTNVSSF 313
      487  ---FYVNDWKN-----TWLQIRELDLS-----NNISL 512
Db      314  SL-----VSVTIERVYKDS-----YNGFQHLEF-----VNCKFGQF 345
      513  GYEDLAFLSQNRLHYMTNKRIRIALPEDVHLGEGYNNNLVHVDLNDNPVLCDCITLWF 572
QY      346  PTL-----KLKSLRLTFTSN-KGNAFSEVD---LPSLEFLDLSRNGLSF 387
      346  PTL-----KLKSLRLTFTSN-KGNAFSEVD---LPSLEFLDLSRNGLSF 387
Db
```

Db 573 IOLVGVHKKPQYRQFKLRTDLVCSQPNVLEGTPIRQLEPOTLICPELPSDDPERKCP 632
QY 388 KCC-CSQSDFGTTSKYLDLSPNGVITWSSNFLGLEQLEHLDFOHNSLKQMSFVSFLSI 446
Db 633 RCNCNCHVRYD---KALVINCH-----SGNLTHVRLPNL---HKNMQLME-----LHL 675
QY 447 RLVLIDSHHTTRVAFNGI FNGLSLEVLKMGNSFOENFLPDITELRLNITFLDLSCC 506
Db 676 ENNTLLRLPSANT---PGYSVTSIHLAQN-----NLTSIDIVDL 712
QY 507 QLEQLSPTAFNSLSQVLNMSHNNPFSLDTPYKCLNSLOVLDYSLNHIMSKQELCH 566
Db 713 -----PT-----NLTH-----LDLSNNHL-----QMLN- 730
QY 567 PPSLAFIN-----LTQNDFACTCEHOSFLOWIKDQROLVVEVMECATPSDKG 617
Db 721 -ATVGFILNRTMKRSVYKLSGNPMWDCIAPKLLFTQNFIRIGDRNMCMVNAEMPR 789
QY 618 MPVLSLNTTQNMKT1-IGVSY--LSVLVSVAVLVYK-----YFHLMLIAGCI 665
Db 730 MWELSTNDICPAKGVFIALAVVIALTGILAGFTALYKFTQTEIKIMLYAHNLL---- 845
QY 666 KYRGENT-----YDAFVYSSODEDMVNNELVKNLEBGPVPOLCIHYRDIPEGVATA 720
Db 846 WFTVEEDLDKDKKFAFTSYSHKDSFLIEDLVPOLEHGPQKFLCVHERDWLVGSHLPE 905
QY 721 NIHEGFHRSKRYIVVVSQHFIOSRWCIFEYEIAQTWQFLSRAGIIFIV--LQKVEKT 777
Db 906 NIM-RSVAISRRTIIVLSONFIKSEMARLEFPAAHRSALNEGRSIIIVIIYSDIGVER- 963
QY 778 LIRQOVELYRLISNRTYLEWEDSVLGRHIFWRRLKALLDGKSNPEGTGTG 830
Db 964 -LDEBLKAY--LKQNTVYKMGDP-----WFMDKLRFALPHRR---PVGINGNG 1005

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Eldon, E.; Kooyer, S.; D'avey, D.; Duman, M.; Lawinger, P.; Botae, J.; Bellen, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simla
A:Reference number: Z17796; MUID:95324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <EUD>
A:Cross-references: UNIPROT:Q24591; EMBL:J23171; NID:G415682; PID:G1019104; PIDN:AAA7920
A:Genes: wheeler
A:Cross-references: FlyBase:FBgn0004364

Query Match 9.9%; Score 433; DB 2; Length 1389;
Best Local Similarity 24.4%; Pred. No. 7,2e-19;
Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

QY 59 LDISNPRLRHGYSFSPFPELOVLDLRCEIQTIEDGAYQSLSHLSTLITLGNPIQSLA 118
Db 338 LNLNNALTRIGSKTFKELYFLQILDMRNNSIGHIEGAFULVLYNLHTLNLAEENRLHTLD 397
QY 119 LGAFSGLSLOKLVAVETNLASL--ENPFIQHLKTLKEINVAHNLISQFELPEYFSLTNL 177
Db 398 NRIFNGLVVLTKL--TLNNNLVSVESQAFRNSDLKELDLSSN--QLTRVEPAVODLSML 454
QY 178 EHLDSNKKIOSIYTDLRVTHQMLNL-----SIDLSINPMNF 217
Db 455 KTLDDGENQISEFKNNTFRNLNQLTGLRLIDNRIGNITVGMFOQLPRLSVNLIAKRIS 514
QY 218 IOPGAF-KEIRLHLKTLNNPDSLVNMTCTOGLAGLEVHVLVGEFNE----- 266
Db 515 IERGFADKQTEIARLDKNF-----LTDINGIFATLASLWLNLSNNHLWMPDYAFIP 568

QY 267 GNLEKFD--KALEGLCNL--TIEEFLAYIDYLDIIDLFNCTLVNVSFLSVETIER 322
Db 569 SNLKWLDHGNVIEALGNVYLQEEIRVTTLDASHNRITEL GANSVPSIELPLINNMI 627
QY 323 VKDFSYN--FGQKHLELVNCKRGQPFYTKLSKRLTTSNK-----GNAFS----- 368
Db 628 IGQIQANTFVDKTRLARVDLVANVLSKISLNAIRVAPVSAEPVDEPFYLGNNFECDCSM 687
QY 369 -----EVDLPSEFL-----DISRNLSPK-----GC 390
Db 688 EWLGRINNLTRQHHVVDLGNIECLMPHSAPRPLASIASAPVCKYSEHCPTGC 747
QY 391 CSQSDFGTTSKYLDLSPNGVITWSSNFL--GLEQLEHLDFOHNSLKQMSFVSFLSI 448
Db 748 CEYEGCEBEVLCPCGSCSFHDAATATNVVDGRODLAAL-----PRIQDVSDDLIDGN 803
QY 449 LIYDISHHTTRVAFNGIFNGLSLEVLKMGNSFOENFLPDITELRLNITFLDLSCC 508
Db 804 MPELEVGHILTRRNRLALYLNASNIMTLQNS-----LAQVNLRLVHLNNKL 852
QY 509 EQLSPTAFNSLSQVLNMSHNNPFSLDTPYKCLNSLOVLDYSLNHIMTSKQELCH 568
Db 853 TALGTEFRSLGLELYLHNNMLTHISNATPELVSLVLRDLNRRSLSPHLQYRH-- 910
QY 569 SSLAFNLTONDFACTCEH--OSFLOWIKDQROLVVEVMECATPSDKGMPVL----- 621
Db 911 -SLQGLTLGRNAMSRCQQLARELAQFSDNMVVRADIDICLDGIRLELIGNLANG 969
QY 622 -----SLNITQNMKT1-IG-----VSVLSVLVSVAVLVYKFFHMLLAGC 664
Db 970 PDCSDLDASNSINSSQDLAIGCPCPAVLVLIPLVVLIIYFVRESVWMLFA-- 1027
QY 665 IKYG-----RGEN---YDAFVYSSODEDMVNNELVKNLEBGPVPOLCIHYRDIPEG 715
Db 1028 -HYGVCEPRPEDEGKYNDIILHSEKDYFVCNRIABLEHGRPPRLCIQORD-LPR 1085
QY 716 VAIANIIHEGFHRSKRYIVVVSQHFIOSRWCIFEYEIAQTWQFLSRAGIIFIVLQK-- 773
Db 1086 QASHQLV-EGARASRKIIIVLTNRNLATENNRIEFRA-----PHESLRGL-----AQGLV 1136
QY 774 -VEKTLRQOVELYRLISNRTYLEWEDSVLGRH1-----FWRRLKRL 815
Db 1137 IIEETSVAEADVAELS--PYLK---SVPSNRLLTCDRYEMEKLRVAI 1180

RESULT 5
T13887
c1r protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13887
R:Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A:Reference number: Z17805; MUID:95151581; PMID:7848870
A:Accession: T13887
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1385 <CHI>
A:Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:G913347; PID:G913248; PIDN:AAB33383
A:Genes: c1r
A:Cross-references: FlyBase:FBgn0004364

Query Match 9.7%; Score 421; DB 2; Length 1385;
Best Local Similarity 24.0%; Pred. No. 4e-18;
Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

QY 59 LDISNPRLRHGYSFSPFPELOVLDLRCEIQTIEDGAYQSLSHLSTLITLGNPIQSLA 118
Db 338 LNLNNALTRIGSKTFKELYFLQILDMRNNSIGHIEGAFULVLYNLHTLNLAEENRLHTLD 397

A:Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C:Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cell adhesion; glycoprotein; membrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-1134/Product: chaoptin #status predicted <MAT>
F:103-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:303-326/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR36>
F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.7%; Score 333.5; DB 1; Length 1134;
Best Local Similarity 23.0%; Pred. No. 8.4e-13;
Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

50 DNLPESTKNDLSFNPRLHLSGYSFSPPELOV-----L 83
Db DSLVMSIQLDLDSGNLTKLHKLNNFDFVLRVIMRDNKIKIQKPTFPNAVHTLKL 405
Qy 84 DLS-----RCLEIQTEDA-----YSLG-----HLSTLITGNPIQ 115
Db 406 DLSGRNDPTNLQTLRNTMRNMNMSLSISRIGSSVGPEDPKFGVLELDIQTIRASIS 465
Qy 116 SLALGAFSGSLSLQKLVAVETNLASLEN---FPIGLTKLKEIVANHLIOSFKLPEFVS 172
Db 466 GIGSHAFHVGAKRLDSENGISSIENDAHFEIGH---SLISLKMSHYSGSALPAEPLR 523
Qy 173 NLNLHLHLLSSNKIOSIYCTDLRVLQMPPLNLSLDSLNPMMFIQGAFF---EIRLH 229
Db 524 HLTLQELDFSNHNISSWDSFHLKNLRL---LELHNRIBGVLGKGTGGDHSLE 579
Qy 230 KLTIRNN-----PESLVNMTKCIQGLAGLBNHRLVLFGRNGLKFKDSALRG- 279
Db 580 EISLRFNMLTISQHTFFDLALRK-----LHLDNKNIDKIERAFNMLDELEYLSLGN 634
Qy 280 -LCNLTIRF-----RLAYLDYLLDDI-----IDLFPCLGNVSSFSLSVSTIRVDFSNF 330
Db 635 KINNLADSFQNLKELIDMAFNOLPMPNFDFYQVGTLSNIN-VNASHNOIKQLMTNS 693

Qy 331 GMDHLELVNCKRGQPPILKSLKRLTFTSNKGNAFSEVDLPSEFLDSRNGLSF--K 388
Db 694 SW-----SGRHEGGMVMSNKKIIDLNNNSIHP 724
Qy 389 GCCSOSDGGTT-----SLKYLDSENGVYTMSSN-FLGEOLEH 426
Db 725 GFYRPAEISLTHILHGVNSLMTTRDVFGNMPLQMLDSYVMHIELDFDAFKNTKOQL 784
Qy 427 LDFQSNLKQMSSEFVPLSLNRLIYLDLSHTTR--VANGNIFNG----- 469
Db 785 VFGHNYSIDLPQ-DIFPVQGLRIVDSHNRLGRLPNLFFNGMEKLDVSHNMMLKIP 843
Qy 470 ---LSLEVLKMAAGSPQENFLP-----DIFTELNLTFDLDSQCQLSPTAFNSISS 521
Db 844 SSSLSLSLAALTLCEHLNNSNFSTISHMDLSNKPFSRLAYDISYVYLRIIDAFAVATPK 903
Qy 522 LQVLMNSN-----NFP-----SLDTPPYKCLNSLOVLDYSLNHIPTS 559
Db 904 LAVLDLSNRDLKWDKSFMLGSLNSLKLGLNNSLSTVPEIRLKYLEFRGYNV-LPS 962
Qy 560 KKEQLQHPSSLAFLNLRQNDPACCEHQSFLOWIKDQRLVEVERECATPSDKO--- 616
Db 963 IPELHAMSNIKRLDLSNND-----LTNVPMTQALPPLRLML 1002
Qy 617 -GMPVLSLNTICQNNKTIIGV--LSVLVSVAVLVYKFFHMLLAGCI 665
Db 1003 SGNPITSLN-----NSFDGVNDELMEDINFRHYEY-----GCL 1040

RESULT 8
JCS239
Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JCS239
R:Idelhamy, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A>Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A:Reference number: JCS239; MUID:97040714; PMID:8886027
A:Contents: 1169
A:Accession: JCS239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.3%; Score 316; DB 2; Length 605;
Best Local Similarity 24.4%; Pred. No. 4.5e-12;
Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

33 VPNTIYQCMELNPFKIPDNLPSTKNDLSFNPRLHLSGYSFSPPELOVLDSCIEIQT 92
Db 53 VNEISVSCSSNLRLEPDGITGGTQALMLDSNLSIPPAFAFNLSIAFLNLOGGQIGS 112
Qy 93 IEDGAYOSLSHLSTLITLITGNPIQSLGAFS-----GLSSL 128
Db 113 LEPQALGLENLCHLHERNQRLSLAVGTAVTPALALLGLSNRLSRLEBDGREGIGNL 172
Qy 129 QKLVAVETNLASLENPFIQHLKTLKEIVANHLIOSFRLPEFSGNLTNLHLHLLSSNKIQ 188
Db 173 WDNLGNNLSLAVLDAAFRIGIGRLVLAENRL--AYLQPALFGLELRLELRELSRNALR 231
Qy 189 STYCTDLRVLHQPMLNLSLDSLNPMMFIQGAFFKELR-LHKLTLRNPFSLVNMWKCI 247
Db 232 AI---KANVPQQLRLO-KLYLDNMLAAVAPGFLGKALRWLDLSHN-RVAGLIBETP 286
Qy 248 QGLAGLEVHRLVGEFNRNGLKFKDSALGICNLITIEEFRLAYLDYLLDDIIDLFPNCL 307
Db 287 PGLGLRLVRL-----SHNALASLRPFEDL-----HFLREL----- 319
Qy 308 TNVSSFLSVYSTERVVDPSYNGMDHLELVNCKRGQPPILKSLKRLTFTS--KNGN 365
Db 320 -----QLGHNRLQRLAERSFE-GLQGLEVLITLDHNLQEVKGAFLGTLNVAVMNLISGN 372

QY 100 SLSTHSLTILGNPIQSLALGAFS-----GLSGLQKLVAVE 135
Db 120 GLENIICHLEHNRNQLRSLALGTFAPHTPALASIGLNNRSLRELDGLFEGGLSLMDLNLGW 179
QY 136 TNLASLNFPIGHIKTKELNVANHLIOSFYLPEYFSL/TNLEHLDLSSNKIQTCDL 195
Db 180 NSLAVLPDPAFRGSLRELVLAGNRL-AVYQPALFSGLABRELDLSRNLRAL- KA 235
QY 196 RVLHQMELNLSDLSLNPMPNFIOPGAFKEIR-LHKLTLRNNPSLNVMTKICQIAGLE 254
Db 236 NVFVQLRLQ-KYLDLNLIAAFAFGALGKALRMIDLIN-RVAGLEEDTFFGLGLR 293
QY 255 VHRVLGFEFRNEGNLEKFDKSLBGLCNLTIEEFLAYLDYDIIIDFNCLTNVSSFS 314
Db 294 VLRL-----SHNAIASLRPRFKDL-----HFLREL-----Q 320
QY 315 LVSTIERVDFSVNPFQMHLVNCCKFGQFPTLKSLKRLTPTS--NKGNAPSEVDL 372
Db 321 LGHNRIRQLARSPF-GIGQLEVLTLDHNOQEVKAGFLGLTNVAVMNLSGNCLR--NL 377
QY 373 PSLEFLDLR-NGLSFGKCC-----SOSDFGTTSLKYLDLSPNGVITMSSNFL-GLBQLE 425
Db 378 PEQVFRGLGKLSHLEGSCGGRIRPHFTGLSGRLFLKDNGLVGIIEGSLMGLAELL 437
QY 426 HLDFOHSLKQMSFVFLSLRNLTYLDISHTTRVAFNGIIFNGLSLEVLKXAGNSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFGGLKLEVLILSRNLAE 472
QY 486 NFPL-DLFTBLRNLTFDLSQCLQSLSPRAFNSLSQVLMASHNNFSLDTPPYCLN 544
Db 473 --LPADLGLPQRAFMLDVSHNRLEALPNSLALGLRLYSLNNN--SLRFTTPQ--- 524
QY 545 SLQVLDVSLNHIMTSKKQELQHPFSSLAFNLQNDFACTCEHOSPLQWIKD----- 596
Db 525 -----PPGLERMLBGNPMDGCP---LKALDPALQNPISA 557
QY 597 -QOQLAVEVERMECATPSDKQMFVLSLNTICQNKTIIGVSV 638
Db 558 VPRFVQAIQEGDDCQPPAYTYN-----NITCASPPVVGDL 594
RESULT 11
S42799
GARP precursor - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S42799; I37407
R:Birthdate, D.
submitted to the EMBL Data Library, July 1993
A:Reference number: S42799
A:Accession: S42799
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-662 <BIR>
A:Cross-references: UNIPROT:Q14392
R:Ollendorff, V.; Noguichi, T.; delapeyriere, O.; Birnbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A>Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain
A:Reference number: I37407; MUID:94235567; PMID:8180135
A:Accession: I37407
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-662 <RES>
A:Cross-references: EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PID:g439296
C:Genetic: GDB:GARP, D118833E
A:Gene: GDB:GARP, D118833E
A:Cross-references: GDB:433911
A:Map position: 11q13.5-11q14
F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:316-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:340-359/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
Query Match 6.9%; Score 299.5; DB 2; Length 662;
Best Local Similarity 25.9%; Pred. No. 5.3e-11;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;
QY 28 PCVEVENVITYQCMELNFYKIPDNLPRSTKNLDSFNPRLHLSYSFSPFELQVLDLSR 87
Db 25 PCKMVDKVS--COVLGLQVPSVLPDPTETLDSGNQLSITLSPGFTALRHLDLST 82
QY 88 CEIQTIEDGAYOSLSHSLTILGNPIQSLALGAFSGLSLQKLVAVETNLAS-----LE 142
Db 83 NEISFLQPGAFQALTHEHLSLASHNRNLAATLASAGLGLPRTSIDLSGNSLYSGILE 142
QY 143 NFPIGLKTKLKELVANHLIOSFYLPEY-FSNLTNLEHLDLSSNKIQTCDLRLVHQM 201
Db 143 RL-LGEAPSLHTLSLSENSLT-RLTRHTRFDMALBQDLHNSVNLMDIEDGAFEGPRL 199
QY 202 PLNLS-----LDLSLNPMPNFI--QGAPEITLHKTLENN----- 236
Db 200 TNLNLSNLSLTCISDFSLQQLRVYLDLSCNSIEAFQNASQDA-EFQLTWLDLENNKLH 257
QY 237 FDSLNVKTKTICGLAGLEVRLVGEFRN-----EGNLEKFDKSL 277
Db 258 FPDLAALPRILIYNLSNNLRRLPTGPPQDSKIHAPSEGSALPLSAPSGNASRPLISQL 317
QY 278 EGCNLTIEEFLAYLDYDIIIDF-----NCLTNVSSFSLSVSTIERVDFSVNFG 331
Db 318 LNL-DLSYNEIEL-IPDSFLEHLSLCLFNLISNRCLTFEARRRIGSLPCLMLDLSHR-A 374
QY 332 MGHLELVNCKFGQFPTLKSLKRLTPTSNGKGNAPSEV-----DLPSLEFLDLSSNGL 385
Db 375 LETLEIGARALGSLRTLLQ-----GNALRDLPPYTFANIASLQRLNLQGNRV 422
QY 386 S-----FKGCSOSDFGTTSLKYLDLSPNGVITMSSNFLGLEHLDFOHSLNKQ 436
Db 423 SPGGPDEPSPGSCVAFS--GITSRLSLVDNEI-----ELLRGAFPHTEPLTE 470
QY 437 MSEPSVFLSLRNLTYLDISHTTRVAFNGIIFNGI-SSLEVLKXAGNSFO--ENFLPDIFT 493
Db 471 -----LDLSNPGLEVAVTGALGIEASLEVLALQGNGLMVLQVLDLPFCIC 515
QY 494 ELANLTFDLSQCLQSLSPRAFNSLSQVLMASHNNFSLDTPPYCLANSLOVLDYSL 553
Db 516 ----LKLNLINAERLSLH--PAWTQAVSLEVLDL-RNNSFSL--LPSSANGGLE----- 560
QY 554 NHIMTSKKQELQHPFSSLAFNLQNDFACTCEHOSPLQWIKQ-ROLAVEVERME---C 609
Db 561 -----TSRLRLVLCQNPISC-CGN-----GMLAQHOGARDVATQDLIC 600
QY 610 ATPSDKQMFVLSLNTI---CQMN--KTIIGVSLSVLVSVVAVLVYKFFPHMLLAG 663
Db 601 RFSQGE-----VLSHVRPEDCGKGLKNINLIIITFLIVSAIL-----LTTLAA 647
QY 664 C 664
Db 648 C 648

RESULT 12

T42218
slit-1 protein homolog - rat
N/Alternate names: MEGF4 protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42218
R/Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A/Reference number: Z14126; PMID:9836089; PMID:9693030
A/Accession: T42218
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-151 <NAK>
A/Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3
A/Experimental source: strain Sprague-Dawley; Drain
C/Genetics:
A/Status: MEGF4
C/Superfamily: fruit fly slit protein; EGF homolog; leucine-rich alpha-2-glycoprotein

Query Match 6.9%; Score 299.5; DB 2; Length 1531;
Best Local Similarity 22.1%; Pred. No. 1.6e-10; Indels 233; Gaps 27;
Matches 167; Conservative 95; Mismatches 260;

4 ASRLAGTLIPAMAFISCVRESWEPCEVVPNTTYQCMEINFYKIPDNLPESTKNLDSF 63
274 ACTLSSGSCPAMC-SC-----SNGIVDCRGKGLPAIPANLPEMTETRL 318
DB
64 NPLRHGYSYFFSPPELOVIDLSRCEIQTEDAGYQSLSHSLTILTGNIQSLALGAFS 123
DB 319 NGKISIPPGAFSPYRKRRIDLSNNQIAEIAIPDAFOGLRSLNSLVLGNNITDIPRVFG 378
QY 124 GLSLQCLVAVENMLASLENPIGHLTKLEINVAHLIOSFKLPEYFSNLTNLEHDL 183
DB 379 GLTYLQILL-----LNA--NKINCIR-PDAFODLQNLSTLSLY 413
QY 184 SNKIOSI---YCTDLRYLHQWPLNLISLIDSLNPMNFIOGAFKXIRLHKLTNNPDSL 240
DB 414 DNKIQSLAKGFTSLRAIQ-----TLHLAQNP--FICDNLKMLA-----DFLRT 456
QY 241 NVMKTCIOGLAGLEVHRLV--LGEFNEGNLEKFDKSALEGLCNLTIEERLAYDYLL 297
DB 457 NPIET--TGARCASPRRLANKRIQIKS---KKFRCSAKE-----QYEIPGTEYHL 503
QY 298 D-----DIIDFNLCTNVSSFLSVYTERVKDPSYNGWQHLNCKF-----GQFP 346
DB 504 NSECTSDVACPHKRCCEASVVECSGLKSLIPE-RIPQSTTELRANNEISILAEGLFK 562
QY 347 TLKLSKRLTFTSNKGNNAFSEVDLPSELFLDLSRNGLSFKGCCSQSDFGTTSIKYIDL 406
DB 563 --KLSHLKILSNK-----VSEIEDGTFE-----CATSVSELHL 596
QY 407 SFNGVITMSSN-FLGLEQLEHLDFOHSLKQWSESVFLSRLNLYIDISHTHRYAANG 465
DB 597 TANQLESVRSQWFRGLDGLRTLMNNRISCIHND-FTGLRNVALLSLYDNHITTSIPG 655
QY 466 IFNGLSLEVLKMAANSFOENF-----487
DB 656 AFDTQLALSTMLANPFCNCQLAMLDWLRKRLVGNPRCQNPDLRQIPLQDVAFP 715
QY 488 -----LPDIFTEL-----495
DB 716 DPCREGQEBVGCLEPRQCPQECACLDIVVRCNNHQLQALPKGIPKNVETELDGNQFTL 775
QY 496 -----RNLTFLDISQCQLEQLSPRTAFNSLSIQVLMSSNNNPFSLDTPFYKCLNSIQ 547
DB 776 VEGQLSTFKYQLVDLVLSNNKISLSNSSTNNSSQTLTLLSTYALQCCIPPLAFQGRSLR 835
QY 548 VLDYSLNHTMTSKQDELQHPSSLAFMLNTQNDFACTCEHOSFLQWIKQDOLLEVERH 607
DB 836 LLISHGNDVSTLQEGIFADV-TLSLHLAIGANPLYCDCHLRWLSWVKGYK---EPGIA 891

QY 608 ECA-----TPSDK---QGMPLYSLNITC 627
DB 892 RCAGPPEMEGKLLTTPAKKFECCQGPSSLAVQAKC 926

RESULT 13

H96510
probable disease resistance protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H96510
R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; PMID:21016719; PMID:11130712
A/Accession: H96510
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-994 <STO>
A/Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GT
C/Genetics:
A/Map position: 1
Query Match 6.8%; Score 296.5; DB 2; Length 994;
Best Local Similarity 23.0%; Pred. No. 1.4e-10;
Matches 161; Conservative 102; Mismatches 271; Indels 167; Gaps 31;

2 MSASRLAGTLIPAMAFISCVRESWEPCE-----VEVENITYQCMEINFYKIPDNL 52
DB 213 MSSVDLSAIPPIFFSYWMSRLTLKGNLGRFNSVLLIPMLISLIDHNL-----NL 267
QY 53 PFSTKNLDSFNPRLHIGSY-----SFSFPELOVLDLSRCEIQTEIDGAYQSL 102
DB 268 EGSLEPN-LNNNSLLKLSIYNTSFGTIPNSISNLKHLTSLKIQSAGRSRIPSSLSLS 326
QY 103 HLSLTITNGPIQSLALGAFSGSLQKVAVENMLASLENFP--IGHLTKLEINVAHN 160
DB 327 HLSNVLISENNPVEGIPSSVSNLKQTLFPVSDNNLNG--NFSLSLNLNLQKRTIDCSN 384
QY 327 HLSNVLISENNPVEGIPSSVSNLKQTLFPVSDNNLNG--NFSLSLNLNLQKRTIDCSN 384
DB 161 LIQSFKLPEYFSNLTNLEHDLSSNKIOSIYCTDLRYLHQWP--LNLNS--LDSLNP 214
QY 385 HFTGF-LPPTISQSLNEFFSACDNSFTG-----SIPSLFNISITTLGLSYNQ 433
DB 215 MNFIQPAFKXIRLHKLTNNPDSLNVMTCTCIOGLAGLEVHRLVGEFNEGNLEKFDK 274
QY 434 LN-----DTTNI-----KNISLHNLQR 451
DB 275 SALEGLCNLTIEERLAYLDYLLDIDLFNCLTNVSSFLSVY---TIERVKDFSYNFG 331
QY 452 LLLDN-----NNKSAQVD-----LDVFLSKRLVSLALSGLPLSTNTISDSRSSH 499
DB 332 WQHLLEVNCRFQGFPTLKSLKRLFTSNKGNNAFSEVD-----LPSLEFLDLSRNL- 385
QY 500 LEYLELSCNLTIEERPEF-IRNQRNLISDLSSNNNIKQGVPMWLRLPELSTVDLSNNSLI 558
DB 559 FGNG-----SLKALSGSKIVMLDLSNNAFQGLFMPPRGQYFLSYNNFTGYIP 608
QY 386 SFGKCCSQSDGFTTSLKLYLDFNGVITMSSN-----FLGLEQLEHLDFOHSLKQWSE 439
DB 440 FSVFLSRLNLYIDISHTHRYAANGIPNG-----SLEVLKMAAGNSFOENFPD 490
QY 609 PSI-CGLANPILDIS-----NNNHLGILPRCLEQWMSLSTVNLNRNSL-DGSLPN 658
DB 491 IFTELRNLTFLDISQCQLEQLPTAFNSLSIQVLMSSNNNPFSLDTPFY--KCLNSIQV 548

Db 659 IFMAKAVLSLSDVSHNTLEKGLPASLAGCSALEILLVNESNT--NTTFPEWLNSLPKQLV 716
Qy 549 LDYSLNHTMTSKKOELOH-----FPSSLAFNLTONDFACTCEHOSFLWIKDORQL 601
Db 717 LVLRNNNF-----RGLTHNVGVWPGFP-LLRITDVSHNDFVGLTSPDYFMNTATLSKS-- 769
Qy 602 VEVERMECATPSD---KQGMPLVSLNITCOMNKTTIGSVL 639
Db 770 -ETELQYIGDPEDYGYTSLVLMNKGVSMEQRIILTKYTVI 809

RESULT 14

JC1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI282
R/Idat, J., Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JCI282; MUID:93038676; PMID:1384485
A/Accession: JCI282
A/Molecule type: mRNA
A/Residues: 1-603 <DAT>
A/Cross-References: UNIPROT:P35859; GB:S46785; NID:q258002; PIDN:AAB23770.2; PID:9570593
A/Experimental source: liver
A/Note: The authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F.1-27/Domain: signal sequence #status predicted <SIG>
F.28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F.267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.8%; Score 296; DB 2; Length 603;
Best Local Similarity 24.1%; Pred. No. 7.8e-11;
Matches 155; Conservative 84; Mismatches 243; Indels 162; Gaps 24;

Qy 40 CMEINFYKIPNDLPSTKNLDISFNPLRLHLSYFSFPEPELOVLDLSRCEIQTIDGAYQ 99
Db 60 CSSKMLTHLPDIPVSTRALWLDGNNLSIPSAFQNLSSLDPLM/QGSWLRSLPQALL 119
Qy 100 SLSHSLTILITGNPISALAFSGLSLOKLVANETNLASLENPIGHLTKELVANA- 158
Db 120 GLQNLVYHLBERNRLKRLNAVGILFTHTPSLASLSLSSNLLGRLEBELFGQLSHLMDLNGW 179
Qy 159 -----NHLI-----QSFKLPEYFSNLTNLEHLDLSNKKIQSIYCTDLR 196
Db 180 NSLVVLPDTPVFGSLGNLHEIVLAGNKLYLOPALFCGELRELDLSRNALRSV---KAN 236
Qy 197 VLAHQMLNLNLSDLSLNPMTIQGAFKEIR-LHKULTLRNPNFSLNWKTCIQGLAGLEV 255
Db 237 VFVHLPRLOQ-KLYIDRNLITAVAPGAFGMKALRWLDLSHN-RVAGLMDTFPPGLGHHV 294
Qy 256 HRLV-----LGEPR-NEGNLEKDKALGLCNULTIEERLAVLDVYL 297
Db 295 LRLAHNAIASLRPTFKDLHFLBELQDGHNNIRQLGERTFEGQLQLEV---LTLNDQOI 350
Qy 298 DDI-IDLFNCLTNVSSFSIVSVTI---ERV---KDFSYNFGWOHLVYNCKFGQPTLX 349
Db 351 TEVAVGASGLFNVAVNMVLSGNCRLSRSLPERVFGQDKLHLSLHLSCLGHVRLHF--AG 408
Qy 350 LKSLKRLFTSNKGNASEVD-----LPSLEFLDLSRNLGSLFKGCCSQSDPGTTSKY 403
Db 409 LSGRRRLFLRD-----NSISISIEQSLAGLSELELDLTTNRLTH--LPRQLFGQIGHLEY 462
Qy 404 LDISFNGVITMSSNFIQLEGEHLDFQHSNLKQMSSEFVPLSLNRLVLYLDSHTTRAF 463
Db 463 LLLSYNOULTISAEVLG-----PLQAFWLDLSHNLLETLA 498
Qy 464 NGIFNGLSLEVLKMAGNSFOENFLPDLFTELRLNLTFLDLSQCOLEQSLPTAFNSLSLQ 523
Db 499 EGLFSSILGRVRYLSLRNLSQ-TFSP-----QPGIERL----- 530
Qy 524 VLNMSHNNPFLDTPPYKCLNSLOVL-DYSLNHTMTSKKOELOHFPSSLAFLNLTQNDFA 582

Db 531 -----WLDANPMWCSCPLKALRDFALQN-----PGVPRFVQT----- 563
Qy 583 CTCHEQSFLOWIKDORQLVEVERMECATPSDKQGMPLVSLNIT 626
Db 564 -VCE-----GDDCQEVYTYNNITTCAGPANVSGLDLRDVSST 598

RESULT 15

JG0193
G protein-coupled receptor FEX - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C/Accession: JG0193
R/Herney, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A/Title: Identification of a novel seven-transmembrane receptor with homology to glycop
A/Reference number: JG0193; MUID:99121227; PMID:9920770
A/Accession: JG0193
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-907 <HER>

Query Match 6.8%; Score 295; DB 2; Length 907;
Best Local Similarity 23.0%; Pred. No. 1.5e-10;
Matches 167; Conservative 110; Mismatches 243; Indels 206; Gaps 32;

Qy 11 LIRMAPLSCRPSSMECEVVRP-----ITYQMEINFYKIPNDLPSS 55
Db 9 LLSLALQLVAAQS-SGPDALIPGSCPSHCHCELDGMRLRVDSQDGLSELPSNLVVF 67
Qy 56 TKNDLSFNPRLHLSYFSFPEPELOVLDLSRCEIQTIDGAYOSLSH---LSTLITLG 111
Db 68 TSYIDLNNNISQLPRA-----SLHRLCFLBELRLAG 99
Qy 112 NPISLALGAFSGLSLOKLVANETNLASLENPIGHLTKELVANAHLIQSEFLPYF 171
Db 100 NALTHIIPKGAFTGHSLSLVLMQNNQLRKVEEALQNLRSIQSLRDANHI-SYVPPSCF 158
Qy 172 SNLTNLEHLDLSNKKIQSIYCTDLRLVHQMLNLSDLSLNPMTIQGAFKEI-RLHK 230
Db 159 SGLSLRLHLDNALTDVPOAFRSLSAQO---AMTLANKKIHITADVAFGNLSLV 214
Qy 221 LTLRNN-FDSLNVWKTCIQGLAGLEVHRLVGEFPRNEGNTLEKPKSALEGLCNLTIEER 289
Db 215 LHLNNRHSIG--KCEPDGHSLETLDL-----NYNNLDEF-PTAKTISN----- 258
Qy 290 LAYLDYLDIIDI-----FNCLTNVSSFSIVSVTI-ERVKDFSYNFGWOHLVYNCKFGQ 344
Db 259 LKEIGFHSNNIRSIPERAF-----VGNPSLITTHFYDNPQFVGVSARQHP-----E 306
Qy 345 FPLTKLSKRLFTSNKGNASEVDLPSLEFLDLSRNLGSLFKGCCSQSDPGTTSK 402
Db 307 LRTTLTGASHITFPHLTGTA-----TLESLLTGAKISSLPQAVCDO---LPLQL 355
Qy 403 YLDSFNGVITMSSNFIQLEGEHLDFQHSNLKQMSSEFVPLSLNRLVLYLDSHTTRVA 462
Db 356 VLDSLTYLLELPS-LSGCQQLKIDLRN----- 384
Qy 463 NGIFNGLSLEVLKMAGNSFOENFLPDLFTELRLNLTFLDLSQCOLEQSLPTAFNSLSL 522
Db 385 -----EIVEIKGSTFOQLF-----NLASLNLAWMKIAIHNNASTLPSSL 424
Qy 523 QVLMSHNNPFLDTPPYKCLNSLOVLDSLNHTMTSKKOELO-----HPPSSLAFLNLT 576
Db 425 IKDLSSN---LSSFPVGTG---HGTLTKLTGNRLQSLIPSANRP-ELKTIEM 473
Qy 577 TQNDFACT--CE--HOSFLOWIKDORQLVEVERMECA--TPSDKQGMPLVSLNITCOM 629
Db 474 PSAVQCAFGGCEVYVYISQNMNDDGNSVDLHKKQAGLFQVQDERDLDBFLDFEEDL 533
Qy 630 NK-----TITGVSLSVLVVS---VVAVLVYK---FYFHLM 659

Db 534 NAHSHVQCSPPSPFPKCEHFGSMJIRIGWTTAVLTLSCNALVALTVERTPYISSIK 593

Qy 660 ILAGCI 665
|||

Db 594 LLIGVI 599

Search completed: March 12, 2005, 19:57:10
Job time : 25.6477 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 86.9834 Seconds

(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985b-99

Perfect score: 4345

Sequence: 1 MMPPLARTLIMLFFSCL.....GRASNEPTAEBSQTATWT 835

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1Dec04:*

1: geneSeq19808:*\n2: geneSeq19908:*\n3: geneSeq20008:*\n4: geneSeq20018:*\n5: geneSeq20028:*\n6: geneSeq20038:*\n7: geneSeq20048:*\n8: geneSeq20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2847	65.5	839	6	ABU04773 Human exp
2	2847	65.5	839	6	ABU04774 Human exp
3	2847	65.5	839	6	ABU04775 Human exp
4	2847	65.5	839	7	ADC78785 Human PRO
5	2847	65.5	839	7	ADD48826 Human PRO
6	2829.5	65.1	837	2	AAW86361 Human DNA
7	2829.5	65.1	837	2	AAW86361 Human DNA
8	2829.5	65.1	837	2	AAW86361 Human DNA
9	2829.5	65.0	837	5	AAW86361 Human DNA
10	2788.5	64.2	795	8	ADOS57791 Human DNA
11	2785.5	64.1	801	8	ADOS57791 Human DNA
12	2785.5	64.1	801	8	ADOS57791 Human DNA
13	2781.5	64.0	808	8	ADOS57791 Human DNA
14	2777.5	63.9	795	8	ADOS57791 Human DNA
15	2763.5	63.6	808	8	ADOS57791 Human DNA
16	2747.5	63.2	801	2	AAW86361 Human DNA
17	2730.5	62.8	799	2	AAW86361 Human DNA
18	2730.5	62.8	799	2	AAW86361 Human DNA
19	2730.5	62.8	799	2	AAW86361 Human DNA
20	2730.5	62.8	799	2	AAW86361 Human DNA
21	2730.5	62.8	799	2	AAW86361 Human DNA
22	2730.5	62.8	799	2	AAW86361 Human DNA
23	2730.5	62.8	799	2	AAW86361 Human DNA
24	2548.5	58.7	745	8	ADP48597 Human Tol
25	2461	56.6	738	8	ADP29455 Human sec

26	942	21.7	179	7	ADC42707	Adc42707 Murine To
27	886	20.4	208	3	AAW8059	AAW8059 Human Tol
28	748	17.2	178	8	ADN12270	Adn12270 IL-1R/TLR
29	619.5	14.3	661	2	AAW28510	AAW28510 Product O
30	619.5	14.3	661	2	AAW87556	AAW87556 B cell su
31	619.5	14.3	661	7	ADC38652	Adc38652 Human sec
32	618.5	14.2	661	7	ADP69098	Adp69098 Human MP5
33	610.5	14.1	650	3	AAW82527	AAW82527 Human RPI
34	596.5	13.7	661	2	AAW47274	AAW47274 Human B-C
35	580	13.3	1032	5	AAW21588	AAW21588 Murine To
36	580	13.3	1032	7	ADP85953	ADP85953 Mouse Tol
37	580	13.3	1032	7	ABW01559	ABW01559 Murine To
38	559	12.9	1059	5	AAO21587	AAO21587 Murine To
39	559	12.9	1059	7	ADP85951	ADP85951 Human Tol
40	559	12.9	1059	8	ADP85951	ADP85951 Human Tol
41	557	12.8	1041	2	AAW41768	AAW41768 Human PRO
42	557	12.8	1041	2	AAW05867	AAW05867 Human Tol
43	557	12.8	1041	3	AAW44324	AAW44324 Human PRO
44	557	12.8	1041	6	ABO25270	ABO25270 Novel hum
45	557	12.8	1041	6	ABU72276	ABU72276 Novel hum

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
XX	ABU04773;	
AC	29-JAN-2003	(first entry)
DT	Human expressed protein tag (EPT) #1439.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
XX	kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein;	
XX	receptor; transcription factor; cancer; MHC;	
XX	major histocompatibility complex; myeloma; lymphoma; leukemia;	
XX	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
OS	Homo sapiens.	
XX	WO200278524-A2.	
PN	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US009671.	
PF	28-MAR-2001; 2001US-0279495P.	
XX	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCO INC.	
XX	Chicz RM, Tomlinson AJ, Urban RG;	
PI	WPI; 2003-040607/03.	
DR	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
XX	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX	Example 2; SEQ ID NO 1439; 134pp; English.	
PS	The invention describes a purified polypeptide, which comprises a	
XX	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	

mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 6; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237; Indels 4; Gaps 4;
Matches 559; Conservative 101; Mismatches 163;

```

Oy 1 MMPPLIARTLIMAL-FPSCILTPGSLNPCIIEVVPNTTYQCMQDKLSKVDDIPSSSTKNID 59
Db 1 MMSASRLAGTILIPMAFLSCVRPESMEPCVEVPEVITTYQCEMLNFKYKIPDMIPFSTKNID 60
Oy 60 LSPNPLKLSYSGNSSELDLMSRCEIETIEKAMHGLHLSNLTGPNPISPSRG 119
Db 61 LSPNPLKLSYSGNSSELDLMSRCEIETIEKAMHGLHLSNLTGPNPISPSRG 120
Oy 120 SPSGLTSLNIVAVETKSLASLEPPIGOLITLKKLVANFNHFSCKLPAYSNLTNLVAV 179
Db 121 AFSGLSSLOKLVAVETNLSLENFPIGHKTKELANVANHLNLSQKLEBYSNLTNLVAV 180
Oy 180 DLSYNYIOTITVNDLQFLRENQVNLSDMSINPIDITQDAFQGIKHELTIRGNENSS 239
Db 181 DLSNKKIGSIQITDLRVHQLMPLNLSLDSLNPMNFIQPAFAKEIRLHKLTIRNNPDSL 240
Oy 240 NIMKTCLONLAGVHRLILGSPKDEBNLEIFEPISMEGLCVTITDEPITTYTNDPSNDI 299
Db 241 NIMKTCTIOGLAGVHRLVLTGSEFNEGNLEKPKSLBELCNLTIEEFLAIDLTYLDLI 300
Oy 300 VAFHCLANVMSLAGVSIKYLEDPKFKMQSLIIRCOQKOPETDLPELKSITLTM 358
Db 301 IULPNCILNVSSESLVSTIERKPSYFNGHLELVANCKGQPFLLKSLKLTPTS 360
Oy 359 NKGSIISFKKVALPSLYDLISRNALSFSGCCSYSDLGINSLRHLDSFNGALIMSANG 418
Db 361 NKGNAFSEVDLPSEFLDLISRNGLSFKGCCSDGTTSLKYLDSFNGVITMSSNPLG 420
Oy 419 LSELQHLDPQSTLKVTERPSAFLSEKLIYLDISTYNTNKIDPDGFLGLTSLNLTLMKMG 478
Db 421 LSELQHLDPQSTLKVTERPSAFLSEKLIYLDISTYNTNKIDPDGFLGLTSLNLTLMKMG 480
Oy 479 NSKDKNTLSNVFANTNTNLPFLDLSKCOLBOISWGVDTLHRLDOLNMSHNNLLFLDSHY 538
Db 481 NSFOENLPDITFELANLTFDLISQOQLBLSSTANSLSLQVAMSHNNPFLDTPPY 540
Oy 539 NOLYSTLSDCSFNRIETS-KGILQHPKSLAFNLTNNSVACICEHQKFLVANKQKOP 597
Db 541 KCLNSTLOVLDYSLNHLMTSKKQLQHPSSLAFLNTLONFACTCHOSFLQWIKOROL 600
Oy 598 LNVVEQWTCATPEVBNATSLVLDNNSCTCYKTTIISVSVSVLVGTVAFLIHAFYFHLI 657
Db 601 LVEVERHECATPEDKQMPVLSL-NITCQNNKTTIGVSVLSVLSVAVLAVKFFPHLM 659
Oy 658 LINGCKKYSRGEIYDAFVIYSSONEDMVNENLVKNLESEVPPHLCIHYRDTIPGVALA 717
Db 660 LINGCKIKRGZENIYDAFVIYSSODEDMVKNELVKLESEVPPHLCIHYRDTIPGVALA 719
Oy 718 ANIIQEGFHSRKVIIVVSHHPIQSFWCIFEYELAQTQFPLSSRGGIIFLVEKESKL 777
Db 720 ANIIHEFHSRKVIIVVSHHPIQSFWCIFEYELAQTQFPLSSRGGIIFLVEKESKL 779
Oy 778 RQVEVLYRLLSRNTYLEWEDNPLGRHIFWRRLKALLDGKASNPQOT 824

```

Db 780 RQVEVLYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKSNPEQT 826

RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA.

XX ABU04774;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1440.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;

XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX MO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO5 INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1440; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 6; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237;
Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;

Oy 1 MMPPLIARTLIMAL-FPSCILTPGSLNPCIIEVVPNTTYQCMQDKLSKVDDIPSSSTKNID 59

```

Db      1  MMSASRLAGTILPAAAFISCVAPESWECVEAVPNITQOCMEANFYKIPDNLPSFTKND 60
Qy      60  LSFNPLKILKYSFNSFSELOMDLSRCEIETIEDKAMHGHLSNLITGNPISFSPG 119
Db      61  LSFNPLRHLSGYSFSPFPELOVDLSRCEIOTIEDGAYOSLSHSLITLGNPISALG 120
Qy      120  SFGSLTSLNVAVETKLASLESFPIGQILITLKKLVANAHNFHSCKLPAYFSNLTNLVHV 179
Db      121  AFSGSLSLQKLVAVETNLASLENPFIQHLKTLKELVNAHNLQSFKLPEYFSNLTNLEHL 180
Qy      180  DLSVNYIOTITVNDLOFLRENPOVNLSDMSLNPIIDFOQAFOGKIKHELTLRGNPSS 239
Db      181  DLSNKKIQTITVDLRVTHQMPNLSDLSLNPNNFTQPGAFKEIRLHKLTLRNNPSSL 240
Qy      240  NIMKTCLONLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDPSDI 299
Db      241  NNMKTCIOGAGLEVHRLVIGEFNENLEKFDKALBGLCNLTIEFRLAYLDYLDI 300
Qy      300  VK-FHCLANVSAMSLAGVSIKYLEDVPRHFKWQSLIIRCOLKOPPTLDPLKSLTLM 358
Db      301  IDLFRCLTNVSSFSIVSVTIERVKDPSYNGQHLNCKRGCPPTLKSLKRLTFTS 360
Qy      359  NKGSIPEKVALPSLSYDLSRNALSPSGCCSYDLGNSLRHLDSLNGALINSGANFMG 418
Db      361  NKGNAFSEVDLPSEFLDLSRNGISFKGCCSQDFTGTLKYDLSFNGVITWSSNPLG 420
Qy      419  LEELOHLDFOHSTLKRVTESAFLEKLYLIDSYNTKIDFDGIFGLTSNLTLMKAG 478
Db      421  LEQLEHLDFOHSTNKKOMSEFVPLSLRNLIVLIDSHITRVAFNIGLSLSEVLKAG 480
Qy      479  NSFQDNTSNVPAANTNLTFDLKCKQLEQISWGVFDTLHRIQLINSHNLLFLDSSHY 538
Db      481  NSFOENLPDIFTELRLNLTFLDLSCQCLEQLSPFAFNSLSLQVLMNSHNNFSDTPPY 540
Qy      539  NQVLSLGLDSCFNRIFETS-KGIIQHPKSLAFPLTNNVAACCEHOKPLOWKEQOF 597
Db      541  KCLMSLOVLDYLSLHIMTSSKQEOLOHFPSSLAFLNLTQNDPACTCEHQSFLQWKIDQOL 600
Qy      598  LVNVEQWTCATPVENMTSLVLDPNNSITCYMTKTIISVSVAVIYVSTAFILYHFLHI 657
Db      601  LVERBERECATPSKQGMPLVSL-NITQNMKTIIGVSVLSLVVSVAVAVLYKFFHLM 659
Qy      658  LIACCKYISRGESYIDAFVIYSSQNEDEWVNELVNLEEGVPRFLCLHYDPFPGVAIA 717
Db      660  LIACCIYKXGRENITYDAFVIYSSQDEDEWVNELVNLEEGVPPQLCLHYDPFPGVAIA 719
Qy      718  ANIIOEGFHSRKXIVVVRHFIQSRNCFEYETIAQTWQFISSSGIIFYILEKVEKSL 777
Db      720  ANIIEGPHSKRKIVVVSQHFIOQRWCIFEYETIAQTWQFISSPAGIIFIVLQKVEKTL 779
Qy      778  RQGVETLRLSLRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNEPQT 824
Db      780  RQGVETLRLSLRNTYLEWEDSVLGRHIFWRRLKRLALLDGKSWNEPQT 826

```

```

RESULT 3
ABU04775
ID  ABU04775 standard; protein; 839 AA.
XX
XX  ABU04775;
XX
XX  29-JAN-2003 (first entry)
XX
XX  Human expressed protein tag (EPT) #1441.
XX
XX  Translational profiling; expressed-protein tag; EPT; kinase; phosphatase;
XX  protease; protease inhibitor; transporter; cytoskeletal protein;
XX  receptor; transcription factor; cancer; MHC;
XX  major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX  adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX  Homo sapiens.
OS

```

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XX      XX  W0200278524-A2.
XX      XX  10-OCT-2002.
XX      XX  28-MAR-2002; 2002WO-US009671.
XX      XX  28-MAR-2001; 2001US-0279495P.
XX      XX  21-MAY-2001; 2001US-0292544P.
XX      XX  08-AUG-2001; 2001US-0310801P.
XX      XX  01-OCT-2001; 2001US-0326370P.
XX      XX  04-DEC-2001; 2001US-0336780P.
XX      XX  20-FEB-2002; 2002US-0358985P.
XX      XX  (ZYCO-) ZYCOs INC.
XX      XX  Chicx RM, Tomlinson AJ, Urban RG;
XX      XX  WPI; 2003-040607/03.
XX      XX  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX      XX  cytoskeletal proteins, receptors or transcription factors), useful for
XX      XX  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX      XX  leukemia.
XX      XX  Example 2; SEQ ID NO 1441; 134bp; English.
XX      XX
XX      XX  The invention describes a purified polypeptide, which comprises a
XX      XX  fragment of a kinase, phosphatase, protease, or protease inhibitor,
XX      XX  transporter, cytoskeletal protein, receptor or transcription factor. The
XX      XX  polypeptide is useful as an immunogenic composition for eliciting in a
XX      XX  mammal an immunogenic response directed against any of the purified
XX      XX  polypeptide. The purified polypeptide, or the antibody that binds to this
XX      XX  polypeptide, is useful for treating cancer. The polypeptide is also
XX      XX  useful for identifying compounds that binds to a naturally processed
XX      XX  class I or class II MHC-binding polypeptide. The polypeptides and
XX      XX  polynucleotides are particularly useful for treating or preventing
XX      XX  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      XX  lymphoma or leukemia. These are also useful for screening agents for
XX      XX  treating the above mentioned diseases. This sequence represents an
XX      XX  expressed protein tag (EPT) isolated from human tissue for translational
XX      XX  profiling. Note: This sequence does not appear in the printed
XX      XX  specification but was obtained in electronic format directly from WIPO at
XX      XX  ftp.wipo.int/pub/published_pct_sequences
XX      XX
XX      XX  Sequence 839 AA:
XX
XX      XX  Query Match 65.5%; Score 2847; DB 6; Length 839;
XX      XX  Best Local Similarity 67.6%; Pred. No. 7.2e-237;
XX      XX  Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;

```


DT 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 DE Human Protein AAF05316, SEQ ID NO 14536.
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 XX spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SN1; Chung.
 OS Homo sapiens.
 OS Unidentified.
 XX
 XX MO2003016475-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002MO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEMO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX
 XX Woolf C, D'Urso D, Befort K, Costigan M,
 XX WPI; 2003-268112/26.
 XX GENBANK; AAF05316.
 DR
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX
 XX Example 1; Page; 1017pp; English.
 PS
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 XX or human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
 XX comprising the vector, a method for identifying a nucleotide sequence
 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially expressed in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 XX injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
 XX therapy). The sequence presented is a human protein (described in Table 3
 XX of the specification) which is differentially expressed during pain.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 839 AA;
 SQ
 Query Match 65.5%; Score 2847; DB 7; Length 839;
 Best Local Similarity 67.6%; Pred. NO. 7.2e-237;
 Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;
 QY 1 MPPMLARTLIML-FPSCLTPGSLNPCIENVNITVQCMQKSKVDDIPSTKNIID 59
 DB 1 MMSASRLAGTILPAMAFISCPSWECVENVNITVQCMELNPKIKPDLNLPSTKNIID 60

QY 60 LSFNPKILKISYSFSGNFSELOMLDLSRCEIETIEDKAMHGLHLSNLITGNPIOSFSPG 119
 DB 61 LSFNPLRLGYSFSPFPELOVLDLSRCEIETIEDGAVQSLSHSLITLITGNPIOSLALG 120
 QY 120 SFGSLTSLNIVAVETKASLESPIGOLITLKLAVANHTHCKLPAVYSNLTVLVH 179
 DB 121 AFSGLSSLOKIVAAVETNLASLENFPIGLKTLKEINVAHNIIOSFKLPEYFSNLTLNHL 180
 QY 180 DLSVYIQTITVNDLOFRENPOVNLSDMSINPDIPODAFOGIKLHELTIRGNFSS 239
 DB 181 DLSNKKIOSICTDLRLVHOMPLNLSDLSNPNFIOPGAFKIRLHKILTRNPFSL 240
 QY 240 NIMKTCLOMLAGLHVHRLIIEGFDERNLKEIPEBSIMEGLCVTIDERLTYTNDPFSDI 299
 DB 241 NIMKTCIOGLAGLEVHRLVIEGFRNENLEKFDKSALEGLCNLTIEERLAVLDYLDI 300
 QY 300 VK-FHCLANVAMSLAGSITKYLEDVPHFQMSLITRCQLKQPTLDPFLKSLITM 358
 DB 301 IDLFNCLTNVSSFSLVSTIERKDFSYNFGMOHLELVNCKRFGQPTLKLKSLRLPETS 360
 QY 359 NKGISFVKVALPSLSYDLISRNALSPGCSYSGLGNSLRHDLSPNGAIIINSANFPG 418
 DB 361 NKGANAPSEVLPSELPDLISRNGLSPKCCSOSDFTTSLKYLDLSPNGVITMSSNPLG 420
 QY 419 LLEIQLHDPQHSSTLKRVTFESGAPLSLEKLYLDISYNTKIDPDIPLGTLSTLTKNAG 478
 DB 421 LEQLEHLDFOHSNKKOMSEFVFLSLNRLIYLDISHFTTRVAFNGIFNGLSLEVLKNAG 480
 QY 479 NSFKDNTLSNVPATNTLTPDLISKCOLSQSMGVPTDILHLQLNLSHNNLLPDSHY 538
 DB 481 NSFQENFLPDIETELRLNLTFLDLSQCOLEQSLPFAFNSLSLQVLYNMSHNNFSLDTPPY 540
 QY 539 NOLXSLTLDSCSPRIETS-KGILOHPKSLAFNLTNNSVACICEHOKFLOVWYEOKOF 597
 DB 541 KCLNSLOVLDYSLNHTSKKQELQHPSSALFNLQNDPACTCEHOSFLQMKDQRL 600
 QY 598 LVNVEQWTCATPEVEMNTSLVLDNFNSSTCYMYKTIISVSVSVIYSTVAFPLIYHFFPLI 657
 DB 601 LVEVERMECATPSPDKQGMPLVSL-NITQNMKTIIGVSVLSVAVAVLVYKFFILM 659
 QY 658 LIACKKYSRGSSTYDAFVYSSQENEMWVNLKALEEGVPRHLCLHTRDPIPGVAIA 717
 DB 660 LLAACITYGRENITDAFVYSSQDEDMVRELKMLEEGVPPQLCLHTRDFTPGVAIA 719
 QY 718 ANIOEGFHSRKATVIVVSRHFIOSRMCIFEYEAQTOMPLSSSGIIFVLEKVERSL 777
 DB 720 ANIHGEFHSRKATVIVVSRHFIOSRMCIFEYEAQTOMPLSSRAIIFVLEKVERSL 779
 QY 778 RQVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALDGRASNPDEOT 824
 DB 780 RQVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGRASNPDEGT 826
 RESULT 6
 ID AAW86361 standard; protein; 837 AA.
 XX
 XX AAW86361;
 AC
 XX 15-MAR-1999 (first entry)
 DT
 XX
 XX Human DNAX toll-1-like receptor DTLR4.
 DE
 XX
 XX DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; Il-1 receptor;
 KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KW modulate inflammatory function; morphological effect;
 KW immunological disorder.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO9850547-A2.
 XX
 XX 12-NOV-1998.
 PD

XX 07-MAY-1998; 98WO-US008979.
 XX 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
 PI MPI: 1999-059670/05.
 DR N-PSDB; AAV80675.
 XX Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 PT metabolism, modulate inflammatory function or innate immunity responses.
 XX Claim 3; Page 147-149; 171pp; English.
 XX The present invention specifically describes human DNAX toll-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 XX Sequence 837 AA;
 SQ
 Query Match 65.1%; Score 2829 5; DB 2; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2.4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;
 QY 7 LARTLIMAL-FPSCITPGSLNFCIEVNPITVQCMDQKSLKVPDDIPSSSTKNIDLSFNPFL 65
 DB 6 LAGTILPMAFLSCVRPESWECVE-VNPITYQCEMLNYYKIPDLNPFSTKNIDLSFNPFL 64
 QY 66 KILKYSFSGNSFSELOWLDISRCIEETIEDKAWHGLHLSNLLITGNPIQSFSGSGIT 125
 DB 65 RHLSYSFSPPELQVLDISRCEIQTEBDGAYQSSHSTLLITGNPIQSLALGAFSGIS 124
 QY 126 SIENIVAVPTKLASFPPIGQILTKLVANHFHSGKLPAVPSNLTNLVHVDLSVY 185
 DB 125 SIQKLVAVETNLASLENFPIGHLTKLKELVANHLQSKFLPEYFSNLTNLHLDLSNK 184
 QY 186 IOTITVNDIQFLRENQVNLSDMSINPIIDFIDQAFQGIKLBELTLRGFNSSNIMKTC 245
 DB 185 IGSIVCTDRLVHLQWPLNLSDLSLNPNNFIQPGAFKEIRLHKLTIRNNPQSLNVMKTC 244
 QY 246 LGNLAGLHVHRLILGFKDERNLIEPESIMBGLCVTTIDERPLTYTNDPSDDIVK-FIC 304
 DB 245 ICGIAGLEVHRLVIGEFERNENLEKFDKALBGLCMLTIEEPFLAVLDYLDIDLFNC 304
 QY 305 LNVGSMGLAGVSIKYLEVDPKHKFQKOSLSIIRCOLKOPPTDLPFLKSLTILMNKGSIS 364
 DB 305 LTNVSSFLSVSVTIEVKDPSPYVFGWQHLBELVCKFGQFPTLTKSLKRLITFSNKGNA 364
 QY 365 FKVALPPLSYLDLSENALSFSGCSYSDIGTNSLRLHLDLSFNGALIMSANFNGLELOH 424
 DB 365 FSEVDPSPLEFLDLSNGLSFKCCSQSDGCTSLKXIDLSFNGVITWSSNFIQLGQLH 424
 QY 425 LDFQHSHTLKRVTFSAFLSLKLLLYLDISYTNKIDPDGIFGLTSLNTLKAAGSFKDN 484
 DB 425 LDFQHSNLTQMSSEFVFLSLRNLIYLDISHTHTRVAFNGIFNGLSLEVLKWAAGSFOEN 484
 QY 485 TLSNVTANTNTNLFLDLSKQLEQISGWVDTLHRLQLLMSNNLLFLDSSHYNDLSL 544

DB 485 FLDPDIFTELRLNLFLLDSQQLLEQLSPTAFNSLSLQVLNMSHNNFSDTFPYKCLNSL 544
 QY 545 STIDCGENRIETS-KGILQHPFKSLAFPNLTNNNSVACIEHQKFLQMVKROQFLVNVQ 603
 DB 545 QVLDYSINHLMTSKKLOHFPSSLAFNLNTQNDFACTCHOSFLQWIKDQRLVVER 604
 QY 604 MTCATPVENNTSLVLDPNNSCTCYMTIISVSVSVYVSTVAFLLYHFFYHLLIAGCK 663
 DB 605 MECHTSPDKQGMVLSL-NITCOMKNTIIGVSLVSLVYVVAVLVYKFFHMLLAGCI 663
 QY 664 KYSGESIDYAFVYSSQNDWVRNEIVKNLEEGVPEPHLCIHYRDFIPGVALNANTIOE 723
 DB 664 KYGGENITYDAFYSSQDEDMVRNEIVKNLEEGVPEPHLCIHYRDFIPGVALNANTIE 723
 QY 724 GFHKSRVITYVSRHFVQSRWCIPEYELAQTWQFLSRSGIIFLYLEKVEKSLRQVEL 783
 DB 724 GFHKSRVITYVSRHFVQSRWCIPEYELAQTWQFLSRSGIIFLYLEKVEKSLRQVEL 783
 QY 784 YRLSRNTYLEMEDNPLGRHIFPRLKALLDGSANPEQT 824
 DB 784 YRLSRNTYLEMEDSVLGRHIFPRLKALLDGSANPEQT 824
 RESULT 7
 ID AAE16102 standard; protein: 837 AA.
 AC AAE16102;
 DT 26-MAR-2002 (first entry)
 DT Human DNAX Toll like receptor (DTLR) 4 #2.
 DE Human, DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KW interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX Homo sapiens.
 XX OS WO200190151-A2.
 XX 29-NOV-2001.
 XX 23-MAY-2001; 2001WO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 XX Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 XX MPI: 2002-083085/11.
 XX N-PSDB; AAD26292.
 XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX Claim 3; Page 41; 297pp; English.
 XX The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAB16116). However these sequences differ
 CC at several locations

XX Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 5; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2,4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```

QY 7 LARTLIMAL-FPSCITPGSLNPCIIEVVPNTTYQCDMDKLSKVDDIPSSSTKNIDLSFNPL 65
DB 6 LAGTLIPAMAFILSCVRESMEPCVE-VPNITYQCMELNPFYKIPDNLFPSTKNIDLSFNPL 64
QY 66 KILKYSFSPNSELOMDLSRCEIETIEDKAMHGLHLSNLIITGNPIQSPSPSGSLT 125
DB 65 RHLSYSFSPFPELOVDLSRCEIOTIEDGAYOSLSHSLTILITGNPIQSLALGAFSGLS 124
QY 126 SLENVAEETKLASIESPFIQOLITLKKLVANHFISCKLPAYSNLNLVHVDLSNYX 185
DB 125 SLQKIVAVETNLASLENPFIGHLKITKELVANHILIOSKLPBYSNLTNLHLIDLSNKK 184
QY 186 IQTITVNDLQFLRENPOVNLSDMSLNPIIDFIDQAFQGIKLEHETLRGNFSSNIMKTC 245
DB 185 IQSIVCTDLRVLHQMPNLNLSDLSLNPNFIQPGAFKIRLHKILTRNPFSLNVMKTC 244
QY 246 IQNLAGLHVHRLILEFDEKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDSDDIYK-FHC 304
DB 245 IQGLAGLEVHRLVLDGFVREGNLEKFRDKSALLEGTLNLTIEEPRLVLDYLDIDILFNC 304
QY 305 LANSVAMSILAGYSIKYLEDPVPHGFKMOSLSIIRCOLKOPETDLPEFLSLTLTMKSGSIS 364
DB 305 LTNVSPFSLVSTTIRKVDPSNFGKMHLELVNCKFGQPIKLKSLKRLTYSNKGNA 364
QY 365 FKVALPSELVLDLSRNALSPSGCCSYSDLGTSNRHLNHLDSFNCAIIMSANFMGLEIOLH 424
DB 365 FSEVDLPSELFLDLSRNGLSFKGCCSQSDPGTSLKAYIDLSNGVITMSNSNLGLGLELH 424
QY 425 LDFOHSTLKRVTEBFAFLSLEKLYLDISYNTKIDFGICFGLTSLNTLMKAGNSPKDN 484
DB 425 LDFOHSTLKRVTEBFAFLSLEKLYLDISYNTKIDFGICFGLTSLNTLMKAGNSPKDN 484
QY 485 TLSNVEANTNLTPLDLSKCOLEOISWGVEDTLHRLQILMNSHNHLFLDSHNYQLYSL 544
DB 485 FLPLDFTLRLNLTFLDLSQCOLEOISWGVEDTLHRLQILMNSHNHLFLDSHNYQLYSL 544
QY 545 STLDGSENRIS-EGILQHPFKSLAFPNLTNSVACICEHQKFLQWVEQKQFLVNEYQ 603
DB 545 QVLDSYLNHIMTSKKQELQHPFSSLAFLNLTQNDPACCEHQSFLQWIKDQQLVVER 604
QY 604 MTCATPVEMNTSLVLDENNSTCYMYKTIISVSVAIVSVTAFLIYHFFYLIIIAACK 663
DB 605 MECAITPSKQKQMPVLSL-NITCOMNKTIIGVSLVSVAVAVLYKFEFLMLACGI 663
QY 664 KYSGESTIYDAFVLYSSQNEBDMVRELKYNLEEGVPRPHLCIHYDPIFGVAILANITQE 723
DB 664 KYSGESTIYDAFVLYSSQNEBDMVRELKYNLEEGVPRPHLCIHYDPIFGVAILANITQE 723
QY 724 GFHSRKAVIVVVRHFIQSRWCIPEYEIAQTWQFLSSRGGIIFYLEKESILRQOVEL 783
DB 724 GFHSRKAVIVVVRHFIQSRWCIPEYEIAQTWQFLSSRGGIIFYLEKESILRQOVEL 783
QY 784 YRLISRTYILEWENPLGRHIFWRRLKNAALDGRASNPQOT 824
DB 784 YRLISRTYILEWENPLGRHIFWRRLKNAALDGRASNPQOT 824

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RESULT 8
 ABU04776

ID ABU04776 standard; protein; 837 AA.
 XX
 AC ABU04776;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1442.
 XX
 DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358955P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI: 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, or protease inhibitor.
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 6; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2,4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```

QY 7 LARTLIMAL-FPSCITPGSLNPCIIEVVPNTTYQCDMDKLSKVDDIPSSSTKNIDLSFNPL 65
DB 6 LAGTLIPAMAFILSCVRESMEPCVE-VPNITYQCMELNPFYKIPDNLFPSTKNIDLSFNPL 64
QY 66 KILKYSFSPNSELOMDLSRCEIETIEDKAMHGLHLSNLIITGNPIQSPSPSGSLT 125
DB 65 RHLSYSFSPFPELOVDLSRCEIOTIEDGAYOSLSHSLTILITGNPIQSLALGAFSGLS 124

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QY 126 SLENVAVETKLASLSPFPIGQILITLKKLVANAHNFHSCKLPAYFSNLTNLVHVLDISTNY 185
DB 125 SLQKVAVENTNLASLENFPIGHLKTLKELNVAHNLIQSPFLPEYFSNLTLEHDLSSNK 184
QY 186 IQTTIVNDLOFLRENPOVNLSDMSLNPIDFIDQAFQGIKHELTIRGNFSSNIMKTC 245
DB 185 IQSIYCTDLRVLHQMPNLNLSDLSLNPANFIQGAKEIRLHKLTLRRNPDLSLNVKTC 244
QY 246 LQNLAGLHVRLILGEFKDERNLEIFPSPIMEGLCDVTIDEFRLTYTNDSDDIK-FHC 304
DB 245 IQGLAGLEVRLVGEFRBGNLEKFKSALBGLCNLTIEFRFLAYLDYLDIDIDLFNC 304
QY 305 LANVSAMSLAGVSIKYLEDEVPRKFKWQSLIIRCOLKOPPTLDPLKSLITLTMKGSIS 364
DB 305 LTNVSSFLSVSVTERKXDSYVNGQHLVNCFKQFPPLTKLSLKRLLFTFSNKGNA 364
QY 365 FKXVALPSLSTYDLSSNALSPSGCCSYSDLGTSNLRHLDSFNCAITMSANFMGLELOH 424
DB 365 FSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKTLDSFNGVITMSSNFLGLEOEH 424
QY 425 LDPQHSITLKRTEESAPFLSEKLYLDISYNTKIDFPGIPLGLTSLNTLMAGNSFKDN 484
DB 425 LDPQHSITLKRTEESAPFLSEKLYLDISYNTKIDFPGIPLGLTSLNTLMAGNSFKDN 484
QY 485 TLSVVPANTTNLTFLDLSKCOLBQISWGVFDTLRLQLLNNSHNNLLFLDSSHYNQYSL 544
DB 485 FLPIPIFELRLTLFLDLSQCOLBQISWGVFDTLRLQLLNNSHNNLLFLDSSHYNQYSL 544
QY 545 STLDGSRRIETS-KGIIQHPKSLAPNLTNNVACICEHOKFLOWKEOKOPLVNVEQ 603
DB 545 STLDGSRRIETS-KGIIQHPKSLAPNLTNNVACICEHOKFLOWKEOKOPLVNVEQ 603
QY 545 QVLVYSLNHLNITSKQELQHPSSLAFLNLTQNDPACCEHOSFQMKDQOLVVER 604
DB 545 QVLVYSLNHLNITSKQELQHPSSLAFLNLTQNDPACCEHOSFQMKDQOLVVER 604
QY 604 MTCATPVMNTSLVLDNNSTCYMYKTIISVSVSVIYVAVFLIYHRYTHLILJACK 663
DB 604 MTCATPVMNTSLVLDNNSTCYMYKTIISVSVSVIYVAVFLIYHRYTHLILJACK 663
QY 605 MECATPSPKQGMPLVSL-NITCQNMKTIIGSVLSVAVVAVLYVFYHMLMAGCI 663
DB 605 MECATPSPKQGMPLVSL-NITCQNMKTIIGSVLSVAVVAVLYVFYHMLMAGCI 663
QY 664 KYSRGESIYDAFVIYSSQNEDEWVNELVKNLEEGVPRFHLCLHYRDFIPGVAIANIIE 723
DB 664 KYSGRENIYDAFVIYSSQDEDEWVNELVKNLEEGVPRFHLCLHYRDFIPGVAIANIIE 723
QY 724 GFHSKRKYIVVVSRIQSRMCIFEYELAQTMQFLLSSSGIIFYLEVEKESILMQOVL 783
DB 724 GFHSKRKYIVVVSRIQSRMCIFEYELAQTMQFLLSSSGIIFYLEVEKESILMQOVL 783
QY 724 GFHSKRKYIVVVSRIQSRMCIFEYELAQTMQFLLSSSGIIFYLEVEKESILMQOVL 783
DB 724 GFHSKRKYIVVVSRIQSRMCIFEYELAQTMQFLLSSSGIIFYLEVEKESILMQOVL 783
QY 784 YRLLSRNTYLEMEDNPLGRHIFMRRLKXNLLDGKASNPBQT 824
DB 784 YRLLSRNTYLEMEDNPLGRHIFMRRLKXNLLDGKASNPBQT 824
QY 784 YRLLSRNTYLEMEDNPLGRHIFMRRLKXNLLDGKASNPBQT 824
DB 784 YRLLSRNTYLEMEDNPLGRHIFMRRLKXNLLDGKASNPBQT 824

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
XX AAE16116;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
XX
XX Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 211
XX
XX FT /label= Unknown
XX
XX FT /note= "Encoded by AAY"
XX
XX PN MO200190151-A2.
XX
XX 29-NOV-2001.
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XX 23-MAY-2001; 2001MO-US016766.
PF
XX
XX 25-MAY-2000; 2000US-0207558P.
PR
XX
XX (SCHE ) SCHERING CORP.
PA
XX
XX Hardman GT, Rock FL, Bazan JF, Kaetelein RA, Ho SWK, Liu Y;
PI
XX
XX WPI; 2002-083085/11.
DR
XX
XX N-PSDB; AAD26306.
XX
XX
XX Claim 3; Page 240-243; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
XX
XX human DNAX Toll like receptor (DTLR) protein and their corresponding
XX
XX nucleic acids. The DTLR is useful for treating conditions exhibiting
XX
XX abnormal expression of the receptors of their ligands. Such abnormality
XX
XX is manifested by immunological disorders. In particular, the DTLR is
XX
XX useful for treating various disease or disorders associated with abnormal
XX
XX expression or abnormal triggering of response to a ligand. The DTLR is
XX
XX also useful as an immunogen for the production of antisera or antibodies
XX
XX specific, e.g., capable of distinguishing between other interleukin (IL)-1
XX
XX receptor family members, for the DTLR or its various fragments. The
XX
XX purified DTLR can be used to screen monoclonal antibodies or antigen-
XX
XX binding fragments. The antibodies are useful for screening expression
XX
XX libraries for particular expression products. These are useful for
XX
XX detecting or diagnosing various immunological conditions related to
XX
XX expression of DTLR or cells that express it. The present sequence is
XX
XX human DTLR4 protein, alternative version. The DTLR4 gene is located on
XX
XX chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
XX
XX be similar to the sequence shown in page 41 (AAE16102). However these
XX
XX sequences differ at several locations
XX
XX
XX Sequence 837 AA;
XX
XX
XX Query Match 65.0%; Score 2822.5; DB 5; Length 837;
XX
XX Best Local Similarity 67.6%; Pred. No. 9.5e-235;
XX
XX Matches 555; Conservative 101; Mismatches 160; Indels 5; Gaps 5;
XX
XX
XX 7 LARTLTMAL-FPSCITPESLNPCTEYVNPNTYQCCMDQLSKVPDIPSTKXIDLSFNPPL 65
XX
XX 6 LAGTLIPAMARLSCVRPSWEPVE-VENITYQCELNIFYKIPDLPSSTXKIDLSFNPPL 64
DB
XX
XX 66 KILKSYSPNSFSELOMDLSRCEIETIEDKAMHGHLNLTGNPIQSPSPGSPSGLT 125
XX
XX 65 RHLSYSFSPFPELDVLDLSRCEIOTIEDGAYQSLSHLSTLITGNPIQSLALGAFSGLS 124
DB
XX
XX 126 SLENVAVETKLASLSPFPIGQILITLKKLVANAHNFHSCKLPAYFSNLTNLVHVLDISTNY 185
XX
XX 125 SLQKVAVENTNLASLENFPIGHLKTLKELNVAHNLIQSPFLPEYFSNLTLEHDLSSNK 184
DB
XX
XX 186 IQTTIVNDLOFLRENPOVNLSDMSLNPIDFIDQAFQGIKHELTIRGNFSSNIMKTC 245
XX
XX 185 IQSIYCTDLRVLHQMPNLNLSDLSLNPANFIQGAKEIRLHKLTLRRNPDLSLNVKTC 244
DB
XX
XX 246 LQNLAGLHVRLILGEFKDERNLEIFPSPIMEGLCDVTIDEFRLTYTNDSDDIK-FHC 304
XX
XX 245 IQGLAGLEVRLVGEFRBGNLEKFKSALBGLCNLTIEFRFLAYLDYLDIDIDLFNC 304
DB
XX
XX 305 LANVSAMSLAGVSIKYLEDEVPRKFKWQSLIIRCOLKOPPTLDPLKSLITLTMKGSIS 364
XX
XX 305 LTNVSSFLSVSVTERKXDSYVNGQHLVNCFKQFPPLTKLSLKRLLFTFSNKGNA 364
DB
XX
XX 365 FKXVALPSLSTYDLSSNALSPSGCCSYSDLGTSNLRHLDSFNCAITMSANFMGLELOH 424
XX
XX 365 FSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKTLDSFNGVITMSSNFLGLEOEH 424
DB
XX
XX 365 FSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKTLDSFNGVITMSSNFLGLEOEH 424
```

QY 425 LDFOHSTIKRVTESAFSLSEKTLIDISYNTKIDPDCIFLGSLTSLNTKMAKNSFKDN 484
 DB 425 LDFOHSTIKRVTESAFSLSEKTLIDISYNTKIDPDCIFLGSLTSLNTKMAKNSFKDN 484
 QY 485 TILSNFANTMTLFTDLSCQLEQISWGVFTDLHLLQLLNMGHNNLLFLDSSHYNQYSL 544
 DB 485 TILSNFANTMTLFTDLSCQLEQISWGVFTDLHLLQLLNMGHNNLLFLDSSHYNQYSL 544
 QY 545 STLDSCFNRIETS-KGIIQHPKSLAFNLTNNSVACICEHOKFLQWVEKQKPLVNEQ 603
 DB 545 QVLDSYLNHIMTSKQOELOHFPSSLAFLNTQNDPACCEHQSFLQWIKDQQLLVEVER 604
 QY 604 MTCATPVMNTSLVDPNNTSTYMTKTIISVSVSIVYVSTAFLIYHFFLLIAGCK 663
 DB 604 MTCATPVMNTSLVDPNNTSTYMTKTIISVSVSIVYVSTAFLIYHFFLLIAGCK 663
 QY 605 MECATPSPKQMPVLSL-NITCQNMKTIIIGVSVLSVVAVAVYKFFHMLAGCI 663
 DB 605 MECATPSPKQMPVLSL-NITCQNMKTIIIGVSVLSVVAVAVYKFFHMLAGCI 663
 QY 664 KYSRGSSTYDAFVIYSSQNEBVRNELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIE 723
 DB 664 KYRGENIYDAFVIYSSQNEBVRNELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIE 723
 QY 724 GFHRSKRVIVVSRHFIOSRMCIFEYELAQTWQPLSRSGIIFIVLEKESKILRQVEL 783
 DB 724 GFHRSKRVIVVSRHFIOSRMCIFEYELAQTWQPLSRSGIIFIVLEKESKILRQVEL 783
 QY 784 YRLLSRNTYLEWEDNPLGRHIFWRRLKVALLDGKASNPBQT 824
 DB 784 YRLLSRNTYLEWEDNPLGRHIFWRRLKVALLDGKASNPBQT 824

RESULT 10

ID ADOS7791 standard; protein; 795 AA.
 XX AC ADOS7791;
 XX 12-AUG-2004 (first entry)
 DT Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
 XX Macaca mulatta.
 OS Key Location/Qualifiers
 FH Misc-difference 635
 FT /label= Lys, Asn
 XX MO2004042365-A2.
 XX 21-MAY-2004.
 PD 03-NOV-2003; 2003WO-US036247.
 PF 01-NOV-2002; 2002US-0423113P.
 PR (EVOL-) EVOLUTIONARY GENOMICS LLC.
 PA Messier W;
 PI WPI; 2004-400726/37.
 DR N-PSDB; ADOS7789, ADOS7790.
 XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX Disclosure; SEQ ID NO 12; 111pp; English.
 PS The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World

CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents rhesus monkey TLR4.

SQ Sequence 795 AA;

Query Match 64.2%; Score 2788.5; DB 8; Length 795;

Beet Local Similarity 68.3%; Pred. No. 7.7e-232;
 Matches 543; Conservative 98; Mismatches 151; Indels 3; Gaps 3;

QY 31 VVPNTTCQMOQKLSKVPDDIPSSSTKNDLSFNPILKISYFSFSELOMDLSRCRE 90
 DB 1 VVPNTTCQMOQKLSKVPDDIPSSSTKNDLSFNPILKISYFSFSELOMDLSRCRE 90
 QY 91 TIEDKAWHGLHLSNLITGNPIOSFSPGSGSLSENVAVERKLASLESFPIGOLIT 150
 DB 61 TIEDKAWHGLHLSNLITGNPIOSFSPGSGSLSENVAVERKLASLESFPIGOLIT 150
 QY 151 LKCANVAFHSHCKLPAYPSNLTNLVHVDLSYNYIQITTVNDLOFLBNPQVNLSDMS 210
 DB 121 LKCANVAFHSHCKLPAYPSNLTNLVHVDLSYNYIQITTVNDLOFLBNPQVNLSDMS 210
 QY 211 LNPIDFIDQAFQGIKHELTIRGNFNSNMKTCLQWLAGHVRLLTGEFKDERNLEI 270
 DB 181 LNPIDFIDQAFQGIKHELTIRGNFNSNMKTCLQWLAGHVRLLTGEFKDERNLEI 270
 QY 271 FEPSTMEGLCDVTIDEFRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEVDPKHF 329
 DB 241 FEPSTMEGLCDVTIDEFRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEVDPKHF 329
 QY 330 WQSLIIRCOLKOPFTLDPFLKSLITLTMKSGISFPKVALPSLSYLDLSRNALSFSGCC 389
 DB 301 WQSLIIRCOLKOPFTLDPFLKSLITLTMKSGISFPKVALPSLSYLDLSRNALSFSGCC 389
 QY 390 SYSDLGTSLHLLDLSFGALITMSANFPGLELOHLDFOHSTIKRVTESAFSLSEKTL 449
 DB 361 SYSDLGTSLHLLDLSFGALITMSANFPGLELOHLDFOHSTIKRVTESAFSLSEKTL 449
 QY 450 LDISYNTKIDPDCIFLGSLTSLNTKMAKNSFKDNLTNNSVANTMTLFTDLSCQLEQ 509
 DB 421 LDISYNTKIDPDCIFLGSLTSLNTKMAKNSFKDNLTNNSVANTMTLFTDLSCQLEQ 509
 QY 510 SWGVFTDLHLLQLLNMGHNNLLFLDSSHYNQYSLSTDCSFPNRIETSKG-ILQHPKSL 568
 DB 481 SWGVFTDLHLLQLLNMGHNNLLFLDSSHYNQYSLSTDCSFPNRIETSKG-ILQHPKSL 568
 QY 569 AFPNLTNNSVACICEHOKFLQWVEKQKPLVNEQMCATPEVNTSLVDPNNTSTYMT 628
 DB 541 AFPNLTNNSVACICEHOKFLQWVEKQKPLVNEQMCATPEVNTSLVDPNNTSTYMT 628
 QY 629 KTIISVSVSIVYVSTAFLIYHFFLLIAGCKKTSRGSISYDAFVIYSSQNEBWRN 688
 DB 600 KTIISVSVSIVYVSTAFLIYHFFLLIAGCKKTSRGSISYDAFVIYSSQNEBWRN 688
 QY 689 ELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIOGPFHRSKRVIVVSRHFIOSRMCIFE 748
 DB 660 ELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIOGPFHRSKRVIVVSRHFIOSRMCIFE 748
 QY 749 YEIAQWQPLSRSGIIFIVLEKESKILRQVELYRLLSRNTYLEWEDNPLGRHIFWR 808
 DB 720 YEIAQWQPLSRSGIIFIVLEKESKILRQVELYRLLSRNTYLEWEDNPLGRHIFWR 808
 QY 809 LKVALLDGKASNPBQT 823
 DB 780 LKVALLDGKASNPBQT 823

RESULT 11

AD057797
ID AD057797 standard; protein; 801 AA.
XX
AC AD057797;
XX
DT 12-AUG-2004 (first entry)
XX
DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS Saimiri sciureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /label= leu, phe
XX
FN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PP 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Meslier W;
XX
XX WPI; 2004-400726/37.
DR N-PSDB; AD057795; AD057796.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents squirrel monkey TLR4.
XX
SQ Sequence 801 AA;
XX
Query Match 64.1%; Score 2785.5; DB 8; Length 801;
Best Local Similarity 68.3%; Pred. No. 1.4e-231;
Matches 544; Conservative 90; Mismatches 159; Indels 3; Gaps 3;
XX
QY 31 VVPNTTYQCMQDKLSKVPDDIPSTYNDLSFNPILKLSYSFSNFSLEQWLDLSCRELE 90
DB 1 VVPNTTYQCMELNXXKIPDNIRPSTKNLDSLFPRLHLSHSPFNPRELQVLDLSRCDIQ 60
XX
QY 91 TIEDKAMHGLHLSNLIITGNPIQSPSPSGSLTLENLVAETKGLASLESFPIQOLIT 150
DB 61 TIEDGAYGSLSHSLITLGNPIQLNALGAFSGLSLQKLVAVETHLLENPFIQHLXT 120
XX
QY 151 LKLVAVAHFHSCTLPAYFSNLTNLVHYDLSYNYQTIVNDIQFLRENPQVNLSDMS 210
DB 121 LKDLVAVAHNLIOFSLPEYFSNLTNLHDLSSNNIQLNYCKDLQVLRHQPPLNLSLDLS 180
XX
QY 211 LNPIDPFDQAFQGIKLHETLRLGNFSSNIMKTCQLQNLAGLHVRLLIGFEDERNLEI 270
DB 181 LNPINIQGAFREIRHLHKLTLRNNFDSLAMKTCIQGLAGLEVHRLVIGEPNNENIED 240

QY 271 FEPISMEGLCDVTIDFRLTYTNDPSDDIYK-FHCLANYSAMSLAGVSIKYLEDPGRHFK 329
DB 241 FDKSALBGLCNLTINERLAIYDDFLDDIIDLNCLANYSFPLVNVHIMKRVDFPSYNNFR 300
XX
QY 330 WQSLIIRCOLKQPTLIDPFLKSLTLTNKKSISFEKVALPSLSTYDLSRNALSEGCC 389
DB 301 WQHLLEVNCVFOQFPFLKLSLRKLTFTANKGNHNSSEVLPPLSEFLDLSRNGLSFPGCC 360
XX
QY 390 SYSDLGTSNLSRHLDSLNGAMIMSANFMGLEEHLQHDFOHSTLKRVRVFAFLSEKLLY 449
DB 361 SOSDFGTSLSKYLDSLSPNDVITGNSNPLGLEJLHLDFOHSNLSKQNSFVSFLSRMLY 420
XX
QY 450 LDISYNTKXIDFDGIFGLTSLNTLTKAAGNSFKONTLSNVFANTNLTFDLRSQOLEOI 509
DB 421 LDISHTHTRVAFNGITFNGFLPSLKLTKAAGNSFQGNFEDJFTDLNMLIFDLSECOLEQL 480
XX
QY 510 SWGVFDTLHRLQLINMSHNNLLFLDSHYNQLYSLSLTDGSPNRIETSKG-ILQHPKSL 568
DB 481 SPTAFDSLPRRLRLIMSHNNFPALDTPPYKGLYSLQVLDVSLNHIQTSKQELQHPSSL 540
XX
QY 569 AFPLTNNNSVACTCEHOKFLQWYKCKOPLVNTVEOMTCATPVENNTSLVDFNNSTCMY 628
DB 541 AFLNLTQNDFACTCEHOSFLOMTKQRRLLVEYQMECAPLNRKGIPVLSL-NITCOMS 599
XX
QY 629 KTIISVSVSYIVVSTVAFILYHFYFLILILAGCKTSRGESIYDAFVIYSSQNEDEWVRN 688
DB 600 KTIIGSVLSLVVSVVAVLVYKFFHMLLAGCITKRGRENTYDAFVIYSSQNEDEWVRN 659
XX
QY 689 ELVKNLEGVPRFLCLHYRDFIPGVAIIANIIOEGHKSARKVIVVSRHETGRCWCFE 748
DB 660 ELVKNLEGVPRFQCLHYRDFIPGVAIAANIIHEGFHKSARKVIVVSRHETGRCWCFE 719
XX
QY 749 YEIQOTQWPLSSRGIIIFVLEKYEKSLRQOVELYLLSNTYLEMEDNPLGRIHFWRR 808
DB 720 YEIQOTQWPLSSRGIIIFVLEKYEKSLRQOVELYLLSNTYLEMEDNPLGRIHFWRR 779
XX
QY 809 LKNALLDGKASNPQOT 824
DB 780 LKNALLDGKASNPQOT 795
XX
RESULT 12
AD057803
ID AD057803 standard; protein; 808 AA.
XX
AC AD057803;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PP 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Meslier W;
XX
XX WPI; 2004-400726/37.
DR N-PSDB; AD057801; AD057802.
XX

PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 PS Disclosure; SEQ ID NO 24; 11pp; English.
 XX
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Query Match 64.1%; Score 2785.5; DB 8; Length 808;
 Best Local Similarity 68.2%; Pred. No. 1.4e-231;
 Matches 543; Conservative 99; Mismatches 151; Indels 3; Gaps 3;
 QY 31 VPPNTTTCQMDKLSKVPDDIPSSSTKNDLSFNPPLKILKSYFSNPSLQMDLSRCIE 90
 DB 1 VPPNTTTCQMDLNFYKIPDNLPSSTKNDLSFNPPLKILKSYFSNPSLQMDLSRCIE 60
 QY 91 TIEDKAMHGLHLSNLILTGNIQSFSGSFGSLSTLENLVAVETKLASLSPFGQLIT 150
 DB 61 TIEDGAYOSLSHLSLITLITGNPIQSLALGAFSGSLQKLVAVETNLASLENFPIGHKLT 120
 QY 151 LKKLVANFNHSHCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENQVNLSDMS 210
 DB 121 LKELVAVANHLIQSFKLPEYFSNLTNLEHDLSSNNKIQSYCTDRLVHQMPLNLSLDS 180
 QY 211 LNPIDFIQDAQOGKHELTARGNPNNSIMKTCLQNLAGLHVHRLIIGFEKDERNL 270
 DB 181 LNPMPFIQGAKEKRLHKLTLTRNNPDSLNVMKTCIOGAGLEVHRLVIGERNEENLEK 240
 QY 271 FEPSIMEGCDVTIDEFRLTYTNDSPDDIVK-FHCLAVNSAMSLAGVSKYLEVDYPRKHK 329
 DB 241 FDKSLBEGICNLITIEFRLAYIDYLDLIDLPNCILTNVSSSLVSVTKSYKXDSPYNG 300
 QY 330 WQSLIIRCOLKQFPFLDLPLKSLTLTNMKGSIKFKVVALPSLYLDSRNALSPSGCC 389
 DB 301 WQHLVAVCKEFGQFPLTKLSKRLTLFNSKGNAPSEVDLPFLDLSRNGLSFKGCC 360
 QY 330 SYSIDGTSNLRHLDSFNGALIMSNFNGLEBLQHLDFQHSHTLKVTEFSAFLSLEKLY 449
 DB 361 SOSDEGTSLSKYLDSFNGVIMSSNFIQLEHLEHDFQHSNLMKQMSSEFSVFLSRNL 420
 QY 450 LDISYTNKIDPDGIFLGITSLNLTLMKAGNSFKDNTLSVFNANTNLPLFLDLSKCOLBOI 509
 DB 421 LDISITHIRVAFNGIFNGLSLEVLKMGANSQENFLPDITELRNLTFLDLSQOLEL 480
 QY 510 SMGVEDTLARLQOLMNSHNLLFLDSHYNQLYSLTLDSCFNRIETS-KGILQHPKSL 568
 DB 481 SPTAENSLSLQVLNMSHNPFSLDTPPYKCLNSLQVLDYLSNHTMTSKKQOLQHPSSL 540
 QY 569 AFNLTNNNSVACICHOQFLQWVKQKQFLVAVEDQMTCAIPVEMNTSLVLDPNSTCYW 628
 DB 541 AFLNLTQNDPACTCHQSFLOWIKDQRLVVERMECATPSDKQGMVLSL-NITCOMN 599
 QY 629 KTIISVSVSVYIVASTVAFLIYHFEYHLILTAGCKKYSRGSIVAPVYISSQNDWNRN 688
 DB 600 KTIIGVSIVSVYIVASTVAFVLYKFFHMLTAGCKKYGSENYIDAFYISSQDDWNRN 659
 QY 669 ELVKNLEEGVRFHLCIHYRDFIPGVAIANIIOGFHKSRYIVVSRHPIQSWCIFE 748
 DB 660 ELVKNLEEGVRFHLCIHYRDFIPGVAIANIHHGFHKSRYIVVSGHPIQSWCIFE 719
 QY 749 YEIAQWQPLSRSQIIFIVLEKVKSLRQVELYRLSRNTYLEMEDNPLGRHIFWR 808

DB 720 YEIAQWQPLSRSQIIFIVLEKVKSLRQVELYRLSRNTYLEMEDSVLGRHIFWR 779
 QY 809 LKNALLDGKSNPEOT 824
 DB 780 LKRALDGKSNPEOT 795
 RESULT 13
 ID ADO57782
 ADOS7782 standard; protein; 808 AA.
 AC ADO57782;
 DT 12-AUG-2004 (first entry)
 DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 OS Pan troglodytes.
 PN WO200402365-A2.
 PN 21-MAY-2004.
 PF 03-NOV-2003; 2003WO-US036247.
 PR 01-NOV-2002; 2002US-0423113P.
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 PI Messier W;
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADO57780, ADO57781.
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 PS Example 1; SEQ ID NO 3; 11pp; English.
 XX
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Query Match 64.0%; Score 2781.5; DB 8; Length 808;
 Best Local Similarity 68.2%; Pred. No. 3.2e-231;
 Matches 543; Conservative 98; Mismatches 152; Indels 3; Gaps 3;
 QY 31 VPPNTTTCQMDKLSKVPDDIPSSSTKNDLSFNPPLKILKSYFSNPSLQMDLSRCIE 90
 DB 1 VPPNTTTCQMDLNFYKIPDNLPSSTKNDLSFNPPLKILKSYFSNPSLQMDLSRCIE 60
 QY 91 TIEDKAMHGLHLSNLILTGNIQSFSGSFGSLSTLENLVAVETKLASLSPFGQLIT 150
 DB 61 TIEDGAYOSLSHLSLITLITGNPIQSLALGAFSGSLQKLVAVETNLASLENFPIGHKLT 120
 QY 151 LKKLVANFNHSHCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENQVNLSDMS 210


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Db 121 LKELNVAHNLIOSEKLEPEYSNLTNLEHLDISSNKIOIYCTDRLVHOMPLNLSLDS 180
Qy 211 LNPIDFIDODAFQGIKIHLELTLRGFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db 181 LNPINFIOPGAFAKRIHLKHLTLRNNFDSLNMKTCIGLAGLEVHRLVLGEFRNEGULEK 240
Qy 271 PEPIMEGLCVTIDEPFLTYTNDPSDDIVK-FHCLANVSAMSLAGVSIKLEVPKHF 329
Db 241 FDKSALBGLCNLTIEEFLTYLDYLDIIDLFPCLNTVSSFSVSVYIKSVKDFSYNFG 300
Qy 330 WQSLIIRCOLKOPFTLDPLFKSLTLTMNKGSIISPKVALPSLSDLSNNALSPSGCC 389
Db 301 WQHLLEVNCCKGQPPTLKSLKRLTFSNKGNAFSEVDLPSEFLDLSNNGLSFKGCC 360
Qy 390 SYSDLGTSNLRHLDSFNGAIIIMSANFNGLELQHLDPQHSHTLKVTEFSALISLEKLY 449
Db 361 SOSDFGTSLSKYLDSFNGVITMSNFIQLBQLEHLDFOHSNLKQMSBFSVFLSRNLY 420
Qy 450 LDISYNTKIDPDGIFLGLTSLNTLKMAKNSFKDNTLSNVANTNLFLDLSCQLEOI 509
Db 421 LDISHTHTRVAFNGIFNGLSLLEVLKMAKNSFOENFLDIFTELRLNLFLLDSQQLBQL 480
Qy 510 SMGVPTLHRLQLLMSHNNLLFLDSHYNOLYSLTDCSPNRIETS-KGILQHPKSL 568
Db 481 SPTAFNLSLSLQVLNMSHNNPFLDTPPYKCLNSLQVLDLSLNHMTSKQELQHPSSL 540
Qy 569 AEFNLTNNSVACICEHOKFLQWKEOKQFLVNVNQTCATPEVEMNTSLVDENNSTCYW 628
Db 541 AFLNLTQNDFACTCEHOSFLQWIKQORQLVEVERMECATPEDKQGMPLSLV-NITCQNA 599
Qy 629 KTIISVSVSIVVSTVAFLIYHFFHLLILGCKKYSNGESIYDAFYIYSSQNDVARN 688
Db 600 KTIIGVSIVSVIVVAVLVYKFFHMLLAGCIRYGENIYDAFYIYSSQDDVARN 659
Qy 689 ELVKNLEBVRPFHCLHYRDFIPGVALANIIIOEGFHKSRYIVVSHHFIOSEWCIPE 748
Db 660 ELVKNLEBVRPFOLCLHYRDFIPGVALANIIHBSGFHKSRYIVVSHHFIOSEWCIPE 719
Qy 749 YEIAQTCQFLSSRSGLIIFVLEKVEKSLRQOVELYRLSRNTYLEMEDNPLGRHIFWR 808
Db 720 YEIAQTCQFLSSRAGIIFVLOKVEKTLRQOVELYRLSRNTYLEMEDSVLGRHIFWR 779
Qy 809 LKNALIDGKASNEQOT 824
Db 780 LKKALLDGKSNMEGT 795

RESULT 14
AD057800
ID AD057800 standard; protein; 795 AA.
XX
AC AD057800;
XX
DT 12-ANG-2004 (first entry)
XX
DE Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
OS Papio hamadryas.
XX
PN MO2004042365-A2.
XX
PD 21-MAY-2004.
XX
XX 03-NOV-2003; 2003MO-USG036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
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PI Meslier W;
XX WPI; 2004-400726/37.
DR N-PSDB; AD057798, AD057799.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure, SEQ ID NO 21, 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of a human. The
XX monkey which corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents hamadryas baboon TLR4.
XX
XX Sequence 795 AA;
XX
XX Query Match 63.9%; Score 2777.5; DB 8; Length 795;
XX Best Local Similarity 68.2%; Pred. No. 6.9e-231;
XX Matches 542; Conservative 95; Mismatches 155; Indels 3; Gaps 3;
Qy 31 VVNPITYQCMDOKLSKVPDDIPSTKXNDLSFNPDLTKLKSFSNFBELQHLDSRCEIE 90
Db 1 VVNPITYQCMELNFKYKIPDNIPFSTKXNDLSFNLRIHGSYFRLPELQVLDLSRCEIQ 60
Qy 91 TTEBKAMGLHLSNLTITGNPIOSFSGSGSLTSENVAVETKLASLSPFICOLIT 150
Db 61 TTEBQAYOSLSHLSLTITGNPIOSLAGASGSLQKLVAVETNLSLNLFGHILKT 120
Qy 151 LKKNVANPNFHSCKLPAYFNSLNTLVHVDLSYNYITQITVNDILOFLRENQVNLSDMS 210
Db 121 LKELNVAHNLIOSEKLEPEYSNLTNLEHLDISSNKIOIYCTDRLVHOMPLNLSLDS 180
Qy 211 LNPIDFIDODAFQGIKIHLELTLRGFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db 181 LNPINFIOPGAFAKRIHLKHLTLRNNFDSLNMKTCIGLAGLEVHRLVLGEFRNEGULEK 240
Qy 271 PEPIMEGLCVTIDEPFLTYTNDPSDDIVK-FHCLANVSAMSLAGVSIKLEVPKHF 329
Db 241 FDKSALBGLCNLTIEEFLTYLDYLDIIDLFPCLNTVSSFSVSVYIKSVKDFSYNFG 300
Qy 330 WQSLIIRCOLKOPFTLDPLFKSLTLTMNKGSIISPKVALPSLSDLSNNALSPSGCC 389
Db 301 WQHLLEVNCCKGQPPTLKSLKRLTFSNKGNAFSEVDLPSEFLDLSNNGLSFKGCC 360
Qy 390 SYSDLGTSNLRHLDSFNGAIIIMSANFNGLELQHLDPQHSHTLKVTEFSALISLEKLY 449
Db 361 SOSDFGTSLSKYLDSFNGVITMSNFIQLBQLEHLDFOHSNLKQMSBFSVFLSRNLY 420
Qy 450 LDISYNTKIDPDGIFLGLTSLNTLKMAKNSFKDNTLSNVANTNLFLDLSCQLEOI 509
Db 421 LDISHTHTRVAFNGIFNGLSLLEVLKMAKNSFOENFLDIFTELRLNLFLLDSQQLBQL 480
Qy 510 SMGVPTLHRLQLLMSHNNLLFLDSHYNOLYSLTDCSPNRIETS-KGILQHPKSL 568
Db 481 SPTAFNLSLSLQVLNMSHNNPFLDTPPYKCLNSLQVLDLSLNHMTSKQELQHPSSL 540
Qy 569 AEFNLTNNSVACICEHOKFLQWKEOKQFLVNVNQTCATPEVEMNTSLVDENNSTCYW 628
Db 541 AFLNLTQNDFACTCEHOSFLQWIKQORQLVEVERMECATPEDKQGMPLSLV-NITCQNA 599
Qy 629 KTIISVSVSIVVSTVAFLIYHFFHLLILGCKKYSNGESIYDAFYIYSSQNDVARN 688
Db 600 KTIIGVSIVSVIVVAVLVYKFFHMLLAGCIRYGENIYDAFYIYSSQDDVARN 659
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QY 669 ELVKNLEGGVPRFHLCIHYRDPFIPGVAIAANIIOEGFHKSRAVIYVNSHFIQSRWCIFE 748
Db 660 ELVKNLEGGVPRFQCLHYRDPFIPGVAIAANIHHGFFHKSRAVIYVNSHFIQSRWCIFE 719
QY 749 YEIAQTWQFLSSRSGIIFIVLEKYEKSLRQOVELYRLSHNTYLEMEDNPIGRHIFMR 808
Db 720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLRQOVELYRLSHNTYLEMEDSVLGQHI FMR 779
QY 809 LKNALLDGKASNPQ 823
Db 780 LKRALLDGRSWNPEE 794
RESULT 15
AD057785
ID AD057785 standard; protein; 808 AA.
XX AC AD057785;
XX 12-AUG-2004 (first entry)
XX DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; gorilla.
XX OS Gorilla gorilla.
XX PN MO2004042365-A2.
XX PD 21-MAY-2004.
XX PF 03-NOV-2003; 2003WO-US036247.
XX PR 01-NOV-2002; 2002US-0423113P.
XX PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX PI Messier W;
XX DR WPI: 2004-400726/37.
XX N-PSDB; AD057783; AD057784.
XX PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX PS Example 1; SEQ ID NO 6; 111pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents gorilla TLR4.
SQ Sequence 808 AA;
Query March 63.6%; Score 2763.5; DB 8; Length 808;
Best Local Similarity 67.8%; Pred. No. 1.2e-229;
Matches 540; Conservative 99; Mismatches 154; Indels 3; Gaps 3;
QY 31 VVNNITQCMQDKSKVPDDIPSSSTKXNDLSFNPPLKIKSYSFNSFELQWMLDSRCEIE 90
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QY 91 TIEBKAMHGLHLSNLITGNPIQSFSPGSGLTLENLVAVETKLASLESFPIGLIT 150

Db 61 TIEBAYOSLSHLSLTLITGNPIQSLAGAFSGLSLQKLVAVETNLSLENFPIGLHKT 120
QY 151 LKKNVANPNFHSCKLPAYFSNLTNLVHVDLSYNYIGOTITVNDLQFLBNPOVNSLQMS 210
Db 121 LKELVANPNLQSFELPFPYFSNLTNLVHVDLSYNYIGOTITVNDLQFLBNPOVNSLQMS 180
QY 211 LNPIDFIDQAFQGIKHELTLRGNFNSSNIMKTCLQNLAGLHVHRLTIGEFKDERNDEI 270
Db 181 LNPWFIIQPGAPKEIRLHKLTLRNNFDSLNMWKTICIGLAGLEVRLVLTGEFRNGNLEK 240
QY 271 FEPSIMEGLCDVITDEFPLTITNDPSDIYK-FHCLAVSAMSAGVSIKTIEDVPKHK 329
Db 241 FDKSALBGLCNLTIEEFLAVLDYLDIDLFNCLITVSSSPSLVSVTIERKDPSSYNG 300
QY 330 WQSIIIRCOLKOPFTLDPFLKSLTLMNKGSIKFKVVALPSLSYTLDSRYALSFSQGC 389
Db 301 WQHLVAVCKFGQFPFLTKSLKRLTFSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 360
QY 390 SYSIDGINSRLHLSFNGALIMSNFMLELQHLDPQHSCLKRVTEFSAFLSLEKLY 449
Db 361 SQSDRGTTSLAKYLDLSFNGVITMSNFIQLQLEHLDQHNLMQMSFVSFLSRNLILY 420
QY 450 LDISYTNKXIDPDIPLGLTSLNLTLMKAGNSPKDNTLSNFPANTNLTFLDISKQLEQT 509
Db 421 LDISHTHRAVAFNGIFNGLSLEVLKMAAGNSFOENFLPDITELNLTFLDLSQCLEQL 480
QY 510 SMGVPDTHRLQOLNMSNNLLFLDSSHYNDLXSLTDCSFNRETS-KGILQHPFSL 568
Db 481 SPTANSLSLQVLMNSNNPSSLDTPPYKCLNSLRVLDLSLNMHTSKKQELQHPFSL 540
QY 569 AAFNLTNNSVACICEHQKFLQWVKEQKFLVNVQMTCAVEWNTSLVLPFNNSTCYMY 628
Db 541 AFINLTQNDFACTCEHQSFLOMIDQRLIVEVERMECATPSDKQMWVLSL-NITCGMN 599
QY 629 KTIISVSYSVYIVSTVAFILYHFFHLLIAGCKTSKSGSIYDAFVITYSSQNEBWYN 688
Db 600 KTIIGSVSLVLYVSVAVLVYKFFHLMILAGCIKYGRGNVYDAFVITYSSQNEBWYN 659
QY 689 ELVKNLEGGVPRFHLCIHYRDPFIPGVAIAANIIOEGFHKSRAVIYVNSHFIQSRWCIFE 748
Db 660 ELVKNLEGGVPRFQCLHYRDPFIPGVAIAANIHHGFFHKSRAVIYVNSHFIQSRWCIFE 719
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Db 720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLRQOVELYRLSHNTYLEMEDSVLGQHI FMR 779
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Job time : 90.9834 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds

(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985b-99

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2786.5	64.1	844	4	US-09-949-016-9438
2	619.5	14.3	661	1	US-08-514-014-4
3	619.5	14.3	661	2	US-08-833-823-4
4	494	11.4	784	4	US-09-983-308B-23
5	432.5	10.0	775	4	US-09-949-016-8799
6	317.5	7.3	603	1	US-08-190-802A-50
7	317.5	7.3	603	3	US-08-477-346-50
8	317.5	7.3	603	4	US-08-473-089-50
9	317.5	7.3	603	4	US-08-487-072A-50
10	316.5	7.3	603	3	US-09-063-950-5
11	291.5	6.7	605	3	US-08-190-802A-49
12	291.5	6.7	605	3	US-08-477-346-49
13	291.5	6.7	605	3	US-08-473-089-49
14	291.5	6.7	605	4	US-08-487-072A-49
15	291.5	6.7	605	4	US-09-538-092-1087
16	291.5	6.7	623	4	US-09-949-016-10995
17	287.5	6.6	1119	4	US-09-907-794A-294
18	287.5	6.6	1119	4	US-09-905-125A-294
19	287.5	6.6	1119	4	US-09-902-775A-294
20	287.5	6.6	1119	4	US-09-906-700-294
21	287.5	6.6	1119	4	US-09-903-603A-294
22	287.5	6.6	1119	4	US-09-904-920A-294
23	287.5	6.6	1119	4	US-09-909-064-294
24	287.5	6.6	1119	4	US-09-905-381A-294
25	287.5	6.6	1119	4	US-09-906-618-294
26	286.5	6.6	1112	3	US-09-353-585-2
27	285.5	6.6	1112	3	US-09-353-585-3

28	285.5	6.6	1525	3	US-09-191-647-2	Sequence 2, Appli
29	285.5	6.6	1525	3	US-09-540-245A-2	Sequence 2, Appli
30	285.5	6.6	1525	3	US-09-540-153-2	Sequence 2, Appli
31	282	6.5	1529	4	US-09-312-283C-396	Sequence 396, App
32	273	6.3	1480	3	US-09-191-647-7	Sequence 7, Appli
33	273	6.3	1480	3	US-09-540-245A-7	Sequence 7, Appli
34	273	6.3	1480	3	US-09-540-153-7	Sequence 7, Appli
35	273	6.3	1480	5	PCR-US91-09055-2	Sequence 2, Appli
36	271	6.2	1480	3	US-09-182-024A-5	Sequence 5, Appli
37	269.5	6.2	1059	4	US-09-907-794A-290	Sequence 290, App
38	269.5	6.2	1059	4	US-09-905-125A-290	Sequence 290, App
39	269.5	6.2	1059	4	US-09-902-775A-290	Sequence 290, App
40	269.5	6.2	1059	4	US-09-906-700-290	Sequence 290, App
41	269.5	6.2	1059	4	US-09-903-603A-290	Sequence 290, App
42	269.5	6.2	1059	4	US-09-904-920A-290	Sequence 290, App
43	269.5	6.2	1059	4	US-09-909-064-290	Sequence 290, App
44	269.5	6.2	1059	4	US-09-905-381A-290	Sequence 290, App
45	269.5	6.2	1059	4	US-09-906-618-290	Sequence 290, App

ALIGNMENTS

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RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match      64.1%, Score 2786.5; DB 4; Length 844;
Best Local Similarity 68.3%; Pred. No. 1.8e-238;
Matches 544; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY      30 EVNNITTYQCMDOQLSKVPDDIPSTKNIDISFNPDIKLSYSPNSFELQMLDSRCEI 89
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      36 EVNNITTYQCMELNPKYKIPDNLPSSTKNLDSFNPDLRLGYSFSPFELQVLDISRCI 95
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      90 ETIEDKAWHGHHLSNLTGNPIQSPGSPGSGTSLNENVAETTKLASLESPIGOLI 149
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      96 QTIIDGAVQSLSHSLTILITGNPIQSLALGAFSGSLSQKLVAVETNLASLENPIGHLK 155
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      150 TLKLVANAHNFHSCKLPAYSNSLTNLVHVDLSYNYQITITVNDLOFLRENPOVNLSDM 209
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      156 TLKELNVAHNIQGFKEJPEYFSNLTNLEHDLSSNKLQSIYCTDLRVLHQMPNLNLSTD 215
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      210 SLNIDIPDOPAFGKIKLHETLTCGNPNSSIMTCTONLAGLAVHRLILGEFDERLLE 269
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      216 SLNPNMTIQPGAFKIRLHKLTLLNNPDSLVNMTCTCQGLAGLGHVHRLVLGEFNRGULE 275
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      270 IFESINIEGCDVYITDEFRLTYTNDPSDDIYK-FHCLANYSAMSLAGYSIKYLEDPVPGH 328
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      276 KFDGSALEGLCNLTIEFRRLAYLDIYDDIIDLNCLTNSSPFLSVVTTIERVDFSYNF 335
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      329 KWQSLSTIRCOLKOPFLTDLDFLKLSTLTWNKGSISFKVVALPSLSYLDLSRNALSPSGC 388
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Db	396	CSQSPGTTLSLKYTLDSFNGVITMSNSNFGLEQOLEHLDQOHSUHLKQMSSEFVPLSLRNL	455
Qy	449	YLDISYNTKIDFDEGIPLGLTSLNLTLMKAGNSFKONTLSNVFANTNLTLFLDISKCOLEQ	508
Db	456	YLDISHTHTRAVAFNGIPLNGLSLSEVLKMGAGNSFOENFPLDPIFELNELNLTLFLDISQCOLRO	515
Qy	509	ISWGFPTDLHRLQOLMNSHNNLLFLDSSHYNOLYSTLDCSPNRLETS-KGILGHFPPS	567
Db	516	LSPTAFNSLSSLOQVITMNSHNNFSLDTPFYKCLNLSLOQVLDYSLNHMTLSKQEOLEHPPS	575
Qy	568	LAFNLITNNSVACICEHQKFTOMVYEQOKOPLVNVBEOMTCATPEVNMNTSLVLPFNNSCTYK	6272
Db	576	LAFNLTLQNDPACTGCEHOSFLOMIDQORDLIVBEVMECATBPEDKQGMPLSL-NITCQM	634
Qy	628	YKTIISVSVSIVVSTAVELIYHFYFHLILLAGCKKISRGESITYAFVYSSQNEDWYR	687
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Qy	688	NELVNLBERGVRFHLCIHYRDPFIPVATAANITOGFPHSKRVYIVVSSHFIQSRKICF	747
Db	695	NELVNLBERGVPPFOCLCHYRDPFIPVATAANITIHGFHKSRYIVVSOHFIOSSKICF	754
Qy	748	EYEIAQWQFLLSSRSGLIPIVLEKYEKSLRQOVELYRLLSRNTYLEWEDNPLGRHI FWR	807
Db	755	EYEIAQWQFLLSSRAGIIFIVLQKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFWR	814
Qy	808	RLKNAALDGRKANPEQT	824
Db	815	RLRKAALDGRKANPEGT	831

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1      RESULT 2
2      US-08-514-014-4
3      ; Sequence 4, Application US/08514014
4      ; Patent No. 5707829
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Jacobo, Kenneth
7      ; APPLICANT: McCoy, John
8      ; APPLICANT: Kellner, Kerry
9      ; APPLICANT: Carlin, McKeough
10     ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
11     ; TITLE OF INVENTION: ENCODED THEREBY
12     ; NUMBER OF SEQUENCES: 12
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
15     ; STREET: 87 CambridgePark Drive
16     ; CITY: Cambridge
17     ; STATE: Massachusetts
18     ; COUNTRY: USA
19     ; ZIP: 02140
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/08/514, 014
27     ; FILING DATE:
28     ; CLASSIFICATION: 514
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Brown, Scott A.
31     ; REGISTRATION NUMBER: 32, 724
32     ; REFERENCE/DOCKET NUMBER: GI6000
33     ; TELECOMMUNICATION INFORMATION:
34     ; TELEPHONE: (617) 498-8224
35     ; TELEFAX: (617) 876-5851
36     ; INFORMATION FOR SEQ ID NO: 4:
37     ; SEQUENCE CHARACTERISTICS:

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; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

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Query Match	14.3%;	Score 619.5;	DB 1;	Length 661;
Best Local Similarly	28.6%;	Pred. No. 4.4e-46;		
Matches 187;	Conservative 126;	Mismatches 296;	Indels 45;	Gaps 18;

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RESULT 3
 US-08-833-823-4
 ; Sequence 4, Application US/08833823
 ; Patent No. 5963093
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacoby, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Callin, McKeough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; TITLE OF INVENTION: ENCODED THERAPY
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA

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; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-823-4

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Query Match      14.3% Score 619.5; DB 2: Length 661;
Best Local Similarity 28.6%; Pred. No. 4,4e-46;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

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DB 88 QINNIHETFOSSHQSLTVLGNPLIEMETSLNGPSLKLFLIQGISNLEFIPVHN 147
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DB 148 LENESLYLGSNHSISIKFPPDF-ARULKYLDPONNAIHYSRDMASLEQ-AINSL 204
QY 208 DMSINPDIQDQAFQIKIHELTLRGNFNSNIMKTCLQNLAGLHVHRLIIGERKDERN 267
DB 205 NFNANNVAGIELGAFSTVFSQNLNGTPNLSVLPNG-LQNST--TQSLMLGTEDIDD 260
QY 268 LEIEPESIMEGLCVTIDEPRLTYTNDSD-DIYKHCGLAVNSAMSLAGVISIKYLEDVPK 326
DB 261 EDI-SSAMLKGLCEMSVESLNL-OEHRFSDISSTTFQCFQLOEIDLTAAT--HLKGLPS 315
QY 327 HFKQSLIIR-----COLK--OEPPLDLRPLKSLTLTMNKGSSISFKKVALPS 372
DB 316 GMR--GLNLKGLVLSVNHFPQDLCISANFSLTHLYTRGNVKKLHLGVGCLER-LGN 371
QY 373 LSYLDLSRNALSFSGCCSYSDLGTSNLSHLIDLSFNGAI-IMSANFMGLEEIOHLDFOGST 431
DB 372 LQITDLSHNDIEADCCSLQKNSLHQTNLSHNEPLIGLOSQAFKECPQLELDIAFTR 431
QY 432 LKRTESAPLSLEKLYLIDSYNTYKIDPFGIFGLTSLNTLQKAGNSFQDNTL--SNV 489
DB 432 LHNAPSPFQNLHFLVNLTYCFLDTSNOHLNLAGLPLVRLHNLKGNHFDGTITTKNL 491
QY 490 FANTTNLTFDLISCKOLEQISWGVFDTLHRLQOLNMSHNNL--FLDS-SHYNDLQSLST 546
DB 492 LQYVGSLEVLILSSCGSLSDIOQAFHSLGKMSHYDLSHNSLTCSDLSLSHLKGIY--- 547
QY 547 LDCSFNRIETSKGILQHFPSKLAFFNLTNNSVACICEHOKFLQWVECKQFLVAVEQWTC 606
DB 548 LNLANSINIIISPLRILSQOSTINLSHNDLCTCSNHFLLTWYKEMHLKLBESSEETJC 607
QY 607 ATPENK-----TSVLDPNNSTCYMYKTIISVSIVSVIYVSTVAFLLYHFFHL 656

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DB 608 ANPSELGVKLSDVKLSGCTAIGIFFLIVFLLALILLFAVKYLLRWKYOH 661
RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Pan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavodny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JBO601QC
; CURRENT APPLICATION NUMBER: US/09/982,308B
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-982-308B-23

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Query Match      11.4% Score 494; DB 4: Length 784;
Best Local Similarity 25.9%; Pred. No. 8.2e-35;
Matches 218; Conservative 131; Mismatches 319; Indels 174; Gaps 34;

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QY 44 LSKVPDDIPSSSTKNIDLSFNPRLIKSYSPFSELOMIDL SRCIEFIEDKAMHGHLS 103
DB 43 LNSIPSGLEAVKSLDLSNNRITYISN-----SDIQRCV-----NL 78
QY 104 SNLITGNPIOSFSGSGLSLENVAVETKLASLESFPIGQITLTKLVANFNHIS 163
DB 79 QALVLTSGNITIEDSFSSLSGLEHLDLSYNYLSNLSWFKPLSLTFLNLGNPKYT 138
QY 164 CKLPAYFNSLTNLVHVDL-----SYNYIQTITVNDLQFLRNPOVNLSDMSINPDIQD 219
DB 139 LGETSLFSHLTKQLIRGNMDTFTKIQKDFAGLTFLEB-----LEIDASDQSYEP 191
QY 220 QAFQGI-----KLHELTLRGNFNSNIMKTCLQ-----NLAGLHVHRLIIGEPD- 264
DB 192 KSLKSLQNVSHLILAMQHILLLEIFVDVYSVE-CLELRPTDLDTFPSLSGTETSL 250
QY 265 -----ENLIEFESIME-----GLCDVTIDEPRLTYYTNDF--SDIYKHCGLANV 308
DB 251 IKKFTFNVKLTDESIRFQMKLNLQISGLELEFDDCTLNGVGRASDN----- 300
QY 309 SAMSLAGVISIKYLEDVKKHFMQSLITRQLKQFPL-DLPFLKSLTLTMNKGSSISFKK 367
DB 301 -----DRVIDPGVETLTIIRLHIPEFYLDSTLSTYSILTERKRTIVENSK 347
QY 368 V-----ALPELSYLDLSRNA-----LSFSGC-CSYSDLGTSNR--HL-DLSFNGA 409
DB 348 VFVLPCLLSOHLKSLRFLDLSLENLMBEYLYKNSACEDAMBSLOTLILRQNLASLEKGE 407
QY 410 IMSANFMGLEEIOHLDFOGSTLKRVTESAFSLKLYLIDSYNTYKIDPFGIFGLT 469
DB 408 TLLT-----LKNLTINIDISKNSFSHMPETCOM--PERKXYLNLSSST----- 446
QY 470 SLNTLKAAGNSFQDNTLSNVPANTTNLTFDLISCKOLEQISWGVFDTLHRLQOLNMSHNN 529
DB 447 -----RHSVTGCIPT--LEIIVDSNHNILFSL--NLPLQKELYISRNK 488

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QY	530	LLFLDSSHYNOLYSLSTLDCSPNRET-SKLILOHPFSLAFPMJLNNVACICEHOKEL	588
Db	489	LMFLPDA--SLFLPMILVLIKSRNMTITFSKQOLDSF-HTLTLLEAGGNPFISCE---FL	542
QY	589	QWVEOKOFLVNV-----EQMTCAIPVEMNTSLVLD--FNNSTCYMTKITISVSVVSVIV	641
Db	543	SFTQEO-QALAKLIDWPANLYCDSPSHVHVGQVDVRLSYSEGHRIALVSGMCALFL	601
QY	642	VSTVAFLIYHE---YFHLI--LIAGCKKYSRGS---TYDAFVYSSGONEWPMNVELVK	692
Db	602	ILLGVLCRHFGHGLWYMMQMMWAMLQAKKRPKAPAPRNICYDAFVSYSERDAYVWNLWQ	661
QY	693	NLEBSVPPFHLCLHVRDTPGVALANIIQESFHSKRVIYVSSHPIOSRQICEYEYLA	752
Db	662	ELENNPNPFCKLHHRDFIPGRMIIDNII-DSIEKSHKVFPLSBNFVSEWCKTELDS	720
QY	753	QTWQFLSRSGIIFVLEKVEKSLRQO--VEYLRILSRNTYEWEMDNPLGRHIFWRRLKN	811
Db	721	HFRLEDDENDDAIIILILEPIEKKALPQRCCKLRKIMNTKITYLEMPNDEKQRGSGFWNLBA	780
QY	812	AL 813	
Db	781	AI 782	

```

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

```

Query Match	10.0%;	Score 432.5;	DB 4;	Length 775;
Best Local Similarity	25.4%;	Pred. No. 2.3e-29;		
Matches 207;	Conservative 116;	Mismatches 290;	Indels 201;	Gaps 33;

[illegible]

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QY 309 SAMSLAGVSIKXLEVDPRHFWOSLTIIRCOLKOPFTL-DLPEYKSLTUTNMKGSIFSKX 367
Db 336 -----DVIDPGKVEVETLIRRHIFRFLIFLFDLSYLLTERVYRIVTEMSK 382
QY 368 V-----ALPSISYLDISRNA-----LSFGSC-CSVSDLGTSNLR--HL-DLSFNCA 409
Db 383 VFLVPCLSLOHKLSLEYIDLSENLMBEYLKNSACEDAMPSLOTLILRQHLHLSLEKTGE 442
QY 410 IIMSANFGLBELOHDFHSHSTLKVTEPSAFSLSEKLYLDISYNTNTKIDPFGIFLGLT 469
Db 443 TLLT-----LKNLTIDISKNSFHSMBETCOM--PEKMKYTLNLSJT----- 481
QY 470 SLNTLKMGNSPKDNTLSNVFANTNTLITFLDLSKCOLEQJSMGWPFTHRLLOLNMSHN 529
Db 482 -----RHISVGCIPKT--LEILDVSNMNNLPSL--NLPOLKELYISRK 523
QY 530 LLEFDSHYNOLYSLTDCSPFNRIET-SKGILHOPKSLAFPNLTNNSVACICEHOKEL 588
Db 524 LMTLPDA--SLLPMLLVLTKISRNALTTPSKQULSF-HTLKTELAGNNTICGE---FL 577
QY 589 QAWKEOKOFLVNV-----EQMTCAIPYEMNTSLVLDENNSTCYWYKTIISVSVSVIIVS 643
Db 578 SFQEO-QALYAVLIDMFRANTJCDSBPSHYRQOVQDVRVLSSECHRALVSGMCCAL--- 633
QY 644 TVAFLIYHFVPHIILIAG--CKKY-----SRGESIYDAFVLY 678
Db 634 -----FLTILITGLVCHRFGILGYMMKMMAMMLOAKKRPKRABSR-NICDAVSVY 682
QY 679 SSONEMWVKNELVKULBEVPRFNHCLHYRDPFGVALLAANIIOEGFHSKRKYVIVVSRH 738
Db 683 SERDAYVWNLWMOELTENENPFKJCLHKRDPIDPEKWTIIDNII-DSIEKSHKYFVLSBN 741
QY 739 FIOSRWCIFFEYELAQTOWFLSRSGIIFIVLEKV 772
Db 742 FVKSBEWCKIELDSHRFLPDEMDNDAIILILEPI 775

```

RESULT 6
 US-08-190-802A-50
 Sequence 50, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dosit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190, 802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fablian, Gary R.
 REGISTRATION NUMBER: 33, 875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ. ID NO.: 50:
 SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-190-802A-50

Query March 7.3%; Score 317.5; DB 1; Length 603;

Best Local Similarity 24.1%; Pred. No. 2.6e-19;

Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;
 QY 39 CMDOKLSKVPDDISSTKNDLSFNPILKLSYFSNFSLEQWDLSCETIETEDKAWH 98
 Db 60 CSSKNLTHLPDDIVSTRALMDGNLSSIPSAFQNLSSLDPLNQSWSLRSEPOLL 119
 QY 99 GLHLSNLILTGPNIQSFSPSGLSLENLVAVETKLASLESFPIGQITLTKKNVAH 158
 Db 120 GLQNLVYIHLERNRLRNLAVALFTHTPSLASLSNMLGRLEBGLFQGLSHLMDNLGW 179
 QY 159 NF-----IHSCCL-----PAYFSNLTNVHVDLSYNYQITTVNDLQ 195
 Db 180 NSLVLPDVTYFQGLGNLHVLNAGNKLTYLOPALFCGELRELDLSRNALRSYKAVFV 239
 QY 196 FLRENPOV-NLSLMSLNPIIDFIDQAFQGIK-LHETLRGNFNSSNMKTCLQNLAGLH 253
 Db 240 HL---PRLQKLYLDRNL--ITAVAPGAFGLKALRWLDLSIN-RVAGLMETFPGLGLH 293
 QY 254 VHRLLGEFKDERNLLEIFEPSIMEGLCDVTIDEFRLTYTNDPSDDIVKFCIANVSAMSL 313
 Db 294 VLR-----LAHNAIASL 305
 QY 314 AGVSIKYLEDPKHKFKQSLIIRCOLKQPTLDLPFLKSLTLMNK-----GSISPKVA 369
 Db 306 R-----DLHFLBELQIGHNRIRQGERTFE--G 336
 QY 370 LPSLSYDLNRNAL-----SFGCCSYS--DLGTNSLRHDLDFNGAIIIMSANPMGLEE 421
 Db 337 LGQLEVLTLNDNOTTEVRVAGFSGLFNVAVMNLSCNLRSLP-----ERFQGLDK 387
 QY 422 LQHLDPQSTLKRVTESAPLSLEKLYLDISYNTKIDPFGIFLGLSLNTLMAQNSF 481
 Db 388 LHSIHLBHSCLGHVRLHT-----FAGLSGARLFL----- 417
 QY 482 KQNTLSNV-----PANTNLTFLDLSKOLEISWGVPTTLRLQLLMSHNNLLFLDSSH 537
 Db 418 RDNSSISIEBQSLAGLSELLELDLTYRLTLPQLFQGLHLELYLLSYNQLTTLSEV 477
 QY 538 YNOLYSITLDCSFNRIET-SKGILQHPKSLAFPNLTNNSVACIHCQKFLQWKEO-- 594
 Db 478 LGPQRAFWDISNNHETLAEGLFSSIGR-VRYLSLRNNS-----LQTFSPQPG 526
 QY 595 -KQFLVAVEQMTCATPVE-----MNTSLVLDENNSTC-----YMYKTIISVSYS 638
 Db 527 LERMLANPMWDCSPLKALRDPAQNQGVVRFVQVTCBGDDCQPVYTYNNITCAGPAN 586
 QY 639 V 639
 Db 587 V 587

RESULT 7

US-08-477-346-50

Sequence 50, Application US/08477346

Patent No. 6262023

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,346
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,072
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-477-346-50

Query March 7.3%; Score 317.5; DB 3; Length 603;

Best Local Similarity 24.1%; Pred. No. 2.6e-19;

Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDOKLSKVPDDISSTKNDLSFNPILKLSYFSNFSLEQWDLSCETIETEDKAWH 98

Db 60 CSSKNLTHLPDDIVSTRALMDGNLSSIPSAFQNLSSLDPLNQSWSLRSEPOLL 119

QY 99 GLHLSNLILTGPNIQSFSPSGLSLENLVAVETKLASLESFPIGQITLTKKNVAH 158

Db 120 GLQNLVYIHLERNRLRNLAVALFTHTPSLASLSNMLGRLEBGLFQGLSHLMDNLGW 179

QY 159 NF-----IHSCCL-----PAYFSNLTNVHVDLSYNYQITTVNDLQ 195

Db 180 NSLVLPDVTYFQGLGNLHVLNAGNKLTYLOPALFCGELRELDLSRNALRSYKAVFV 239

QY 196 FLRENPOV-NLSLMSLNPIIDFIDQAFQGIK-LHETLRGNFNSSNMKTCLQNLAGLH 253

Db 240 HL---PRLQKLYLDRNL--ITAVAPGAFGLKALRWLDLSIN-RVAGLMETFPGLGLH 293

QY 254 VHRLLGEFKDERNLLEIFEPSIMEGLCDVTIDEFRLTYTNDPSDDIVKFCIANVSAMSL 313

Db 294 VLR-----LAHNAIASL 305

QY 314 AGVSIKYLEDPKHKFKQSLIIRCOLKQPTLDLPFLKSLTLMNK-----GSISPKVA 369

Db 306 R-----DLHFLBELQIGHNRIRQGERTFE--G 336

QY 370 LPSLSYDLNRNAL-----SFGCCSYS--DLGTNSLRHDLDFNGAIIIMSANPMGLEE 421

Db 337 LGQLEVLTLNDNOTTEVRVAGFSGLFNVAVMNLSCNLRSLP-----ERFQGLDK 387

QY 422 LQHLDPQSTLKRVTESAPLSLEKLYLDISYNTKIDPFGIFLGLSLNTLMAQNSF 481

Db 388 LHSJLHSHSCIGHVRLHT-----FAGLSGLRRLFL----- 417
Qy 482 KDNTLSNV-----PANTNLTFLDLSKQLEISGVEDTLHRLOLMSNNLLFLDSSH 537
Db 418 RDNSISSEIEOQSLAGSELDELDTNRLTLHPROLFGHGEYLLSYNOQLTTLSAEV 477
Qy 538 YNOLYSLTDCSEFNRIET-SKGILQHPKSLAFNLTNNSVACICEHQKFLQWKEQ-- 594
Db 478 LGPLQRAFWLIDISHNHLETLAEGLFSSLSGR-VRLSLRNNS-----LQTFSPQPG 526
Qy 595 -KQPLVNEQWTCATPYE-----NMTSLVLDFFNNSTC-----YMYKTIISVSVS 638
Db 527 LERLMLDANPMDSCPLKALRDPAIQNPVPRVQVCEGDQCQPYTYNNITCAGPAN 586
Qy 639 V 639
Db 587 V 587
RESULT 8
US-08-473-089-50
; Sequence 50, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473.089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-fat, Fig. 33
US-08-473-089-50
Query Match 7.3%; Score 317.5; DB 3; Length 603;
Best Local Similarity 24.1%; Pred. No. 2.6e-19;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;
Qy 39 CMDQLSKVDDIPSTKNIDISFNPDLKLSYFSNPFSELCWLDISRCEITIEDKAWH 98
Db 60 CSSKNLTHLPDDIPVSTRALWLDGNNLSISPSAFAQNLSSLDPLNLQSGWLRSLPQALL 119

Qy 99 GLHLSNLTITGNPIQSPSPGSGLTSLNLTVAVETKLASLSPFIQGLITLTKLVAAH 158
Db 120 GLQNLVYIHLERRRLNLAVALGFTHTPPLASLSLSSNLLGRLEEGHFOGLSHLMDINTLGW 179
Qy 159 NF-----IHCKTL-----PAYFSNLTUVAVDLSYNYIQITTYNDLQ 195
Db 180 NSIVVLPDVTFOGLGNLHVLVLAGNKLTYLOPALFGGLBELRLDLSRNLRVKNANVFV 239
Qy 196 FLRENPOV-NLSLMSINPIDIPIQDAFOGIR-LHETLTGNNSSNIMKTCQNLAGLH 253
Db 240 HL---PRQLYLYDRNL--ITVAPGAFGLMKLRLHLDLSH-RVAGIMEDTTPGLLGLH 293
Qy 254 VRLIIGEEFDEBERNLEIFEBSINEGLCDVTIDEFRLLTYTNDFSDDIVKFCANVASMSL 313
Db 294 VLR-----LAHNAIASL 305
Qy 314 AGVISIKLIDVPEKFKKQSLSTRCOLKQPTLIDPLKSLITLTMK-----GSISPKVA 369
Db 306 R-----PRTFK-----DLHFLLEELQGHNRIRQLGERTFE--G 336
Qy 370 LPSLSYLDLSRNAL-----SFGCCSYS--DLGTNSLRHLDSFNCAITMSANFMGLRE 421
Db 337 LGQLEVLTLNDNQITTEYRVGAFSGLFNVAVANLSCNCLRSLP-----EKVFGSLDK 387
Qy 422 LQHLDPQSTLAKRTEBSAFLSEKLYLDISYNTKIDPDGIFLGLTSLNTLKMAGNSF 481
Db 388 LHSJLHSHSCIGHVRLHT-----FAGLSGLRRLFL----- 417
Qy 482 KDNTLSNV-----PANTNLTFLDLSKQLEISGVEDTLHRLOLMSNNLLFLDSSH 537
Db 418 RDNSISSEIEOQSLAGSELDELDTNRLTLHPROLFGHGEYLLSYNOQLTTLSAEV 477
Qy 538 YNOLYSLTDCSEFNRIET-SKGILQHPKSLAFNLTNNSVACICEHQKFLQWKEQ-- 594
Db 478 LGPLQRAFWLIDISHNHLETLAEGLFSSLSGR-VRLSLRNNS-----LQTFSPQPG 526
Qy 595 -KQPLVNEQWTCATPYE-----NMTSLVLDFFNNSTC-----YMYKTIISVSVS 638
Db 527 LERLMLDANPMDSCPLKALRDPAIQNPVPRVQVCEGDQCQPYTYNNITCAGPAN 586
Qy 639 V 639
Db 587 V 587
RESULT 9
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-487-072A-50

Query Match 7.3%; Score 317.5; DB 4; Length 603;
Best Local Similarity 24.1%; Pred. No. 2,6e-19;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDOKLSVPPDIPSTKNIDLSFNPILKISYFSNFSNLSQMDLSRCETIEDKXMH 98
DB 60 CSSKNTLHPDIPSTKNIDLSFNPILKISYFSNFSNLSQMDLSRCETIEDKXMH 119
QY 99 GLHLSNLILGNPIQSPFSFSGLSLEMLVAVETKLALESFPIQQLITLKKLVANH 158
DB 120 GLQNLVYHLBRNRLNLAVALFTHTPELASLSSNLGRLEBEPQGLSHMLNIGW 179
QY 159 NF-----IHSCKL-----PAYSNLTNLVHVDLSYNYIQTITVNDLQ 195
DB 180 NSLVVLPDPTVEQGLNHLVLAQNKLTLYLPALFCGGLRELDLSHNAISVAVANFV 239
QY 196 FLRENPQV-NLSLMSLNPIDIDQAFQGIK-LHELTLRGNFNSNMKTCLQALAH 253
DB 240 HL-----PRQKLYLDRNL-ITAVAPGAFGLMKALRWLDLSHN-RVAGMEPTFPGLGLH 293
QY 254 VHRLLLEFQKDERNLLEFEPSEIMGLCDVTIDEFRLTYTNDPSDDIVKHCIAVNSAMSL 313
DB 294 VLR-----LAHNAISL 305
QY 314 AGVSIKYLEDPKAFKQWSLIRCOLKQPTLDPFLKSLTLMNK-----GSISFKVA 369
DB 306 R-----PRTEK-----DLHFLBELQGLHNRIRQLGERTFR--G 336
QY 370 LPSLYLDSRNAL-----SFGCCSYSS--DLGNSLRHLDSFNGLIIMSANPMGLIE 421
DB 337 LGLLEVTLDNDQITEVRVAGAFSGLPVNAVNLGNCILRSIP-----ERVFGGLDK 387
QY 422 LQHLDPQHSSTLKRVTEFSAPLSLEKLYLDISYNTYKIDFDGIFLGITSLNTLKMAGNSF 481
DB 388 LHSILHBSCLGHVRLHT-----FAGLSGLRLFL----- 417
QY 482 KDNLTLSNV-----PANTNLFLDLISKQOLEISWGVEDTLHRLQLLNMSSHNLFLDSH 537
DB 418 RDNSSISIEQSGLSELLELDLTLRRLTLPRQLFGGLHLYLLISTYQQLTSLAEV 477
QY 538 YNOLYSSTLDCSPNRIET--SKGILQHPKSLAFPNLTNNSVACICEHQKLOVWQO-- 594
DB 478 LGLPQRAFWLIDISHNLLETLAEGLFSSLGR-VRYLSLRNNS-----LQTFSPQPG 526
QY 595 -KQFLVNEQWTCATPVE-----NNTSLVLDENNSTC-----YMYKTIISVSVS 638
DB 527 LERLMLDANPMDSCPLKALRDPAALQNGVPRVPRVQVCEGDDCQPYTYTNNITCAAPAN 586
QY 639 V 639
DB 587 V 587

RESULT 10

US-09-063-950-5
Sequence 5, Application US/09063950C
Patent No. 6225085
GENERAL INFORMATION:
APPLICANT: Holcman, Douglas A.
TITLE OF INVENTION: NOVEL LRGG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MEI-019
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 605
TYPE: PRT
ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.3%; Score 316.5; DB 3; Length 605;
Best Local Similarity 22.2%; Pred. No. 3,2e-19;
Matches 147; Conservative 89; Mismatches 238; Indels 189; Gaps 17;

QY 32 VPNTTYQCMDOKLSVPPDIPSTKNIDLSFNPILKISYFSNFSNLSQMDLSRCETIED 91
DB 53 VNELSVFSSNLTRLPDGIPGTOALWLDNNLSIPPAFRNLSSIAFLNLQGGQLGS 112
QY 92 IEDKAMHGLHLSNLILGNPIQSPFSFSGLSLEMLVAVETKLALESFPIQQLITL 151
DB 113 LEPQHLGLEMLCHHLERNOQLSLAVGTFTPTALLGLSNNKLSLED----- 163
QY 152 KLVNVAHFHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSDMSL 211
DB 164 -----GLFEGELGNLMDNLQWNSLAV----- 184
QY 212 NPIDIDQAFQGI-KHLELTLRGNFNSNMKTCLQALAHVHRLILGEKDERNLEI 270
DB 185 -----LPDAARFGIGLREVLQGN-----RLAY 208
QY 271 FEPSEIMGLC-----DVTIDEFRLTYTNDPSD--DIVKHCIAVNSAMSLAGSIKYLED 323
DB 209 LQPALFSGLAELRELDLSRNALRAIKANVFAQLPRLQLYDRNLIAVAPGA----- 261
QY 324 VPKHFKWQSLISIRCOLKQPTLDPFLKSLTLMNK-----GSISFKVALPSLYLDSRN 381
DB 262 -----FLGLKALRWLDLSHNVAAGLEDTFPGLGLRVLRLSHN 300
QY 382 ALRSFGCCSYSD-----LGTNSLRHLDSFNGLIIMSANPMGLIELOHLDPOHSTLK 433
DB 301 AIASLRPRTEDEHFLBELQGLHNRIRQL-----AERSFGLQLLEVTLDNDHQLQ 351
QY 434 RVTEFSAPLSLEKLYLDISYNTYKIDFDGIFLGITSLNTLKMAGNS----- 480
DB 352 EV-KVGAFLGLITNVAVNMNLGNCILRNLPBOVFRGLKHSIHLEGSCLGIRPPTFAGLS 410
QY 481 -----FKDNTLSNVFANT-----TNLTFLDLISKQOLEISWGVEDTLHRLQLLNMSSHNL 530
DB 411 GLRRLFLKONGLVGIEBQSLMGALBLELDLTLSQHLHLHQFLQGLKLELYLLSHNRL 470
QY 531 LFLDSSHYNOLYSSTLDCSPNRIETSKGILQHPKSLAFPNLTNNSVACICEHQKLO- 589
DB 471 AELPADALGPLQRAFWLIDISHNLLETLAEGLFSSLGR-VRYLSLRNNSLARTPTPOPGLER 530
QY 590 -WYVEQKQFLVNEQWTCATPVE-----NNTSLVLDENNSTC-----YMYKTI 632
DB 531 LNLBEG-----NPMDCSPLKALRDPAALQNGVPRVPRVQVCEGDDCQPYTYTNNIT 582
QY 633 SVS 635
DB 583 CAS 585

RESULT 11
US-08-190-802A-49

Sequence 49, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-SEP-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGIN: SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 6.7%; Score 291.5; DB 1; Length 605;
Best Local Similarity 22.0%; Pred. No. 5.3e-17;
Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;
QY 39 CMDQKLSKVPDDIPSTKNIDLSFNPDLTKLSYFSNSELQMDLSRCEITIEDKMH 98
DB 60 CSSRMLTRLPDGVPGTQALMDGNLSSVPPAAFGONLSLGLFNQGGQLSLEPQALL 119
QY 99 GLHLSNLTLTGNPLOSFGSGFSGLSLENIVAVETKLASIEPFIQGLITLKKLVANH 158
DB 120 GLENLCHLHLEKQSLALGTFATHPALASLGLSNRRSLRLEDGLFEGLSGLMDNLGM 179
QY 159 NFTH-----SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDIQ 195
DB 180 NGLAVLPDAFRELGLRELVLVAGNRLAYLPALFGLAELRELRLDLSRNALRAIKAN--V 237
QY 196 FLRENPQVNLSDMSLNPTDFIODAFQGIK-LHEITLKGNFSSNMKTCLONLAGLAV 254
DB 238 FVQLPRLQKLYLDRNL--IAAVAPGAFGLKALRWLDLSHN-RVAGLEBTPFGLGLGRV 294
QY 255 HRLILGEFDERNLEIFEPBSIMGICDVTIDEFRLTYTNDFSDDIVKFLANVSAMSLA 314
DB 295 LRL-----SNNALA 303
QY 315 GVSIXYLEDPKFKFKQSLIIRCOLKOPFTLDPFLKSLTTLTMNGKSIISFKVALPSLS 374
DB 304 SLR-----PRIFK-----DLHFLBEL----- 319
QY 375 YLDLSRNALSFSGCCSYDLGTNSLRHLDLSPNGAIITMSANFGLBELQHLDFQHSITLKR 434

DB 320 -----QLGHRIRQL-----AERSFGLQLLEVLTLDHNOLOE 352
QY 435 VTEFSAPLSLEKLYLDISTYNTKIDPDGIFLGJTSINTLKAAGNS----- 480
DB 353 V-KAGAFGLITVNAVWNLGNCRLNPEQVFRGLGKLSLHLEGSCLGIRIRPTFTGLSG 411
QY 481 -----FKDNTLSVFPANT-----TNLTFDLSKQLEQISGWVDPDTHRLQLNMSSHNL 531
DB 412 LRLFLKNDGLVGIRESQSLMGLAELLEDITSQTLHPRLRFOGLKLEYLLLSRRLA 471
QY 532 FLDSHYNQLYSLSTDSPNRISYTSKGLQHPKSLAFENLTNNSVACICEHQKFLQ-- 589
DB 472 ELRADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRRLYSLNNNSIRFTPOPGLERL 531
QY 590 WKREKQFLVNVHOMTCATVE-----MTSLVYDFNNSTC-----YMYKTIIS 633
DB 532 WLEG-----NPMDCGFLKALRDPALONPSAVPRFVALCEGDDCPPAYTNNTTC 583
QY 634 VSVSVI 640
DB 584 ASPEEV 590

RESULT 12

US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGIN: SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

QY 634 VSVSVI 640
Db 584 ASPEEV 590

RESULT 14
US-08-487-072A-49
Sequence 49, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEFAX: (202) 887-1500
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYDROTHERICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Query Match 6.7%; Score 291.5; DB 4; Length 605;
Best Local Similarity 22.0%; Pred. No. 5.3e-17;
Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;
QY 39 CNDOKLSKYVDDIPSTKNIIDISFNPLKIKSYFSNFSFELQWLDISRCIEITIEDKAWH 98
Db 60 CSSRNLTRLPDVGPGTQALMDGNLSSVPPAFAQNLSSIGFLNAGQGLSLEFQALL 119
QY 99 GLHLSNLLITGNPIQSFSPGFSGLTSLNVAVETKIASLESFPIGQILITLKKLVNAH 158
Db 120 GLENLCHLHLEKQKSLALGTFAHTPALASIGLSNNRSLRLEDGLFEGIGSLMDLNLGM 179
QY 159 NFTH-----SCKLPAYFSNLTNLVHVDLSYVYIQTITVNDQ 195
Db 180 NSLAVALPDAFRGLGLRELVLVAGNRLAYIQPALFSGLAELRLDLSRNALRLKANK--V 237
QY 196 FLRENPOVNLSTMSINPIDIODAFQGIK-LHEILTRGNFNSSNIMTKCLONTLAGLHV 254
Db 238 FVGLPRLQKLYLDRNL--IAVAAGAFGLGKALRWDLSHN-RVAGLLEDTFFGLGLGRV 294
QY 255 HRLILGEFKDERNLIEFESIMEGLCDVTIDEFLTYTNDPSDDIYKFLCLANVAMSILA 314

Db 295 LRL-----SHNATA 303
QY 315 GVISIKLEDPVPHKFKQKQSIIRCOLKQPTLDLPFLKSLTLTNKGSISFKVALPSIS 374
Db 304 SIR-----DHFLEEL----- 319
QY 375 YDLISRNALSFGCCSYSDIGTNSLRLDLSPNGALIMSANPWGLCHLDFOHSTLKR 434
Db 320 -----QLGHNRIQL-----ARSFEGLOQLVLTLDHNOLOE 352
QY 435 VTEPSAFLSEKLLYDISYTNKIDPDGIFUGITSINTLNAKNS----- 480
Db 353 V-KAGAFGLITVAVANNLSGNCILRNLPBOVFRGLGKLSLHLEGSLGRIRPFTGLSG 411
QY 481 -----FKDNTLSVFANT-----TNLPFLDSKQQLQSIGVDPDTHRLQLNMSHNLL 531
Db 412 LRLFLKDNGLVIGIEQSLWGLAELELDLTSNQLTHLPHRLFGGLKLEYLLSNRRLA 471
QY 532 FLDSHYNOLYSLTDCSFNRLETSGKILQHPKSLAPFNLTNNSVACICEHQKFLQ-- 589
Db 472 ELPADALGFLQRAFWDVSHNRLEALPNLSLALPLGRRLYLSLNNSLRTFTPPQGLERL 531
QY 590 VYKQKQFLVNVBQMTCAPE-----NNTSLVLDENNSTC-----YMKTIIS 633
Db 532 WLEG-----NPWDGCELKALRDPALQNPAPVPRFVQALCEGDCCPAPATYNNITC 583
QY 634 VSVSVI 640
Db 584 ASPEEV 590

RESULT 15
US-09-538-092-1087
Sequence 1087, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (0)-(0)
OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Query Match 6.7%; Score 291.5; DB 4; Length 605;
Best Local Similarity 22.0%; Pred. No. 5.3e-17;
Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;
QY 39 CNDOKLSKYVDDIPSTKNIIDISFNPLKIKSYFSNFSFELQWLDISRCIEITIEDKAWH 98
Db 60 CSSRNLTRLPDVGPGTQALMDGNLSSVPPAFAQNLSSIGFLNAGQGLSLEFQALL 119
QY 99 GLHLSNLLITGNPIQSFSPGFSGLTSLNVAVETKIASLESFPIGQILITLKKLVNAH 158
Db 120 GLENLCHLHLEKQKSLALGTFAHTPALASIGLSNNRSLRLEDGLFEGIGSLMDLNLGM 179
QY 159 NFTH-----SCKLPAYFSNLTNLVHVDLSYVYIQTITVNDQ 195

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Db      180 NSLAIVLPDAFRGLSRLVLAGNRLAYLQPALPSGLAELELDLSRNALPAIKAN--V 237
QY      196 FIRENPQVNLSDMSINPIDFIQDAFOGK-LHEITLRGNFNSSNIMKTCIQNLAGIHV 254
Db      238 FVQLPRLQKLYIDRN--IAAVAPGAFLGKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294
QY      255 HRLIIGEPDERNLEIFERSIMEGLCDVTIDFRLLTYNDPSDDIVKHFCLANVSAMSLA 314
Db      295 LRL-----SHNAIA 303
QY      315 GVSIKYLEDPVPGHFKWQSLIRCOLKQPTLDLPPLKSLTLMKKSISFKKVALPSLS 374
Db      304 SLR-----DLHFLEL----- 319
QY      375 YLDSRNALSFSGCCSYSDLGTSNRHLDSLFGNAILMSANFMGLELQHLDPQHSLEKR 434
Db      320 -----QLGHNRIQL-----AERSFEGIGOLEVLTLDNQLOE 352
QY      435 VTEFSAFLSLEKLYLIDISYNTKIDFDGIFLGITSLNTLKMAANS----- 480
Db      353 V-KAGAFGLTNVAVNMNLGNCIRNI,PROVFRGLGKLSLHLEGSCLGRIRPHTFTGLSG 411
QY      481 -----FKDNTLSNVFANT-----TNLTPLDLSKCOLEQISWGVEDTLHRLQLLMSHNNLL 531
Db      412 LRRLFLKONGLVGIEQSLMGLAELELDLISNQLTHLPHRLPQGLKLEYLLLSRNRRLA 471
QY      532 FLDSHYNQLYSLSTLDCSFNRIETSKGILQHFPPSLAFNLTNNSVACICEHOKFIQ-- 589
Db      472 ELPADALGPLQRAFWLDVSHNRLEALPNSILAPGLRLRYLSLRNNSLRTFTPPQPLERL 531
QY      590 WVKEQKQFLVNEQTCATPVE-----MNTSLVLDPNNSTC-----YMKTTIIS 633
Db      532 WLEG-----NPDCCGPLKALRDFALONPASAVPRFVOAICEGDDCQPRPAYTYNNITC 583
QY      634 VSVVSVI 640
Db      584 ASPPEVV 590
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Job time : 24.9539 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.8956 Seconds
(without alignment)

3727.157 Million cell updates/sec

Title: US-09-396-985B-99

Perfect score: 4345
Sequence: 1 MPEPMLARTLIMLFFSC.....GKASNPQTAEDEGTATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2829.5	65.1	837	10	US-09-950-041-26 Sequence 26, Appl
2	2730.5	62.8	799	10	US-09-950-041-8 Sequence 8, Appl
3	2730.5	62.8	799	14	US-10-128-166-7 Sequence 7, Appl
4	2730.5	62.8	799	16	US-10-732-563-8 Sequence 8, Appl
5	2730.5	62.8	799	16	US-10-732-563-8 Sequence 8, Appl
6	619.5	14.3	661	13	US-10-114-893-10 Sequence 10, Appl
7	619.5	14.3	661	15	US-10-038-854-134 Sequence 134, App
8	612.5	14.1	661	15	US-10-038-854-135 Sequence 135, App
9	612.5	14.1	661	15	US-10-037-417-107 Sequence 107, App
10	580	13.3	1032	10	US-09-954-987B-192 Sequence 192, App
11	580	13.3	1032	14	US-10-272-502A-31 Sequence 31, Appl
12	580	13.3	1032	15	US-10-407-952-32 Sequence 32, Appl
13	559	12.9	1059	10	US-09-954-987B-187 Sequence 187, App

14	559	12.9	1059	15	US-10-407-952-30	Sequence 30, Appl
15	559	12.9	1059	17	US-10-753-267-30	Sequence 30, Appl
16	557	12.8	1041	9	US-09-168-978-3	Sequence 3, Appl
17	557	12.8	1041	9	US-09-978-295A-498	Sequence 498, App
18	557	12.8	1041	9	US-09-978-697-498	Sequence 498, App
19	557	12.8	1041	9	US-09-978-122A-498	Sequence 498, App
20	557	12.8	1041	9	US-09-999-832A-498	Sequence 498, App
21	557	12.8	1041	9	US-09-978-189-498	Sequence 498, App
22	557	12.8	1041	10	US-09-978-608A-498	Sequence 498, App
23	557	12.8	1041	10	US-09-978-585A-498	Sequence 498, App
24	557	12.8	1041	10	US-09-978-191A-498	Sequence 498, App
25	557	12.8	1041	10	US-09-978-403A-498	Sequence 498, App
26	557	12.8	1041	10	US-09-978-564A-498	Sequence 498, App
27	557	12.8	1041	10	US-09-999-833A-498	Sequence 498, App
28	557	12.8	1041	10	US-09-981-915A-498	Sequence 498, App
29	557	12.8	1041	10	US-09-978-824A-498	Sequence 498, App
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37	557	12.8	1041	10	US-09-978-643A-498	Sequence 498, App
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40	557	12.8	1041	10	US-09-978-188A-498	Sequence 498, App
41	557	12.8	1041	10	US-09-978-681A-498	Sequence 498, App
42	557	12.8	1041	10	US-09-978-194A-498	Sequence 498, App
43	557	12.8	1041	10	US-09-999-829A-498	Sequence 498, App
44	557	12.8	1041	10	US-09-978-299A-498	Sequence 498, App
45	557	12.8	1041	10	US-09-978-544A-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OF INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-26
Query Match 65.1%, Score 2829.5, DB 10, Length 837;

Best Local Similarity 67.7%; Pred. No. 3e-224;
Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

Qy	7	LATLITMAU- FFSGLTGPJSLNPCI EEWPNITVYOCMDQJLSVPDDIPBSTKNIDLSFNPJL	65
Qy	6	LACGLLPAMAPLSVCPRESMEPCVE- VPNITVYOCMEALNFYKIPDNLPPSTKNIDLSFNPJL	64
Db	66	KIKUSYFSNPSFELQWIDLRSCEIETIEDKAMGHMLNSLITGNPIQSFSPGSGJLT	125
Qy	65	RHIGSYFSFSPPELQVLDLSRCEIOTIEDAGVQSIHLSHTLITLGNPIQSI LAGFSGJS	124
Db	126	SLNLUVAVEYKIASLESFPIGQJLTIKKLANAHPHNSCKJLPAVSNLTLNHYDLSVNY	185
Qy	125	SLQJLVAVETNLASLENFPIGHLTKLXLANAHNLIQSFKJPEYFSNLTLNHELDLSKX	184
Qy	186	IOTTVNDLOFIRENPQVNLSDLSMNSIDPFIQDAPFOGJKLHELTILKGNFNSNIMKTC	245
Db	185	IQSIYCTDLKXVLOHQMPLNLSLSDLSANPMNFIQBPAPFEIRHKHKLTLKNNPFSJLVMTKC	244
Qy	246	LQNLAGLHVHRLIGEFKDERNLEIFEDSIMEGLCDVTITDEFRLTYNDFSDDIYK-FHC	304
Db	245	IQGLAGLEVHRVLVGEFNRNEGNLEKFDKSALEGLCNLTIEFRLVLYLDYLDIIDLFNC	304
Qy	305	LNVNSAMSLAGVSIKILEDVPRKHFPMQSLSIIRQJLQRPPTLDLPFLKSLTLTNKKGJS	364
Db	305	LTVNSSPSLSVTTERVXDFSYNFMQHELVNCKFGFQPTLKLSLXKRLITVSNKGNA	364
Qy	365	FKKVALPSLSYLDLSRNALFSGQCSYSDLTGNISIRHLDLSFNCAJIMSANPMGLELOH	424
Db	365	FSEVDLPSELFDLSRNGLSFKGCCSQSDPGTSLAKYDLSFNGVITYMSNLFGLGEQLH	424
Qy	425	LDPQHSILKRVTEPSAFLSLEKLYLDISYNTKIDPQDIFLGLTSLNLTLMKAGNSFKON	484
Db	425	LDPQHSNKKQMSFSEVFLSLRNLILYDISHTHTRAVFNQIFNGLSLEVLKMAGNSFOEN	484
Qy	485	TLNSVFAATTNLTLFDLSKCOLEOJSMGVFDTLHLROLNMSHNNLTFDSSHYNLOYSL	544
Db	485	FLPDIETELRNLTFLDLSQCOLEJSLPRAFNSLSIQVLANMSHNNFSLDTPPYKCLNBL	544
Qy	545	STLDQSFNRIETS-KGIIQHPKSLAFPNLTNNSVACICEHOKFLOQVKEQOKFLVNEQ	603
Db	545	QVLDVSLNHHMYSKKQELQHPFSLAFNLQNDFACTGEHGFQIMIKDQRLVEVER	604
Qy	604	MTCATPVENMTSLVIDPNNSTCYMTKTIISVSVSVSYVSTAFLLYHPYFHLILAGCK	663
Db	605	MECAPSPDKQGMPIVSL-NITCOMNKTIIIGVSLSVLVSVAVALVYKFFHMLLAGCT	663
Qy	664	KYSRRESIYDAVAVIYSSQDEDMVRNBLVKNLEGVGRPHLCIHYRDPFIPVALAANIOE	723
Db	664	KYGRRENIYDAVAVIYSSQDEDMVRNBLVKNLEGVGRPPQJCLHYRDPFIPVALAANIIHE	723
Qy	724	GFHKSRKVLVVVSRHFIOGRWCIFEYELAQWQFLSSRGGIPIFVILEKYKSLIQOVEL	783
Db	724	GFHKSRKVLVVVSOHFIQGRWCIFEYELAQWQFLSSRGGIPIFVIOKEYKTLIQOVEL	783
Qy	784	YRLSRLNTYLEWEDNPLGRHIFPRRLKALNLDGKASNPET	824
Db	784	YRLSRLNTYLEWEDSVLGRHIFPRRLKALNLDGKSNPEGT	824

```

RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XN1

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CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 8
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-8

```

Query Match	62.8%	Score 2730.5	DB 10	Length 799
Best Local Similarity	67.9%	Pred. No. 4.2e-216		
Matches 534; Conservative	98	Mismatches 152	Indels 3	Gaps 3

Qy	40	DDQKSLKVPDDIPSTKXKIDISFNDPKLKFSYSPNFSEJLQMLDISREIEITBEKAMHG	99
Db	1	MEANFYKIPDNPSTKXKIDISFNPRLHSGSYSPSFPELOVLDISREIQITIEBGAYOS	60
Qy	100	LHLHLSNLLTGNPIQSPSGSPSGTSLSENLVAETKTLASIEFPFICOLITLKULVANH	159
Db	61	LSHSLTLLTGNPIQSLALGAFSGJSSLOKLVAVETNLASJENPFIGHKTLKELVANH	120
Qy	160	FLHCKLPAVSNSLNVLVHVDLSXYXIOTITVNDQFIREMPQVLSLSDMSLNPIDFIOD	219
Db	121	LLOSKLPEYNSNLNLEHLDSSKIKOSITYTDLRVHLQHPMLNLSLSDLSMPNPNFIOP	180
Qy	220	QAFQSIKHLHETLRGNFNSNIMKTCLONLAGLHVHRLILGEFKDERNLEIFEPBIMGL	279
Db	181	GAFKEIRLHKLTLRNPNFSLNWKTCIOGLGLEVHVRVLGEFNRNEGMLKXDKALBGL	240
Qy	280	CVYITIDERPLATYTNDFSDIYK-FECLNLSMSLSAGSIXKLEVPNPKFKQOSIIRIC	338
Db	241	CNLTIEEFLALDYLDIDIDIFNCLTNVSSFSLSVSTIEKVLQFSTYNGHQHLEIVNC	300
Qy	339	OKQEPFTLDPFLKSLTTLTNMGKGISFKKVALPSLSYLDLSNALSFSQSCGSDLGINS	398
Db	301	KKGQFPTLKLKSLKULFTSNKGNAFSEVDPJSLFELDSRNGLSFKGCSQSDYGTTS	360
Qy	399	LRLHLDSPNGALIMSANPMGLELOLHDPQSTLKRVTFEFAFLSLEKLYLDISYTNRK	458
Db	361	LKYLDISFNGVITMSNFGLEQLBHELDPOHENTLQMSSEVFLSLRNLYLDISHTHR	420
Qy	459	IDPDGFLFLGTSNLTKMAGNSFKDHTLSNVANTNLLEFLDLSKCOLEQISMGVDTLL	518
Db	421	VAPNGFLPGLSLEVLKMAGNSFOENFLPIDITELRNLFELDSOQLEQLSPTARNLS	480
Qy	519	RLQILMNSHNNLLFLDSSHYNOLYSLSYLDCEPNRIETS-KGILQHPFSLAFPNLTNNS	577
Db	481	SLQVLNMSHNNFSLDTPFYKCLINSLQVLDYSLNHIMTSKQELQHPFSLAFPNLTQND	540
Qy	578	VACICEHOPELQWVXKOKOLVNVBEOMTCATPEMNTSLVLDENNSTCYMYKTIISVSIV	637
Db	541	FACLTCHOSLQWIKORQLVEVENMECATBDCQGMVLSL-NITQOMKTIIGVSIVL	599
Qy	638	SVLVSIVAFLIYHFFYHLILAGCKKYSRGSYDAFYIYSSQNEBWRNELVKULBEG	697
Db	600	SVLVSIVAFLVLYKFPHMLLAGCIKYGGENIYDAFYIYSSQDEBWRNELVKULBEG	659
Qy	698	VPRFHLCLHVRDIPGVYLAANILQSGFHKSRKVIYVVRHPIQSMWCFPEVSIATQWF	757
Db	660	VPRFOLCLHVRDIPGVYLAANILHGFHKSRRVIVVSOHFIQSMWCFPEVSIATQWF	719

QY 758 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKALLDGK 817
DB 720 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKALLDGK 779
QY 818 ASNPEQT 824
DB 780 SWNPEGT 786

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0253398
; CURRENT APPLICATION NUMBER: US/10/128.166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Query Match 62.8%; Score 2730.5; DB 14; Length 799;
Best Local Similarity 67.9%; Pred. No. 4.2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY 40 MDQKLSVYDPDIPSTKNIIDSFNPKILKXSFNSFSELOMDLSRCEIETIEDKAWHG 99
DB 1 MEALNFKIPDNLPESTKNIIDSFNPKILKXSFNSFSELOMDLSRCEIETIEDKAWHG 60

QY 100 LHLHSLNLTGNPIQSFGSGTSLLENLVAVEYTKLASLSPPIQOLITLKKLVANAHN 159
DB 61 LSHLSTLITGNPIQSFGSGTSLLENLVAVEYTKLASLSPPIQOLITLKKLVANAHN 120

QY 160 FHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSLNIDPDIOD 219
DB 121 LIOSFKLPEYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSLNIDPDIOD 180

QY 220 QAFQGIKLHBLTLRGNFSSNIMKTCLONLAGLHVHRLILGEFQDERNLLEFBSIMEGL 279
DB 181 GAPEIRILHKLTLRNNFDSLNVMKTCIOGLAGLEVHRLVIGEFPNENGLLEKFKDSALEGL 240

QY 280 CDVTIDEFRLLTYNDPDDIVK-FHCLANVSAMSLAGVISIKYLEDPVPHFKMOSLSIIRC 338
DB 241 CNLTIEFRLLTYNDPDDIVK-FHCLANVSAMSLAGVISIKYLEDPVPHFKMOSLSIIRC 300

QY 339 QAKOFTPLDLPFLKSLTLTNKKSISFKYALPBLSTYLDLSRNALSFSGCCSYSDLGTS 398
DB 301 KFOQFPLTKLKSRLTLFTSNKGNASEVDLPBLSTYLDLSRNALSFSGCCSYSDLGTS 360

QY 399 LRHLDSFNGAIIIMSANFMGLLELOHDPQHSITLKRTESAFSLSEKLYLDISYNTK 458
DB 361 LKYLIDSFNGAIIIMSANFMGLLELOHDPQHSITLKRTESAFSLSEKLYLDISYNTK 420

QY 459 IDPDGIFLGLTSLNTLTMAGNSFKDNTLSNVFANTNLTLFLDLSKCOLEOISWGVPTLH 518
DB 421 VANGNIFNGSLSEVLEVKMAGNSFOENLPDLFTLRHLTLFLDLSKCOLEOISWGVPTLH 480

QY 519 RLQOLANSHNNLLFLDGSHTNOYLSLTDSCFNRIETS-KGLIQHPEKSLAFENLTTNS 577
DB 481 SLQVLNMSHNNFSLDTPFYKCLNSLOVLDYSLNHIMTSKKQBLQHPSSLAFLNLOND 540

QY 578 VAGICEHQKFLQWKEQKQFLVNVVEQNTCATPVEMNTSLVDFNNSCTCYKTTISVSV 637
DB 540 VAGICEHQKFLQWKEQKQFLVNVVEQNTCATPVEMNTSLVDFNNSCTCYKTTISVSV 600

DB 541 FACTCEHOSFLQWIKDQROLVEVERMECAPSPDQKQMPVLSL-NITCOMNKTIGSVL 599
QY 638 SVIVSVTAFLIYHFEYFPHILLIAGCKYRSRGSIDAFVYSSQMEDWRNLVKNLEEG 697
DB 600 SVLVSVTAFLIYHFEYFPHILLIAGCKYRSRGSIDAFVYSSQMEDWRNLVKNLEEG 659

QY 698 VPRFHLCHYRDFIPGVALAANIIOEGFHKSARKVIVVSRHFIQSRWCIFEYEAQWQF 757
DB 660 VPPFOLCHYRDFIPGVALAANIIOEGFHKSARKVIVVSRHFIQSRWCIFEYEAQWQF 719

QY 758 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKALLDGK 817
DB 720 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKALLDGK 779

QY 818 ASNPEQT 824
DB 780 SWNPEGT 786

RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732.563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

Query Match 62.8%; Score 2730.5; DB 16; Length 799;
Best Local Similarity 67.9%; Pred. No. 4.2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY 40 MDQKLSVYDPDIPSTKNIIDSFNPKILKXSFNSFSELOMDLSRCEIETIEDKAWHG 99
DB 1 MEALNFKIPDNLPESTKNIIDSFNPKILKXSFNSFSELOMDLSRCEIETIEDKAWHG 60

QY 100 LHLHSLNLTGNPIQSFGSGTSLLENLVAVEYTKLASLSPPIQOLITLKKLVANAHN 159
DB 61 LSHLSTLITGNPIQSFGSGTSLLENLVAVEYTKLASLSPPIQOLITLKKLVANAHN 120

QY 160 FHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSLNIDPDIOD 219
DB 121 LIOSFKLPEYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSLNIDPDIOD 180

QY 220 QAFQGIKLHBLTLRGNFSSNIMKTCLONLAGLHVHRLILGEFQDERNLLEFBSIMEGL 279
DB 181 GAPEIRILHKLTLRNNFDSLNVMKTCIOGLAGLEVHRLVIGEFPNENGLLEKFKDSALEGL 240

QY 280 CDVTIDEFRLLTYNDPDDIVK-FHCLANVSAMSLAGVISIKYLEDPVPHFKMOSLSIIRC 338
DB 241 CNLTIEFRLLTYNDPDDIVK-FHCLANVSAMSLAGVISIKYLEDPVPHFKMOSLSIIRC 300

QY 339 QAKOFTPLDLPFLKSLTLTNKKSISFKYALPBLSTYLDLSRNALSFSGCCSYSDLGTS 398
DB 301 KFOQFPLTKLKSRLTLFTSNKGNASEVDLPBLSTYLDLSRNALSFSGCCSYSDLGTS 360

QY 399 LRHLDSFNGAIIIMSANFMGLLELOHDPQHSITLKRTESAFSLSEKLYLDISYNTK 458
DB 361 LKYLIDSFNGAIIIMSANFMGLLELOHDPQHSITLKRTESAFSLSEKLYLDISYNTK 420

QY 459 IDPDGIFLGLTSLNTLTMAGNSFKDNTLSNVFANTNLTLFLDLSKCOLEOISWGVPTLH 518
DB 421 VANGNIFNGSLSEVLEVKMAGNSFOENLPDLFTLRHLTLFLDLSKCOLEOISWGVPTLH 480

Db 421 VAFNGIFNGLSLEVLKMGNSFOENFLPDIPTFELRNLTFLDLSQCQLEQSPFAFNLSLS 480
Qy 519 RLQLLMNSHNNLLFLDSSHYNOLYSITLDCSFNRLETS-KGILQHPKSLAFENLTNNS 577
Db 481 SLQVLNMSHNNPFLSDTFFPKCLNSLQVLDYSLNHIMTSSKQELQHPSPSLAFNLQND 540
Qy 578 VACICEHQKFLQWVKQKQFLVNVQMTCAPIVEMNTSLVLDNNSTCYMYKTIISVSV 637
Db 541 FACTCEHQSFLOMFKQKQFLVNERECATPSDKQMPVLSL-NITCQNNKTIIGSVL 599
Qy 638 SVTVSVTAFLIHFYFHLILAGCKKYSRGEIYDAFVIYSSQEDWVNEVLKMLEEG 697
Db 600 SVTVSVTAFLIHFYFHLILAGCKKYSRGEIYDAFVIYSSQEDWVNEVLKMLEEG 659
Qy 698 VPRFHLCLHYRDFIPGVAIAANIIOGPFHKSRYIVVSRHFIOSRWCIEYEYEAQTWOF 757
Db 660 VPRFHLCLHYRDFIPGVAIAANIIOGPFHKSRYIVVSRHFIOSRWCIEYEYEAQTWOF 719
Qy 758 LSSRSGLIIFVLEKVEKSLRQOVELYRLSRNTYLEMENDPGRHIFMRRLKALLDGG 817
Db 720 LSSRSGLIIFVLEKVEKSLRQOVELYRLSRNTYLEMENDPGRHIFMRRLKALLDGG 779
Qy 818 ASNPEOT 824
Db 780 SMNPEGT 786

RESULT 5
US-10-732-796A-8

Sequence 8, Application US/10732796A
Publication No. US20040197865A1
GENERAL INFORMATION:
APPLICANT: Gupta, Shalley K.
APPLICANT: Ghosh, Tarnu K.
APPLICANT: Fink, Jason R.
TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
FILE REFERENCE: 5818205004
CURRENT APPLICATION NUMBER: US/10/732,796A
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-10-732-796A-8

Query Match 62.8%; Score 2730.5; DB 16; Length 799;
Best Local Similarity 67.9%; Pred. No. 4,2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

Qy 40 MDQKLSKVPDDIPSSSTKNIDLSFNPCLKILKSYFSNFSFELQMLDLSRCEIETIEDKAWHG 99
Db 1 MEINLYKIPDNLPSTKNIDLSFNPCLKILKSYFSNFSFELQMLDLSRCEIETIEDKAWHG 60
Qy 100 LHHLSNLTGNPIOSFSPBGSGLTSLLENVAVETKASLESFPIGQULITKIANVAN 159
Db 61 LSHLSTLLTGNPIOSLALGAFSGSLQKLVAVETNLALESNFIQHLKTELAVAN 120
Qy 160 FTHSKLAVPSNLTNIVAVDLSYNYIOTITNDIOPRENPQVNLSDMSINPIDFID 219
Db 121 LIQSFLEPFFSNLTNLEHLDLSNKSIOICTDRLVHQMPLNLSLDLSINPMNFIOF 180
Qy 220 QAFQGIKTLHELTLRGNFSSNIMKTCLQNLAGLHVHRLTIGFPERNLIEFSPIMEGL 279
Db 181 GAFKRIHLKLTLRNPFSLNWKTCIOGLAGLEVHRLTIGFPERNLEKFDKSLBGL 240
Qy 280 CVDITDEFRLTYTNDSDIVK-FHCLANVSAMSLAGYSIKLLEVDYKFKKQSLIIRC 338
Db 241 CNLTIEEFRLAYLDYIDIDLFNCLTNVSSPFLSVIIEVKOPFSYVFGQHLVANC 300
Qy 339 QAKQPPTLDPFLKSLTLTMNKGSLSPKVALPSLSYLDLSRAVLSFGCCSYSDGTNS 398

Db 301 KFGQPTLKLKSLKRLFTSNKGNAPSEVDLPJSLFELDSLNGSLFKCCQSSDFGTTS 360
Qy 399 LRHLDSFNGAIITMSANFMGLEBELDROHSTLKRTEPSAFLEKLTYLDSYNTX 458
Db 361 LKYLDSFNGVITWSSNPLGEBQELHLDFOHSLKQMSFVLSLRNLTYLDSYNTX 420
Qy 459 IDPDGIFLGLTSLNLTLMKAGNSFKDNTLSNVFANTTNLTFLDISKQLEQISMGVDTLH 518
Db 421 VAFNGIFNGLSLEVLKMGNSFOENFLPDIPTFELRNLTFLDLSQCQLEQSPFAFNLSLS 480
Qy 519 RLQLLMNSHNNLLFLDSSHYNOLYSITLDCSFNRLETS-KGILQHPKSLAFENLTNNS 577
Db 481 SLQVLNMSHNNPFLSDTFFPKCLNSLQVLDYSLNHIMTSSKQELQHPSPSLAFNLQND 540
Qy 578 VACICEHQKFLQWVKQKQFLVNVQMTCAPIVEMNTSLVLDNNSTCYMYKTIISVSV 637
Db 541 FACTCEHQSFLOMFKQKQFLVNERECATPSDKQMPVLSL-NITCQNNKTIIGSVL 599
Qy 638 SVTVSVTAFLIHFYFHLILAGCKKYSRGEIYDAFVIYSSQEDWVNEVLKMLEEG 697
Db 600 SVTVSVTAFLIHFYFHLILAGCKKYSRGEIYDAFVIYSSQEDWVNEVLKMLEEG 659
Qy 698 VPRFHLCLHYRDFIPGVAIAANIIOGPFHKSRYIVVSRHFIOSRWCIEYEYEAQTWOF 757
Db 660 VPRFHLCLHYRDFIPGVAIAANIIOGPFHKSRYIVVSRHFIOSRWCIEYEYEAQTWOF 719
Qy 758 LSSRSGLIIFVLEKVEKSLRQOVELYRLSRNTYLEMENDPGRHIFMRRLKALLDGG 817
Db 720 LSSRSGLIIFVLEKVEKSLRQOVELYRLSRNTYLEMENDPGRHIFMRRLKALLDGG 779
Qy 818 ASNPEOT 824
Db 780 SMNPEGT 786

RESULT 6
US-10-114-893-10

Sequence 10, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavalie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Metberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
EARLIER FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-893-10

Query Match 14.3%; Score 619.5; DB 13; Length 661;
Best Local Similarity 28.6%; Pred. No. 5,2e-42;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

Qy 28 CIEVNPNTYQCMDKLSKVPDDIPSSSTKNIDLSFNPCLKILKSYFSNFSFELQMLDLSRC 87
Db 28 CIEKANNTYCNENGLSBIPTLNTTBFLFSFNFLPTIHNRTFSRLMNLTFDLTRC 87

[illegible]

RESULT 7
US-10-038-854-134
Sequence 134, Application US/10038854
Publication No. US2004002781A1
GENERAL INFORMATION:
APPLICANT: Spyeck, Kimberly A
Inventor: Li, Li
APPLICANT: Wolenc, Adam R
Attorney: Verne, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Maiyanbar, Uriel M
APPLICANT: Shkimers, Richard A
APPLICANT: Tcherenev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Guseev, Vladimir Y
APPLICANT: Gangolli, Esha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomo R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smlthson, Glenda
APPLICANT: Miller, Isabelle

```

APPLICANT MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 134
LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-854-134

```

Query Match	14.3%	Score 619.5	DB 15	Length 661
Best Local Similarity	28.6%	Pred. No. 5.2e-42		
Matches 187	Conservative 126	Mismatch 296	Indels 45	Gaps 16
QY	28	CIEVNVNITYOCQDQCLSKVPDDIPSSPTKNIDLSFNPKIKSKYSFNSPSELMQWLDL SRC	87	
Db	28	CIEKANKTYNCENGLSIEIPDTLPNTTBEPLEFSNPLPTIHNKRTFSMLMUTLIDLTRC	87	
QY	88	EIEETIEDKAMHGLHLSNLTGNEPIQSFSPGSEFGLTSENVAVETKASLESFPIQ	141	
Db	88	QIWMIHEDPFGSHHQSTLVTLGNPLIFMAETSLNGPSKLKHLFIQIGISNLEFIPVH	141	
QY	148	LITLTKLNAHNPYHSCKLPAFYNSUTLVYHVDLSYNTQITTYNDLOFLREPNQWLSL	207	
Db	148	LENLESLYLGSHNISIKFPDPFP-ARMUKYDLFQNNAHYISREDDMSLEQ--AINSL	204	
QY	208	DMSLNPIDIFLODAFEGIKLHETLGRNPNNSNIKKTOLOLAGLHVRLLTGEFKERN	265	
Db	205	NFGNNVKGIEIGAFDSTYFQSLNGGTGRNLSVIFNG--LQNST--TQSLMGTFEEDID	266	
QY	268	LEIFEPSEMEGCDVTIDEFRLTYNDSF--DIYFKCLAVNSAMSILAGYSIKYLEDVPK	326	
Db	261	EDL--SSAMLKGCIMSVESLNL--QHRRSIDISSTFQCFQLOLELDLTAT--HLKGLPS	315	
QY	327	HEFMQSLAIR-----CQLK--QRPPLDLPKLKLLTMNKGISFPKVALPS	372	
Db	316	GMLK--GLNLTIKLVLYSVNHFDQLCOISANPSPSLTHETIRGNVKKLHGVGCELEK--LGN	373	
QY	373	LSVLDLSRUALSFSGCCSVSDLTGNSLHNLDSFNGAL--IMSANPMGLEELQHLDPQHS	433	
Db	372	LQTLDSHNDIASDCCSLQDLKNLSHLOTLMLSHNEPRLGLOSOAFKCPQLELDLAFT	431	
QY	432	LKKVTEFSAFLSEKLKLYLDSYTTTKIDPFGIFGLISLNTLMAGNSFKONTL--SNV	489	
Db	432	LHNAPQSPQULHFLQVULNLTLCGLDINSQHLAAGPVLKHNMLKGNHQQDDGITITNL	491	
QY	490	PANTNLTGLDLSKQLEOISMGVDTLHRLQILNMGSHNLL--FLDS--SHYNQVLSLT	546	
Db	492	LQVGSLEVLILSSCGLLSIDQAFNHSIGKSHHLLDLSNLSLTCSIDLSHLKITY---	547	

Qy 547 LDGSPNRIFETSKGILQHPFKSLAFPNLTNNSVACICEHQKFLQWKEQKQFLVAVNEQMTFC 606
Db 548 LNLASINISIPRLPLTPOOSSTINLSHNPIDCTCSNHFLLTWYKKNLHLESGSEETTC 607
Qy 607 ATPBEMN---TSLVDFNNSCTCYMYKTIISVSVSIVVSTVAFLLIHFYFHL 656
Db 608 ANPBLRGVKSVDKSLGCGTATGIFLIVFLLLALITLFFAVKYLLEMKYQHI 661

RESULT 8

US-10-038-854-135
; Sequence 135, Application US/1003854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eiben, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkels, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patuturajan, Meera
; APPLICANT: Gusev, Vladimiy Y
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Elberman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-038-854-135

Query Match 14.1%; Score 612.5; DB 15; Length 661;
Beet Local Similarity 27.0%; Pred. No. 2e-41;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

Qy 12 IMALFF-SC-LTPSLNPCIIEVVPNITYOCMDOKLSKVPDDIPBSTKNIDLSFNPLKILK 69
Db 10 LVNLFPLASCRATSSDDCKICEKVENKTYNCENIGLNEI PGTLPNSTCELFSEFVLPFIQ 69
Qy 70 SYSPFSNPELQMDLSPCEIETTEDKAWHGLHLSNLTGNPIQSPSPSGSLSTLEN 129
Db 70 NTFPSRLINLTFPLDTRCQIYWIHEDTFQSHRIDTLVLAPELPLISGPKALKH 129
Qy 130 LVAVETKLASLESPPICQLITLKKLVANHFHSCKLPAYFSNLTNLVHVDLSYNYIQT1 189
Db 130 LPTIQTGISIDFPLNQKTLSELYGSHNHSIKLPKPEPT- EKLKVIDFQNNALHYL 188
Qy 190 TVNDLQFLRENPOVNLSDMSLNPIDFIQDAFGIKHLELTTRGNFSSNIMTKCLQNL 249
Db 189 SKEDMSGLQ--ATNLSLNGNDIAGIBQAFSAVFQSL---NFGQTQNLVIFKGL 242
Qy 250 AGLVHRLIIGEFDERNLTFEFSIMEGLCDVTIDEFRLTYTNDPSDDIVKEHCLANVS 309
Db 243 KNSTIOSIMTGFEDMDDEDI-SPAVEGLCEMSVESINQKVFYFNSSNTFHCFSGLQ 301
Qy 310 AMSLAGVSIKYLEVDPKHF-----KMSLSIRCOL--KQFTLDPPLKS 353
Db 302 ELDLTAT--HSELPSGLVSLTKLVLSANKFENL---CQISANFSLTHLSIKG 354
Qy 354 LTLTNKGSISPKVALPSLSYDLSRNALSFSCCSYSDLTGNSLRHLDSFGAIIWS 413
Db 355 NTKLELGTGLEN--LENLELDLSHDIDRTSDCCNLQLRNLHLSGLNLSYNEPLSLK 412
Qy 414 AN-FMGLDELQHPQSHTKLVTFEFSRFLSLEKLYIDISYTMKIDFDGIFIGLSIN 472
Db 413 TEAFKECPQLBLDLAFRLKVKDAQSPQNLHLKVLNLSHSLDLSSEDLFGSLPLQ 472
Qy 473 TLKMAQNSFKQNTL--SNVFANTTNLTFPLDSCQLOEIQISGVFDTLRLOLNNSHNL 530
Db 473 HNLQGNHFPKGNIOKTNLSLQTLGRLILVLSFCDLSSIDGHAFTSLKMMNHVDSHRL 532
Qy 531 LFLD---SSHYNOVLSLTDSCFNRIETSKGILQHPFKSLAFPNLTNNSVACICEHQK 587
Db 533 TSSSEIALSHLKGIT---LNLASNHISITLPSLLIPISOORTINLRQNPIDCTCSNIYF 588
Qy 588 LQWKEQKQFLVAVNEQMTCAPEVEMN---TSLVDFNNSCTCYMYKTIISVSVSIVVS 643
Db 589 LEWYKENNQKLEDTEDLCENPPLRGVRLSDVTLTSCSMAVGLFLLIVFLVFAILLIF 648
Qy 644 TVAFLLIHFYFHL 656
Db 649 AVKTYLRMKYQHI 661

RESULT 9
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsebrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patuturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R

```
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyanek, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260, 018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260, 360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272, 411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272, 817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291, 186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303, 231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305, 060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318, 405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318, 700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Query Match 14.1%; Score 612.5; DB 15; Length 661;
Best Local Similarity 27.0%; Pred. No. 2e-41;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

QY 12 IMALFF-SC-LTPGSLNCEIVNITQCMDOQLSKVPDDIPSTKNIIDISFPLKLIK 69
DB 10 LVALFLASCRATSSDQKCEKEVVKYCNENLGNELPGLPSTECLEFSFVNLPTIQ 69
QY 70 SYSFSEFSELOMLDSRCEIETIEDKAWGLHLSNLITGNPQSFGSGSLTSEN 129
DB 70 NTSRRLNLNLFDLTRCOIWIHEDTQSOHRDLTVLNLPMALSGPKALKH 129
QY 130 LVAETKIASLESPPIGQLITLKKLVANFHSCKLPAYFSNLTNLVHVDLSVNYIOTI 189
DB 130 LFFIQTGSSIDFIPLHNQKTLSELYGSHNHSISKLPKFPPT-EKLVLDFOGNAIHYL 188
QY 190 TVNDLQFRENPOVNLSDMSLNPIDFQDAFOGCIKHELTGKNFSSNIMTKCLONL 249
DB 189 SKEDMSSIQQ--ATNLSTNLGNNDIAGIBGAFPSAVFQSL---NFGTONLVITFPGI 242
QY 250 AGLHVHRLILGEFDERNLBIFFPSIMEGLCDVTIDEFRLTYTNDPSDVIKPFCLANVS 309
DB 243 KNSITQSLMGTFFDMODEDI-SPAVFGLCEMGEVESINLQKHFFNINSSTTFHCFSLQ 301
QY 310 AMSLAGVSIKLEVDVPHF-----KWSISITRCQL--KQFPTLDLPFLKS 353
DB 302 ELDLTAT---HLSELPSGLVGLSTLKKLVLSANKFENL---COISANFSLTHLSIKG 354
QY 354 LTLMNKGSISFKVALPSLYLDSRNALSFSGCCSSDSDGTSIRHLDSFNGALIMS 413
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DB 355 NTKRELGTGCLLEN--LENLRELDSHDDIETSDCCNIQLRNLSHQSLNLSYNEPLSLK 412
QY 414 AN-FMGELELOHLDFOHSTLKVETFSAPLSLEKLLYDLSYNTKIDPDGIFLGITSLN 472
DB 413 TEAFKECQLELDLDAFLRLKVKQKQSPQNLHLKLVNLSLSDISEQOLFDELPAHQ 472
QY 473 TLKAGNSFKONTL--SNVPANTNLTFPLDSKCOLEOISWGVPTLRLLOLNNSHNUL 530
DB 473 HNLQGNHFPKGNLOKTNLSQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDSLHRL 532
QY 531 LFLD---SSHNQLYSLSSTLDCSPRIFETSKGILQHPFKSLAFPLYLTNNSVACIEHQKF 587
DB 533 TSSGIEBALSHLKGY---LNLASHNISITILPSLPLISQORTNLRONPLDCTCSNIYF 588
QY 588 LQWVEQKQFLVNVQOMTCATPVENM---TSIVLDPNNSCTCMYKTIISVSVSVIYVS 643
DB 589 LEWYKENNQKEDTEDTLCENPPLRGVRLSDVTLSCSMAVGIFFLVFLVPAILLIF 648
QY 644 TVAFLIYHFYFHL 656
DB 649 AVKYFLRWKYQHI 661

RESULT 10
US-09-954-987B-192
Sequence 192, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954, 987B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233, 035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263, 657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291, 726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300, 210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-192

Query Match 13.3%; Score 580; DB 10; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

QY 2 MPF--WLLARTLIW-----ALFSCSLTPGSLNCEIVPN--ITQCMDOQLSKVPDDIP 52
DB 4 MPQSMILTCFCLSSGTSATFHKANYSRST-PDEIRHNSLVLAECNHRQLHEVPOTIG 62
QY 53 SSTKNIDLSFNPPLKILKSYSFSEFSELOMLDSRCEI-----TIEDKAWGLH 102
DB 63 KYVTNIDLSDNAITHIRKESFOKLQNTKIDLNNAKQOHPNENKGNMNTREGALLSLRN 122
QY 103 LSNLITLGNPQSS---PQSGSLTSENLVAVETR-----LASLESFPIG----- 146
DB 123 LTVALLBDNQLXYTIPAGLPESLKELSLQNNITQVTKNTTFGRLNRLRYLGNMCEYKCN 182
QY 147 -----QITLTKLVANH--FIHSCKLPV----- 168
DB 183 QTFVDEGARKNLIHLKLVLSLSTFNNLFYVPPKLPSSLRKLPVLSNAKIMNTIOEDFKLEN 242
QY 169 -----YF 170
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Qy 670 SIYDAFYVYSSON---EDWVNEVLVKNLEEGVPR-FHCLHYRPDPICVAIAANIIOGCF 725
Db 869 TFYDAVSYDTRKQASVTDVWVNELRHLEESDEKSVLLCLBERDWDPPGPIIDNMQ-SI 927
Qy 726 HKSARKVIWVSRHFIQSRWCIFEYEIACTWQFLS-----SRSGIIFIVLEKYE 773
Db 928 NQSKKTIFFVLTCKY-----AKSNMFKTAFYALQRLMDENNDVIIIFILEPVL 975
Qy 774 KSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALL 814
Db 976 Q-YSOYLRRLQRICKSSIIQWPNPKNPAENLFWQSLKNVVL 1014

RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Query March 13.3%; Score 580; DB 15; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

Qy 2 MPP--WLIARTLIM---ALFSCLPFGSLNPPCLEVVN--ITYQCMDOKLSKVPDIP 52
Db 4 MPQSWILTCFCLSSGSAIFHKANYSRST-PCDEIRHNSLVABCHRHQLEHPDTIG 62
Qy 53 SSTNNIDLSFNPILKILSYFSFNSFSELQWDLSSRCEI-----TIEDKAMHGLIH 102
Db 63 KYVTNIDLSDNAITHIKESFOKLQNTKIDLNNAQOHENKNGNITREGALLSRN 122
Qy 103 LSNILILGNPIQSPS---PGFSGLTSLLENVAVETK---LASLESFPIG----- 146
Db 123 LTVLLLEDNDOLYTIIPAGLPESLKEISLQNNIIFOVTKNNTFGLNRLERLYGNNCYFKN 182
Qy 147 -----QLITLKLNVANH--FLHSCKLP----- 168
Db 183 QTFKVEDGARKNLIHLKVLISFPNLLYVPPKLSLKLFLSNAKIMNTIQEDPKLEN 242
Qy 169 -----SSNFGK--LRSLKLIHLRGVFRLELKKH-----FEH--LQSLPNLATIWDGI 398
Db 243 LTLILDSGNCRCYNAPPTCPCKENSIHHPAFOSLQTLVLYNLSTSLRTIPSTWF 302
Qy 171 SNLTNLVHVLSTNY-IGTITVNDLOFLRENPQVNLSDMSLNIDTIGDOAFQGLKHE 229
Db 303 ENLSNLEKELHLEFYVLOEIASG--AFLTKLPISLQI-LDISFN---FOYKEYLOFINI-- 354
Qy 230 LTLRGFNSSNMKTCLQNLAGLHVHRLIGEFKDEENLEIFEPSIMEGLCDVTIDFRL 289
Db 355 -----SSNFGK--LRSLKLIHLRGVFRLELKKH-----FEH--LQSLPNLATIWDGI 398
Qy 290 TYNNDPSDDIVKPHCLANVSAMSLAGVSITYLEDDVPHFKMQS-----LS----- 334
Db 399 NFLEKI--DPRKAFQNFSEKLDVIYLSGNRIASVLDGTDYSWRNRLRKPLSTDDDEPDPHV 456
Qy 335 -----IRCOLKQF-PTLIDLPF-----LKSULTITNNKGSISFQKV- 368

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Db 457 NFYHSTKLPIKQCTAYGKALDLSLNNIFIICKSQFEGFODIACINLSFNANTQVFNGTE 516
Qy 369 --ALPSTVYLDLSRAALSFSGCCSYSDIGTNSLRHLDSFNCAIIMSAN-----FMEL 419
Db 517 FSSMHPIKYLDTNNRLPDDNNARFSDL--HDEVLDSLHNAHYSIAGVTHRLQPTONL 574
Qy 420 BELQHLDFQHSSTLKAQTE-----FSAFLSLEKLY 449
Db 575 INLRVNLNSHNGIYITLFESELSKISLKEIVFSGNRDLHMANDKWSTIKSLQNLIR 634
Qy 450 LDISTYNTKIDPDGIFGL-TSLNTLKNAGNS--FKDNTLSNVFANTTNLTFLDLSKQOL 506
Db 635 LDLSTNNLQOIPNGAFINLPSLOELISGNKLRFPFNTLLQYF---PHLHLDLSRNL 691
Qy 507 EQISGCVEDTLHRLQOLMSHNNLLFLDSHYNOIXSLSTDGCSNRIE-TSKGILQHP 565
Db 692 YFLPNCLSKPAHSLBTLTSLNHSRHLSPGSLSEARNLVHLDLSFNTIKMINKSLSLQTKM 751
Qy 566 K-SIAFENLTNNSVACICEHOKFLQWYKQKF-----LVNVEQWTCATPEMNTSLVLD 620
Db 752 KTNLSIELHNGYFDCDIDISDFSMIDENLNTITPKLVN---ICSNPGQKSKSISL 808
Qy 621 NNSCTMAKTIISVSVSVIVSTV--AFLIYH-----FYFH--LLIAGCKYSRGE 669
Db 809 DLITCVSDPTAAVAFLEFLFTTSMWMLAALVHHLFYMDVWFYHMCSAKLGKRYTSISQ 868
Qy 670 SIYDAFYVYSSON---EDWVNEVLVKNLEEGVPR-FHCLHYRPDPICVAIAANIIOGCF 725
Db 869 TFYDAVSYDTRKQASVTDVWVNELRHLEESDEKSVLLCLBERDWDPPGPIIDNMQ-SI 927
Qy 726 HKSARKVIWVSRHFIQSRWCIFEYEIACTWQFLS-----SRSGIIFIVLEKYE 773
Db 928 NQSKKTIFFVLTCKY-----AKSNMFKTAFYALQRLMDENNDVIIIFILEPVL 975
Qy 774 KSLRQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALL 814
Db 976 Q-YSOYLRRLQRICKSSIIQWPNPKNPAENLFWQSLKNVVL 1014

RESULT 13
US-09-954-987B-187
; Sequence 187, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-987B-187

Query March 12.9%; Score 559; DB 10; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;

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27 PCIEVVPN--ITYQCMQDKLSKVDDIPSSSTKNIDLSFNPDLKILKSYFSNFSLOMDL 84
53 PCBEKQNDVIAECSNRRLQEVPOQVGVTELDSDNFTIHTNFSFQGLQNLTKINL 112
85 S-----RCEIETEDKAMGHLSNLIITGNPQSPSPSGFGL--TSLEN 129
113 NHPNVOHQNGNPGIQSGNGLNTTGAFLNKNLRELLLEDNQ-----PQIPSGLPESLITE 168
130 LVAVETKLASLESFPIQLITLKKLVANAHN--FIHSCKL-----PAYSNLTNLVHVDLSY 183
169 LSLIQNNIYNTKSGISRLINLKYLAANCYFKNVCEKTIENEDGVETLTNLELSLSF 228
184 NYIQTITVNDIQFLRENPQVNLSDMSLNPIDFIQDQAFQO--IKLHETLRGN-----FN- 237
229 NSLSHVPKLPSSLRK-----LFLSNTQIKYISEDFKGLINTLILDSGNCPCRCFNA 281
238 -----SSNIMTKCLQNLA----- 250
282 PPFCVPCDGGASINIDRAFQNLQOLRYLANLSTSLRKINAMFQMPHKLVDLEFNYL 341
251 -----GLVHRLILGEFK 263
342 VGEIASGAFITMLPRLEILDLSFNVIKGYPOHINISNFSKPLSLRALHLRGVYFOELR 401
264 DE-----RNLFIPEPSIMEGLCDVTIDEFRILTY 291
402 EDDFQPLMQLPNLSTINGINFIKQIDFKLFQNFSGNLBII--YLSBNRISPLVVDKTRQSY 459
292 TN-----DPSDD-----IYKFCILANVSAMSAGVSIKYLEVDPK 326
460 ANSSSFQHIRKRSTDEDFDHSNFYHTRPRLIPQCAAGKALDLSNLSIFFIG--PN 517
327 HPKMQSLIIRCOLKQFPTLDLPFLKSLTLTNKKSISFKKY--ALPESLTLDSRNAL 383
518 QFE-----NLPIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRL 560
384 SFGCCSYSDLGTSNLSRLHLSFNCAIIMSAN-----FMGLBELQHLDFQHSSTLKRYT 436
561 DFDNMSALTEL--SDLEVLDSLNSHYFRIAGVTHLEFIQNFYMLKVLNLSHNNIYTLT 618
437 EBSAFLSLEKLYLDISYNTKID-----PDGIFGLTSLNTLTKAAGSFKDNTLS 487
619 D---KYNLESKSLVELVFSGNRLDILMDDNRYSISFGKLNLTRLDISLRK--HLPN 674
488 NVEFAN--TNLTFLDLSKCOLQEQISWGVFPTLRLOLNNSHNNLFLDSSHYNQLYSLT 546
675 EAPFLNPLASLTETLHINDNMLKFFNMTLQOFPRLBELDRGNKTLFLTLTSLSDFTSSLRT 734
547 LDGSPNRI-----ETSGIILQHPFKS-----LAFNLTNNSVAC 580
735 LLLSHRISHLPSGFLSEVSSLKHLDSLNNLKTINKSALERTYTKLSMELHGNPFC 794
581 IEHQKELQWVWEQKFLVNV-----QMTCAFPVEMNTSVLDFNNSTCYMYKTIISVS 635
795 TCDIGDFRWMDBH---LNVKIPRLVDVLCASPGORGSYSLELTTCVSQVTAIILF 850
636 VVSIVIVSTY--AFILYHFEFH-----LTLIACKKYSGRESIYDAFVLYSQN-- 682
851 FFLFFITTMVLAALAHLEFYMDVWFIVNVCIAKIGYSLSLTSQFYDAIYSYDTPKDS 910
683 -EDWVNEELVKNLEEVPR-FHLCHYRDFIPGVAIPANITQGFHKSRAVIVVSRHFL 740
911 VTDWVINEELRYHLEESRDKVALLCLERDWDPGIATIIDNIMO--SINQSKTIVLTLKCY- 968
741 QSNWCIPEYIQAOTWQFLS-----SRSGIIFVLEKYSKLSAQOVELYILS 788
969 -----ASWMEKTAIFYALQOLMDENMDVILFILLEPVLQH--SQYLRKORIC 1015
789 RNTYLEWEDNPLGRHIFWRILKNALL--DGKASN 820
1016 KSSILQMPDNPKAEGLPWQTLRVVLTENDSRYN 1050

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RESULT 14
US-10-407-952-30
; Sequence 30, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G, U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037 US
; CURRENT APPLICATION NUMBER: US 10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-952-30

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Query Match 12.9%; Score 559; DB 15; Length 1059;

Best Local Similarity 22.3%; Pred. No. 1e-36;

Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;

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27 PCIEVVPN--ITYQCMQDKLSKVDDIPSSSTKNIDLSFNPDLKILKSYFSNFSLOMDL 84
53 PCBEKQNDVIAECSNRRLQEVPOQVGVTELDSDNFTIHTNFSFQGLQNLTKINL 112
85 S-----RCEIETEDKAMGHLSNLIITGNPQSPSPSGFGL--TSLEN 129
113 NHPNVOHQNGNPGIQSGNGLNTTGAFLNKNLRELLLEDNQ-----PQIPSGLPESLITE 168
130 LVAVETKLASLESFPIQLITLKKLVANAHN--FIHSCKL-----PAYSNLTNLVHVDLSY 183
169 LSLIQNNIYNTKSGISRLINLKYLAANCYFKNVCEKTIENEDGVETLTNLELSLSF 228
184 NYIQTITVNDIQFLRENPQVNLSDMSLNPIDFIQDQAFQO--IKLHETLRGN-----FN- 237
229 NSLSHVPKLPSSLRK-----LFLSNTQIKYISEDFKGLINTLILDSGNCPCRCFNA 281
238 -----SSNIMTKCLQNLA----- 250
282 PPFCVPCDGGASINIDRAFQNLQOLRYLANLSTSLRKINAMFQMPHKLVDLEFNYL 341
251 -----GLVHRLILGEFK 263
342 VGEIASGAFITMLPRLEILDLSFNVIKGYPOHINISNFSKPLSLRALHLRGVYFOELR 401
264 DE-----RNLFIPEPSIMEGLCDVTIDEFRILTY 291
402 EDDFQPLMQLPNLSTINGINFIKQIDFKLFQNFSGNLBII--YLSBNRISPLVVDKTRQSY 459
292 TN-----DPSDD-----IYKFCILANVSAMSAGVSIKYLEVDPK 326
460 ANSSSFQHIRKRSTDEDFDHSNFYHTRPRLIPQCAAGKALDLSNLSIFFIG--PN 517
327 HPKMQSLIIRCOLKQFPTLDLPFLKSLTLTNKKSISFKKY--ALPESLTLDSRNAL 383
518 QFE-----NLPIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRL 560
384 SFGCCSYSDLGTSNLSRLHLSFNCAIIMSAN-----FMGLBELQHLDFQHSSTLKRYT 436
561 DFDNMSALTEL--SDLEVLDSLNSHYFRIAGVTHLEFIQNFYMLKVLNLSHNNIYTLT 618
437 EBSAFLSLEKLYLDISYNTKID-----PDGIFGLTSLNTLTKAAGSFKDNTLS 487
619 D---KYNLESKSLVELVFSGNRLDILMDDNRYSISFGKLNLTRLDISLRK--HLPN 674
488 NVEFAN--TNLTFLDLSKCOLQEQISWGVFPTLRLOLNNSHNNLFLDSSHYNQLYSLT 546

```


Db 675 EAFNLPASTLTELHNDNMLKFFNMTLLOQFRLBLDRGNKLLFLDLSLSDFTSSLRT 734
Qy 547 LDCSFNRI-----ETSKGILQHPKRS-----LAFNLTNNSVAC 580
Db 735 LLSHNRISHLPSGFLSEVSLKHLDLSSNLKTKINSKALERTKTTKLSMELHGNPEC 794
Qy 581 ICEHQKFLQWKEQKQFLVNV-----QMTCAPEVANTSLVLDPNNSCTCYMTIISVS 635
Db 795 TCDIGDFRRWMDH-----LNVKIPRLVDVICASPDORCKSVLSLELTTCVSDVAVILF 850
Qy 636 VVSIVIVSTV--AFLIYHFYH-----LILJACKKYSRGESYDAFIYSSON-- 682
Db 851 FFFFTITTMVMAALAHHLFVWDWFIYVNCIAKIKGRSLSTQTFDAYISDTKDAS 910
Qy 663 -EDWVRNELVKNLEGVPR-FHLCIHYRDFIPGVAIAANIIOEGFHRSKRYIVVSRHFI 740
Db 911 VTDWVINEIRKYLESRDKNVLLCJBERMDPGLAIDNLMQ-SINOSKRYVFLTKKY- 968
Qy 741 OSRMCIFREYEAQTQOFLS-----SRSGIIFVLEKVEKSLRQVVELYRLIS 788
Db 969 -----AKSNWFTAFYALQRLMDENMDYIIFLLEPVLQH--SOYLRLRORIC 1015
Qy 789 RNTYLEMEDNPLGRHIFWRRLKALL---DGKASN 820
Db 1016 KSSILQWDPNPKABEGFMQTLRNVVLTENDSRYN 1050

RESULT 15
US-10-753-267-30
Sequence 30, Application US/107533267
Publication No. US20050037946A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Stegallano, Nancy E.
APPLICANT: Healy, Aileen
APPLICANT: Galvin, Katherine M.
APPLICANT: Domoghue, Mary A.
APPLICANT: Rodrigue-Way, Amelie
APPLICANT: Tomlinson, James E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
TITLE OF INVENTION: 32345, 965, 1920, 17318, 1510, 14180, 26005, 554, 16408,
TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
FILE REFERENCE: MP103-003P1RNMNMIM
CURRENT FILING DATE: US/10/753,267
PRIOR APPLICATION NUMBER: 2004-01-08
PRIOR FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/439,683
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/445,216
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/448,036
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/454,189
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/457,541
PRIOR FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/466,411
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/469,041
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: US 60/477,414
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/478,560
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 60/489,772
PRIOR FILING DATE: 2003-07-24
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-753-267-30

Query Match 12.9%; Score 559; DB 17; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;

Qy 27 PCIEVPRV-ITYQMDKLSKVPDDIPSTKNDLSNPLKILKSPSFSBELQMDL 84
Db 53 PCDEKQNDVIAECNSRRLQEVPOTVGKYVTELDSDNFITHITNESFOGLONTKINL 112
Qy 85 S-----RCIEITIEDKAMGHLHLSLILTGPNPISFGSGSPGL-TSLEN 129
Db 113 NNNPNVQHGNGNPGIQSNGNLITDGAFLNKLRLLEDNQL-----PQIPSGLEBSLTE 168
Qy 130 LVAETKLASLESPIGOLITLTKLNVANH--FISCKL-----PAYFSNLTVLVHVDLSY 183
Db 169 LSLIOMNTYNTKGISRLINKULYAMNCEYKNCYCKTNIEDGVETLNLIELSLSF 228
Qy 184 NYIQTIVNDIQFLRENDQVNLSDMSINPJDIFODQFQG-IKLHELTLRGN---FN- 237
Db 229 NSLSHVSFKLPSLSRK-----LFLSNVQTKYSEBDFKGLINTLLDLSGNCRCRFA 281
Qy 238 -----SNIMTKCLQNA----- 250
Db 282 PFCVPCDGGASINIDRAPFQNLQRLVNLSTSLRKINAMFKNMELKVLDELFNVL 341
Qy 251 -----GHVHRLTIGEPK 263
Db 342 VGEIASGAFITMLRLTELIDSPVYIKSGYPOHINISNEKSPSLRKLHLRGVFOELR 401
Qy 264 DE-----RNLEIFEPSIMEGLCDVTIDEFRUTY 291
Db 402 EDDQPLQMLNLTNLGINFIQIDPKLFQNSNLEII--YISENNISPLVKVOTRQSY 459
Qy 292 TN-----DPSD-----IKFHLAVASAMSLAGVSIKYLEDPK 326
Db 460 ANSSSFQHIRKRSTPEEPHSNFYHFTBPLKPOCAAGKALDSLINSIFFG--PN 517
Qy 327 HFKQSLIIRCOQKQFPTDLPFLKSLTLTMNGSISFFKV--ALPSLVLDSRYAL 383
Db 518 QFE-----NLPDIACLANSANSNAQVLSSTESBAIRHVATLIDLTNRL 560
Qy 384 SFGCCSYSDIGTNSLRHLDSFNGALIMSAN-----FMGLEBLQHLDFQHSITLKEVT 436
Db 561 DFNASALTEL--SDLEVLDSLVSNSHYPRAGVTHHLEFIQNFNLKVLNLSHNNIYTLT 618
Qy 437 EFSAFSLSEKLLYDIDISTYTKID-----FDGIFLGTSNLTLMAGNSFSDNTLS 487
Db 619 D--KYNLESKIVELVFSGNRLDILWDDNRRIYSIFPKGNLTRDLSNRLK-HLPN 674
Qy 488 NVFAN-FTNLFTLDSLCOLEQISMGVEDTLHRLOLNMSSNNNLFLDSSHYNOLYSIST 546
Db 675 EAFNLPASTLTELHNDNMLKFFNMTLLOQFRLBLDRGNKLLFLDLSLSDFTSSLRT 734
Qy 547 LDCSFNRI-----ETSKGILQHPKRS-----LAFNLTNNSVAC 580
Db 735 LLSHNRISHLPSGFLSEVSLKHLDLSSNLKTKINSKALERTKTTKLSMELHGNPEC 794
Qy 581 ICEHQKFLQWKEQKQFLVNV-----QMTCAPEVANTSLVLDPNNSCTCYMTIISVS 635
Db 795 TCDIGDFRRWMDH-----LNVKIPRLVDVICASPDORCKSVLSLELTTCVSDVAVILF 850
Qy 636 VVSIVIVSTV--AFLIYHFYH-----LILJACKKYSRGESYDAFIYSSON-- 682
Db 851 FFFFTITTMVMAALAHHLFVWDWFIYVNCIAKIKGRSLSTQTFDAYISDTKDAS 910
Qy 683 -EDWVRNELVKNLEGVPR-FHLCIHYRDFIPGVAIAANIIOEGFHRSKRYIVVSRHFI 740

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Db      911 VTQVWVNLRLRYHLEESRDKNVLLCLERDMDPGIAIIDNLMQ-SINOSKTVFVLTCKY- 968
QY      741 QSRWCIFEYEIAQTWOFLS-----SRSGIIFIYLEKYEKSLRQOVELYRLLS 788
Db      969 -----AKSMNFRTAFYALQRLMDENMDVIIIFILEPVLQH-SQYRLRQRIC 1015
QY      789 RNTYLEMEDNPLGRHIFWRLLKALL--DGKASN 820
Db      1016 KSSILQWPDNPKABGLFWQTLRNVTLTENDSRNN 1050

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Search completed: March 12, 2005, 20:28:08
 Job time : 79.8956 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds

(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985b-99

Perfect score: 4345

Sequence: 1 MPPFWLARTLIMLFPSCLE.....GKSNPEQTAEEDPTATWT 835

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: _pir1: *
2: _pir2: *
3: _pir3: *
4: _pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612.5	14.1	661	2	156258 Rp105 - mouse
2	457.5	10.5	786	2	208664 Toll protein-like
3	406	9.3	1097	2	A29943 Toll protein precu
4	344	7.9	1389	2	T13852 gene wheeler prote
5	342	7.9	1385	2	T13887 citr protein - fru1
6	319.5	7.4	603	2	UC6128 insulin-like growt
7	317.5	7.3	603	2	JC1282 insulin-like growt
8	316.5	7.3	605	2	JC5239 insulin-like growt
9	315.5	7.3	1066	2	T15864 hypothetical prote
10	303.5	7.0	1134	1	A29944 chaptin precursor
11	291.5	6.7	605	2	A41915 insulin-like growt
12	287.5	6.6	1531	2	T42218 silt-1 protein hom
13	283.5	6.5	1112	2	T10504 disease resistance
14	273	6.3	1469	2	B36665 silt protein 2 pre
15	273	6.2	1480	2	A36665 silt protein 1 pre
16	270	6.2	2026	1	OYBY adenylate cyclase
17	269	6.2	1143	2	T10636 hypothetical prote
18	266.5	6.1	1662	2	S42799 garp precursor - h
19	262.5	6.0	1091	2	A58532 glial cell membran
20	260.5	6.0	1523	2	T13953 MEGF5 protein - ra
21	257.5	5.9	1134	2	T04587 hypothetical prote
22	256	5.9	1120	2	B66479 hypothetical prote
23	255.5	5.9	994	2	H96510 probable disease r
24	255	5.9	907	2	UG0193 G protein-coupled
25	254.5	5.9	990	2	T00800 disease resistance
26	253.5	5.8	983	2	G84524 probable disease r
27	249.5	5.7	1027	2	B85089 receptor protein k
28	249.5	5.7	1051	2	T13174 gp150 protein - fr
29	247.5	5.7	603	2	T24315 hypothetical prote

30	247	5.7	907	2	J60176	orphan G protein-c
31	244	5.6	1007	2	C84668	probable receptor-
32	243	5.6	1016	2	T30553	disease resistance
33	242	5.6	853	2	T17461	disease resistance
34	241.5	5.6	1109	2	T18536	receptor-like prot
35	241	5.5	741	2	T05250	probable disease r
36	240.5	5.5	1232	2	T05322	hypothetical prote
37	238	5.5	1039	2	T22117	hypothetical prote
38	235	5.4	1019	2	C96519	hypothetical prote
39	234	5.4	855	2	T17460	probable disease r
40	234	5.4	1068	2	H96769	disease resistance
41	230.5	5.3	910	2	G84648	hypothetical prote
42	230.5	5.3	1692	2	A33988	probable disease r
43	230	5.3	1778	2	AF1116	adenylate cyclase
44	226	5.2	1192	2	T48499	internalin protein
45	222.5	5.1	951	2	A96770	receptor-like prot
						hypothetical prote

ALIGNMENTS

RESULT 1

156258
Rp105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995

A/Title: Rp105, a novel B cell surface molecule implicated in B cell activation, is a me
A/Reference number: 156258; MUID:95204928; PMID:7897216

A/Accession: 156258

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-661 <RES>

A/Cross-references: UNIPROT:062192; GB:D37797; NID:9761711; PIDN:BA07043.1; PID:9761712

Query Match 14.1%; Score 612.5; DB 2; Length 661;

Best Local Similarity 27.0%; Pred. No. 3.3e-30;

Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

QY	12	IMALFF-SC-LTPGSLNFCIEVNTYIOCKMDQKSKVPDDIPSTKNIDLSFNPDLTKL 69
DB	10	LVALFLASCRAVTSDDQKIEKVKYCNGLNIEIPGLPNSTCELSFNVLPITQ 69
QY	70	SYSPSNFSELQWLDLSRCEIETIEDKAMHGLHLSNLITGNPIOSFSPGSSGLTSLEN 129
DB	70	NTPFSRLINTFLDLTRCQIWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129
QY	130	LVAETKLASLSEPPIGOLITLKKLVANAFIHSCKLPAYVSNLTNIVHVDLSVYIQTI 189
DB	130	LFPIQTGSSIDFPIRNQKTLBSLVGSNISSIKLPKGPPT-EKLVLPQNNAIHYL 188
QY	190	TVNDLOFLRENPOVNLSDMSLNPIDFIQDAFOGKIKHELTLGNFNSSNIMTKCLONT 249
DB	189	SKEMSSIQQ--ATNLSTNLNGNDIAGIRPAFSAVFOSL---NFGQTQLLVIFKGL 242
QY	250	AGLHVHRLTIGEFDERNLIFEPSIMEGLCDVITDERRLVYTNDFSDIYKFKHLAVS 309
DB	243	KNSTIQSLWLTGTFEDMDDEDI-SPAVFEGLCSEMVESINLQKHYFNNTSFHCFSGLO 301
QY	310	AMSLAGVSIKYLEDVPKHF-----KMSIATRCOL--KQPTLLDLPFKS 353
DB	302	ELDLTAT--HLSLPSGLVGLSTLKKLVLSANKFENV---CQISANFSFSLTHLSIKG 354
QY	354	LTLTMNKGISLFFKVALPSLYLDLSRNALSPFGCCSYSDIGTNSLRHLDISFGAIIWS 413
DB	355	NTKRLIEGTGLEN--LENLRELDLSHDIETSDCCNLQRLNLSHLSINLSYNEPLSLK 412
QY	414	AN-FMGLBELHNDFOGSLTKRVTEPSAPLSLEKLVLDISYNTTKIDFQDIFIGLTSIN 472
DB	413	TEAFKCPQLELLDLAFLRLKVKDAQSPQNTLILKVLNLSHLSLDISSSEOLFGLPALQ 472

QY 473 TLKMGNSFKDNTL--SNVFANTNLLFLDLSKQLEQISMGVPTDLHRQLAMSHNNL 530
Db 473 HLNIAQGNHFFPKGNIOKNTSLQTLGRLETLVLSFCDLSIDHAATSLKMMHVDLSHRL 532
QY 531 LFLD---SSHNOIYSTLTLDSCFNRIETSKGILOHFFKSLAFNLTNNSVACICEHQK 587
Db 533 TSSSTIALSHLKGTY----LNLASHNISILPSPLLPISQORTINLRQNPIDCTCSNYF 588
QY 588 LQWYKQKQPLVNVFQMTCAIPVENM---TSLVLDPNNSCTMYKTIISVSIVSVYS 643
Db 589 LEWYKKNQKJEDTEDTLCENPFLRGLRVSLDVTLSGMAAVGIFPLIVFLVPAILLIF 648
QY 644 TVAFLLHYHFYFHL 656
Db 649 AVKYLFRMKYQCHI 661

RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C|Species: Homo sapiens (man)
C|Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C|Accession: T08664
R|Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, U.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A|Reference number: Z16466
A|Accession: T08664
A|Molecule type: mRNA
A|Residues: 1-786 <POU>
A|Cross-References: UNIPROT:Q15399, EMBL:AL050262
A|Experimental source: fetal brain; clone DKFZp547I0610
C|Genetics:
A|Note: DKFZp547I0610.1

Query Match	10.5%	Score 457.5	DB 2	Length 786
Best Local Similarity	23.7%	Pred No. 1.6e-20		
Matches	194	Conservative 144	Mismatches 324	Indels 155
			Gaps	31
Db				
88	EIETTEDKAMGHILHLSNLTGNPIQSPSPGSGTSLNLVAVETKLASIESPFIQ	147		
24	EEBFLVDRKNGLIHV-----PKLSQKTIILNI--SQNYISELMTSDLS	67		
Qy				
148	LITLKKLVAAHNFISCKLPANFSNLTNLVHVDLSNTYIQITVNDLQFLREHPQNL	206		
Db				
68	LSKRLIILISHNNIQYLDISVFKEFN--QELSEYLDLSHNKLVKISC-----HPTVNLKH	118		
Qy				
207	LKMSLNPIDFIOQQAQGIKJHELTJRGFNNSNIKTKGLQNLAGLHVH--LIIGEPKD	264		
Db				
119	LDIISFNAFDLPICKEFG--NMSQLKVLG--LSTHLEKSSVLPFAHNLISKVLLVGEITYG	176		
Qy				
265	ERULIEFEPISMEGLCDVTIDBEFLTY--TNFSDDIYKPHCLANVSAMSLAGVSIKLYD	323		
Db				
177	EKE----DPG---GLQDFNESHAIYPPNK-----EHPFILDVSKTVANLELSNICK	223		
Qy				
324	VPRHFKMOSLITRCQLKQEPFLDLPELKSLLTNN-----	359		
Db				
224	VLEDSKSYFLSLAKIQTPKSLSLTIANNIETWNSFIRILLVHHTVWSSISNVKL	283		
Qy				
360	KGSISFEK-----VALPSLSYLDLSRNALSFSGCCSVSDGTSLSH-----	401		
Db				
284	QGQLDFRDPDPSGTSLKALSIHOVSDVSGFPOSYIIEIFSNMNIKNFYSGTRNVAHMLC	343		
Qy				
402	-----LDLSPNGALITMSANFGO---LEELQHLDFQSHTLKRTVESAPLS--LEKLLYL	450		
Db				
344	PSKISPPFLHLDFSNNLITDVIYFENGCGLTLELFTILLQMNQKLSKIAEMTTQMKSIIQL	403		
Qy				
451	DIISTNTKID--PDGIFGLTSLMTLXMAGNSFKDNTLSNVPAANTNLTFJDLKSCQLEOI	509		
Db				
404	DIGNASVYDEKKKDGCSWTKSILSLANSSNLTDTI--PRCL---PPRIKVLDIHNSKIKSI	460		
Qy				
510	SWGVDYTLHLRIQLINMGHNNLLFLDSSHYNQVYSLSTLDCSFNRIETSKGILLQHFPSLA	568		
Db				
461	PKQVY--KLEALQELNVAFNSL--TDLPGCGSFSLSVLIIDHNSVSHPSADFPQSCCKMR	517		

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QY      FFNLTNNVSACICEHOKFLOMWKVEQOKOFLVNVEMT-----CATPEVMNTSLV 617
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      SIKAGDNPFQCTGELGEFK-----NIDQSEBVLGMDPSYKCQYPESRGTLT 567
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
QY      LDEN-----NSTCMTKTIIISVSVSVIVSTAFIHYHFPHLLIAGC---KKTSRG 668
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      KDFMSELSCITLILITVIATMLVLAVTTSLCTIYDLDPWLYLMV---CQMGTGRRA 623
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
QY      ESI-----YDAFVIYSQNEDEWVRNELVKNL-EGVPRPHLCIHRDPIPGVAIA 717
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      RNIFLEBLORNIOPHAEIFSYSGHDSPFWKQELLFNLEKEGN--QICLHEBNFPBGASIV 680
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
QY      ANIFOEGBFKRKRTIYVVWSRHFIOSRMCIFEYEYLACTOWFLSNSGLIIFILEKV-EKSL 776
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      ENII-TCEKSXYSIENVLSRFVQSEWCHEYELPAHHNLFREGNSLIILLIPDIPOYSI 739
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
QY      LRQOVELYRLSRNTYLEMEDNPGRNHFMFRRLKNAL 813
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      PSSYHKLSIMARRTYLEMPEKSKRGTFWMNLTPAI 776
```

QY	41	DOKLSKVPDDIPSTKQID--LSFNPLKIKSYSFNSFSELOMDLSRCBIETIEDKAM	97	9.3%;	Score 406;	DB 12;	Length 1097;
Db	375	NNRLTHLPDSIFAHTTMLTDRLDNLDTGISGDFSLGNLVTLVMSNRLRTIDSRAF	434	Best Local Similarity 23.3%;	Precl. No. 3.8e-17;	Mismatches 263;	Indels 220;
QY	98	HGLHLSNLITVGNPIOSFSGSFSGTSLLENVAETKLASLESFPICQLITLKLQANVA	157	Matches 188;	Conservative 135;	Mismatches 263;	Indels 220;
Db	435	VSTGTGLHHLHDNDIDLOCP-----LLD--IMLQTOINS-----PFGYMHGLITLNLK	481				
QY	158	NN--FHSCSLPVPYFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSLNPI	214				
Db	482	NNSIIFPYVN---DMKMTMLQLRELDLSYNNISLSGYEDLALASQ--RLHYMTHTNKI	534				
QY	215	DFI--QQAQFGQIKLHELTLRGNFNSSNIMKTC-----LQNLAGLHVHRLILGEFYDERN	267				
Db	535	RRILPPEVHLLEGYNNNLVHVDLNDNPVCDCTILMFIQLVRYGVHKPQ--YSNRQFKLRTD	593				
QY	268	LEIFESPIMEGLCDVTIDEFRLLTYTNDFSDDIVKFCILANVSAMSLAGVISIKLEDPVK	326				
Db	594	RLVQSQPVNLVSGTPVQGLEPQTLICPLDFSSDPRERKC-----PR	633				
QY	327	HKFQSLSTIRCOQLKQFTLLDLPLFKSLTLMNKKGISIKRYVALPLSLSYLDSRNALSF	386				
Db	634	G-----CNCHVATYD-----KALVINCHSGNLTH--VPLPNL-----	664				
QY	387	GCCGSYDLGTNSLRDLDSFNCAIMSANFMGLIELOHLDFOHSTLKRYTEFSANFLSLEK	446				

Db 665 -----HKM-----QMLEHLENTLILRPS----- 685
Qy 447 LLYIDISTYTKIDPDGIFLGTLSTLNTLMKAGNSFKDWTLSNVFANTTNLTFELDSKCOL 506
Db 686 -----ANTP-----GYESVTSILHAGNNL-----TSIDVDQLPTNLTHLD----- 720
Qy 507 EGISGCVDTLHRLDOLLMSHNNLLFLDSSHNOYLSLTDSCNNRLETSKGIILQHPK 566
Db 721 --ISM--NHLQMLN-----ATVGLFNRTMKRSV----- 746
Qy 567 SLAFENLTNNSVACICEHQFLQWVKEQKFLVNVQMTCAFPVEMNTSLVDFFNNSTCY 626
Db 747 -----KLSGNPMKCDCTAKPILLFTQDNPERRGDNNEMCVN-AMPTRMWELSTNDICP 800
Qy 627 MYKTI-ISVSVV---SVIVSTVAFLLYHF-----YFH-LILLACCKYSRGSSTYD 673
Db 801 AEKGVFIALAVIALTGLAGFTALYYKFQEIKIMYAHNLMLMFTBEDLDCKKFD 860
Qy 674 AFVYSSQNEQWVRELKYLEGVPRFHLCHYRDFIPGVALAANIIOEGFHSKRYIV 733
Db 861 AFISYSHDQSFIEDYLVPOLEHGPQKPOLCVHERDMLVGHIIPENIMR-SVADSRRFTI 919
Qy 734 VSRHFIQSRWCIFEYELAQTMQFLSRSGIIFIV-----LEKEXSLMQOVELYML 787
Db 920 VLSQNFITSEWAKLEFRALHRSALNEGSRRIIVIIYSDIGVEKLD-----ELKAYL 972
Qy 788 SRNTYLEWEDNPLGRHIFWRRLKNAL 813
Db 973 KMNTYLLKW-----GDPWFMDKLRPAL 993

RESULT 4

gene wheeler protein - fruit fly (Drosophila melanogaster)
T13852
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R/Accession: T13852
R/Eidom, E.: Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botas, J.; Beilen, H.
Development 120, 885-899, 1994
A/Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simlile
A/Reference number: 217796; MUID:95324375; PMID:7600965
A/Accession: T13852
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1389 <EID>
A/Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C/Genetics:
A:Gene: wheeler
A/Cross-references: FlyBase:FBgn0004364

Query Match 7.9%; Score 344; DB 2; Length 1389;
Best Local Similarity 20.6%; Pred. No. 3,6e-13;
Matches 229; Conservative 146; Mismatches 316; Indels 418; Gaps 46;

Qy 41 DQKSKYVDDIPSTKTIIDLSFNLKLIKYSFSNF-----SELO 80
Db 154 DNNIROLPEGWCMSPSIQIQLNTQNRIRSAEFLFSEKLCAGSALSNANGAVGGSBLQ 213
Qy 81 WLDLSRCEIETIEDKAMHG--LHLSNLILGNPISQSPSGGLTSLNLELVAVETKLA 138
Db 214 TLDDSFNELSLPD-AMGASRLRLQTLISLOHNNISITLAPNALGLSLRLVNTSYNHLV 272
Qy 139 SLBS-----PIGQILITLKLINV-----AHNFISCKLPA 168
Db 273 SLSEAFANKELELHQLGNDVLELPKGLHRLLEQLVLVDLSGNQLTSHHVDNST----- 328
Qy 169 YFSULTLVAVHVDLSYNTIQT---TVDLQFLRNPOVNISLDSNLPIDFIDQDAFGI 225
Db 329 -FAQLIRLIVLNTSNNAITRIGSKTFKELYFLQ-----ILDRNNISIGHIEGAFLEPL 380
Qy 226 -KLHELTLRGNFNSNMKTCLONLAGLHVHRLILGFKDRNLNLEIPSPIMEGLCVTI 284
Db 381 YNLHTL-----NLAEHLHTL-----DNR-----IFNELYVLT 408

Qy 285 DEFRLTYNDSDDIVKFEHCILANYSAMSLAGVSIKYLEVDPKHFKQSLIIRC----- 338
Db 409 ---KTLANNLV-SIVESQAFRNCSDLKEBSSNQLEVEBAV---QDLSMKTLIDLGN 462
Qy 339 QLKQPT-----LDLFPKSLITLWAK-GSI---SFKK 367
Db 463 QISEFKONTFRNLQTLRLIDNRIGNITVGMFQDLRLSLVNLAKRRIQSIGIEGARDK 522
Qy 368 -----VALPSLYLDSRAALSFSQCCSYSDIGTNSRLDLSF 406
Db 523 NTEIATLIDKQFLTDINGITATLALSLMLNISENHLW---FDYAFIPSN-LKWLIDHG 578
Qy 407 NGALIMSANFNGLEB---LOHLDPQSHYTKVTERSAFISLEKLYLIDIS-----YTNF- 457
Db 579 N-YIEALGNYYKLDGEIRVTLTLDASHNRITIEGMSVNSIE-LIFINNIIIGQOANTF 636
Qy 458 -----KIDPDGIFLGTSNLTLMK-----GNSFKONTLSNVFANTTNL 496
Db 637 VDKTRLARVDLYANVLKISINALRVAVSAKEVPEFYLGANPECCDSMBWLQRIINL 696
Qy 497 T-----FLDL-----SKOLE 507
Db 697 TTRQHPHYVDIGNIBCLMPHSRSPARPLASLASDFVCKYKSHCPPTCHCCCEYQCECE 756
Qy 508 QISWGVEDTLH----- 518
Db 757 VICQNGSCFHDATWATNIVDQGRDIALPNNRIPQVSDLYLDQNNMPELEVHLTGR 816
Qy 519 RLQLLNMSHNNLLFLDSSHNOYLSLTDSCFNRIETSKG-----IL 561
Db 817 NLRALYNASNLMTLQNGSLAQVLNLRVLENNKLTALBETBPSLGLRELXYLHNNML 876
Qy 562 QH-----FPSLAFPNLTNNSVACICEH-QKFLQWV 591
Db 877 THISNATPEPLVSEVLRDLNDRNLSSLPHLQYRHSLOGLTIGRANWSCRCQOLRELAQV 936
Qy 592 KEQKQFLVNVQMTCAFPVEM-----NTSLVDFFNNST----- 624
Db 937 SDNMMVVRDNDIYCLDAGIRRELELGNLANGDCDLDLSDASNSISSQDLAIGACP 996
Qy 625 CYMTKTIISVSVSIVV---STVAFLYHFYFHLILAGCK-KYSRGSSTYDAFYIY 678
Db 997 CWPALVILFLVVLIIIVFVRESVRMMLFMYGVAV---CPREFEDAKLXDALITLH 1051
Qy 679 SSQNEQWVRELKYLEGVPRFHLCHYRDFIPGVALAANIIO-BGFHSKRYIVVS 736
Db 1052 SEKDYEFVCNRIAALEHGRPPFLCTIQORDLP---QASHLQLVGAGARSRTIIVLT 1107
Qy 737 RHFQSRWCIFEYELAQTMQFLSRSGII--FVLEK-----VEKSLRQOVELY 784
Db 1108 RNLATTEMNIEFPNA---FHELSRLAQKLVIIETSVSAEADVAELSPYLSKPSVN 1163
Qy 785 RLISRNLYLEWEDNPLGRHIFWRRLKNAL 813
Db 1164 RLTLCDRY-----FWEXLRYAI 1180

RESULT 5

clr protein - fruit fly (Drosophila melanogaster)
T13887
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R/Accession: T13887
R/Chiang, C.; Beachy, P. A.
Mech. Dev. 47, 225-239, 1994
A/Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A/Reference number: 217805; MUID:95151581; PMID:7848870
A/Accession: T13887
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1385 <CHI>
A/Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383

C:Genetics:
A:Cross-references: FlyBase:FBgn004364
A:Note: tlr

Query Match 7.9%; Score 342; DB 2; Length 1385;
Best Local Similarity 20.3%; Pred. No. 4.8e-13;
Matches 223; Conservative 151; Mismatches 325; Indels 402; Gaps 43;

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QY 41 DQKSKVPDDIPSTKNIDLSFNPILKISYFSNF-----SELQ 80
DB 154 DNNIRQLPEGVWCSMPSELQNLNQRIRSAEFLGSEKLCAGSALSNANGAVSGSELQ 213
QY 81 WDLRSCEIETIDKAMHG--LHHLNMLITGNPQSPGSGSLTLENVAVENTKA 138
DB 214 TLDSFNELRSLPD-AMGASRLRLQTLISQHNHISTLADNALGLSLRYLNISYHVL 272
QY 139 SLSEFPIGQLITLKKLVANVNFHISCLP-----AYFS 171
DB 273 SLSEAFAGNKEKELHLOQNDLY--ELPYGLRLHRLQVLVLSGNQLDHDHVNSTFA 330
QY 172 NLTVLVHVDLSYNYITQTL--TVNDLQFLRENPOVNLSDMSLNPIDFIQDAFOGI-KL 227
DB 331 GLIRLIYANLSNMLTRIGSKTFEELVFLQ-----ILDWRNNSIGHIEGALPLPYNL 383
QY 228 HELTLRGNFSSNIMKTCLQNLAGLHVHRLIGEFKBERNLIEPESIMEGLCDVTIDEF 287
DB 384 HTL-----NLAEHRLHTL-----DNR-----IFNGLVYLT----- 408
QY 288 RLTYTNDPSDDIVKFLCLANYSAMSAGVSIKYLEDVKHFQMOLSTIIRC-----QLK 341
DB 409 KLTLLNNMLV-SIVSQAFRNCSDLEKEDLSNQLTEVE--AAQDLSMLKTLIDGENQIS 465
QY 342 QEPF-----LDLPFLKSLTLYTNMK-GSI--SPKK-- 367
DB 466 EFKNTPFNALQNLGLRLIDNRIGNITYGMFQDLPRLSLVNLAKRIGISRGADFQKTE 525
QY 368 -----VALPSLYLDSRNALSPSCCYSYDGTMSLRHLDSFPGA 409
DB 526 IEAIRLDKKFLTDINGIPATLASLMLNISEHNLVW--FDYAFIPSN-LKWLTDHGN-Y 580
QY 410 IIMSANFNGLEB---LQHLDPQHSFLKQVTEPSAFLSEKLYLIDIS-----YTNT 457
DB 581 IEALGNVYKLOEIRVTTLDSASHNRTIEIGAMSVNSIE-LIFINNIIIGQIANTFVFX 639
QY 458 ---KIDPDGIFLGTSINTLTKA-----GNSFKDNTLSNVFANTNLT-- 497
DB 640 TRLAVDLYANVLSKISLALRVAVSAKEVPBEFLYLGNPFCDCSMELQIRINMLTR 699
QY 498 ---FLDI-----SKQLEQIS 510
DB 700 QHPHVVDLGNIECLMPHSRSLRPLASLSDPVCKYKESHCPPTCHCEYBQCEVC 759
QY 511 WGVFDTLH-----RLQ 521
DB 760 PNCSCFHDATYATNIVDCGRDIALPNRIPQDVSDLYLDGNMPELEVGHITGRNLR 819
QY 522 LNMASHNMLFLDSHYNQLYSLTLDSPNRIETSKG-----LLOH- 563
DB 820 ALYINASNMTLQNGSLAQVLNRLVLENNKLTALTEGTEPSLGLRELILYNNMLTRI 879
QY 564 -----FPKSLAFNLTNNSVACICEH-QKELQWVXGQ 594
DB 880 SNATPEPLVSLVLRDLNRRSLSLPHLOYRHSLOGLTLGRNAMSRCQOQLRELQAVSDN 939
QY 595 KQPLVNVEMQC-----ATPVEM-----NTSLVLDPNNSCTYV-----YKTIISV 634
DB 940 AMVVRADHDYICLDAGIKRELELIGLNLANGPDCSDLIDASASINISSQDLAAGYRLPLA 999
QY 635 SVASVIVSTVAFLIYHF-----YFHLILAGCKYSGRSIYDAPVIYSSQNDWV 666
DB 1000 AYVAVLFLDVVLLIVVYFRESVMMLEFAHYGAVCEPERPDACKLVDAILIHSEKQYEFV 1059
QY 687 RNELVKNLEBQVPRFHLCLHYRDFIPGVAILANIIO--EGFHKSRYKVIIVVSHRFIOSRW 744

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DB 1060 CNRIAAEELHGRPPFLICIQORDLP-----QASHLOLVGAPASRKILVLRNMLATSW 1115
QY 745 CIFREYIAQTQWPLSRSGII--FVYLEK-----VEKSLRQOVELYRLLSRNTY 792
DB 1116 NRLEPFRNA-----FHESLRGLAQKLVIEETSVSAEADVAELSPYKLSPSNRLLTCDBY 1171
QY 793 LEWEDNPLGRHIFWRRLKNAL 813
DB 1172 -----FWELKRYAI 1180

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RESULT 6

JC6128
Insulin-like growth factor binding complex acid labile chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC6128
R:Bolsclait, Y.R.; Seto, D.; Hejeh, S.; Hurest, K.R.; Ooi, G.T.
A:Title: Organization and chromosomal localization of the gene encoding the mouse acid labile
A:Reference number: JC6128; MUID:96413591; PMID:8816745
A:Accession: JC6128
A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; P1DN:AA017270.1; PID:g162161
C:Comment: This protein is a serum protein and it is of the ternary complex in the physio
C:Genetics:
A:Gene: als
A:Map position: 17

Query Match 7.4%; Score 319.5; DB 2; Length 603;
Best Local Similarity 24.2%; Pred. No. 3.7e-12;
Matches 159; Conservative 85; Mismatches 228; Indels 185; Gaps 23;

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QY 39 CMDQKSKVPDDIPSTKNIDLSFNPILKISYFSNFSLEQWLDLSRCEIETIEDKAMH 98
DB 60 CSSNNLQLPFGIGIVSTRALWLDGNNLISIPSAFQNLISIDPFLNLOGSWLRSLPEQAL 119
QY 99 GLHLSNMLITGNPQSPGSGSLTLENVAVENTKASLSEFPIGQLITLKKLVANH 158
DB 120 GLQMLYHLHRLNRLSLRSLAAGLFHRTPSLASLGNMLGLBEGLPGLSHLMDINLGM 179
QY 159 NF-----HISCKL-----PAYFSNLTNLVHVDLSYNYITQITVNDLQ 195
DB 180 NSLVVLPPTVQGLGNLHVLNAGKLTLYLQPALCGELRELDSRNALRSYVAN--V 237
QY 196 FLRENPOVNLSDMSLNPIDFIQDAFOGIR-LHELTIRGNPNSSNIMKTCLQNLAGLHV 254
DB 238 FHLPRQLKLYIDRNL--ITAVAPRAFLGMALRWLDSHN-RVAGLLEDTPPGLLGLHV 294
QY 255 HRLIGEKDERNLEIEPESIMEGLCDVTIDEFRITYTNDPSDDIVKFLCLANVSAMSLA 314
DB 295 LR-----LAHNAITSLR 306
QY 315 GVSIXYLEDVPRKFMQSLSTIRCOLKQPTLDPFLKSLTLYTNMK-----GSISEKVAL 370
DB 307 -----PRTFK-----DLHFLBELQGNHRIQLGKTFE--GL 337
QY 371 PELSYLDSRNAL-----SPSGCCSYG--DIGTNSLRHLDSFNGALIMSANFNGLEBL 422
DB 338 GQLEVLTLINDNQIHVEVKVAFGLFNVAVMNLSGNCRLSP-----EHVFOQLGR 388
QY 423 QHLDPQHSFLKQVTEPSAFLSEKLYLIDISTYNTNKIDPDGIFLGITSINTLKMAGNSFK 482
DB 389 HSLHLEHSCIGRIRLHT-----FAGISGRRLPL-----R 418
QY 483 DNTLSNV-----PANTTNLFLDLSKQLEQISWGVFDTLHRLQLANMASHNMLFLDSHY 538
DB 419 DNSISIEEQSLANGSELLEDITANQLTHLRQLFGQGLQBYLLSNQQLTMLSEBDVL 478
QY 539 NQLYSLTLDSPNRIET-SKGILOHFPKSLAFNLTNNSVACICEHQFLQWVXQKQRP 597

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Db 479 GELQAFWMLDSHNLLETPEAGLFSSLSGR-LRYILNLRNNSL-----QTFVQPGIERIM 531
QY 598 LVNVEQMTCAFPVE-----MNTSLVLDENNSTC-----YMYKTIISVSVS 639
Db 532 L-DANPMDCSCPLKALRDPALQNPQVPRFVQVCEGDDCCQPVYTYNNITCAGPANV 587

RESULT 7
JCI282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI282
R:Daiz, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A:Reference number: JCI282; MUID:93038676; PMID:1384485
A:Accession: JCI282
A:Molecule type: mRNA
A:Residues: 1-603 <DAL>
A:Cross-references: UNIPROT:P35859; GB:S46785; NID:9258002; PIDN:AAB23770.2; PID:9570593
A:Experimental source: liver
A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 7.3%; Score 317.5; DB 2; Length 603;
Best Local Similarity 24.1%; Pred. No. 4,9e-12;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDQKLVDPDIPSTKNIDLSNPPLKILKSYSPNSFSELOMIDLSCEITIEDKAMH 98
Db 60 CSSKMLTHTLPDIPVSTRALMDGNLSSISPAFQNLSSIDFLNLQSGWLRSLRPAAL 119
QY 99 GLHLSNLILGNPLOSFPSSGSLTLENLVAVETGLASLESPFIQQLTKLTAH 158
Db 120 GLQNLVYHLERNLRNLAIVGLFTPTSLASLSSNLGRLEBGLFQGLSHLMDLNGW 179
QY 159 NF-----IHSCKL-----PAYSNLTNLVAVDLSYNYIQTITVNDLQ 195
Db 180 NSLVVLPDTVFOGLNHELVLAGNKLTYLOPALFCGELRELDLSNLRASVANYFV 239
QY 196 FLRENPQV-NLSLMSLNPIDFIDQAFQGIK-IHELTLRGNSNNIMKTCLQNLAGH 253
Db 240 HL-----PRLOKYLDRNL--ITAVAAGAFGLMKALRWLDSHN-RVAGLMEDTFFELGLH 293
QY 254 VHRLLGFRKDBRNLEIPEPSIMEGLCVTIDFERLTYTNDPSDDIVKFCILANVSANSL 313
Db 294 VLR-----LAHNAIASL 305
QY 314 AGVSIKLYEDVPKFKMQSLIRCOLKOPFLDLPFKSLTLTMNK-----GSISFKVA 369
Db 306 R-----PRIFK-----DHFLEBQLQGNRRKQIGERTFE--G 336
QY 370 LPSLSYLDLSNAL-----SPSGCCSYS--DLGNSLRHLDSFNCAIIMSANFMGLEE 421
Db 337 LGQLEVLTLNDNQITFVAGFSGLEFNVAVMNLISGNCRLSP-----ERVFOGLDX 387
QY 422 LQHLDPQSTLAKRYTEPSAFSLSEKLYLDISYNTKIDPDGIFLGLSLMTLMAGNSF 481
Db 388 LHSLSHLSLSCGHRLHT-----FAGLSGLRRLFL----- 417
QY 482 KDNLTLSNV-----FANTVTLFLDISKQLEQISWGVFTLRLQLLNNSHNNLFLDSSH 537
Db 418 RDNSSISSIEBQSLAGLSLELDLTLNRNLTHLPQGLGHLBELLSYQQLTSLAEV 477
QY 538 YNQLYSISTLDCSNRRIET-SKGLIQHFKSLAFNLTNNSVACICEHQKFLQWYKEQ-- 594
Db 478 LGPQRAFWMLDSHNLLETPEAGLFSSLSGR-VRYLSLRNNS-----LQFSPQPG 526
QY 595 -KQFLVNVQMTCAFPVE-----MNTSLVLDENNSTC-----YMYKTIISVSVS 638

Db 527 LERMLDANPMDCSCPLKALRDPALQNPQVPRFVQVCEGDDCCQPVYTYNNITCAGPAN 586
QY 639 V 639
Db 587 V 587

RESULT 8
JCS239
Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JCS239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A:Reference number: JCS239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JCS239
A:Molecule type: mRNA
A:Residues: 1-605 <DBL>
C:Comment: This factor is structurally related to proinsulin and have insuline-like meta

Query Match 7.3%; Score 316.5; DB 2; Length 605;
Best Local Similarity 22.2%; Pred. No. 5.7e-12;
Matches 147; Conservative 89; Mismatches 238; Indels 189; Gaps 17;

QY 32 VENTTYQMDKLSKVPDPDIPSTKNIDLSNPPLKILKSYSPNSFSELOMIDLSCEIT 91
Db 53 VNEISVFCSSKMLTRLPDIPGIFGTQALWLDNSNLSIPPAFRNLSIAFLNLQGGQGS 112
QY 92 IEDRAMGLHLSNLILGNPLOSFPSSGSLTLENLVAVETGLASLESPFIQQLITL 151
Db 113 LEPQALLGLNLCHEHLERNQRLSLAVGTFAVTPALALGLSNRLSLRD----- 163
QY 152 KKLAVANFPIHCKLPAYFSNLTVLVAVDLSYNYIQTITVNDLQFLRENPQVNLSDMSL 211
Db 164 -----GLFEGIGNLMDNLGMSLAV----- 184
QY 212 NPIDFIDQAFQGI-KHELTFLRGNSNNIMKTCLQNLAGLHVRLLGFRKDBRNLEI 270
Db 185 -----LPDAFRGAGLRELVLAGN-----RLAY 208
QY 271 FEPSEIMEGLC-----DVTIDFERLTYTNDPSD--DIVKFCILANVSANSLAGSIKYLED 323
Db 209 LQPALFSGLABRELDLSRNLRKAIKANVFQQLRLOGLYDRNLIAVAGA----- 261
QY 324 VPKHFKMQSLIRCOLKOPFLDLPFKSLTLTMNK--GSISFKVALPSLSYLDLSRN 381
Db 262 -----FLGKLKALRWLDSHNRVAGLLEDTFFGLGLRVLRLSHN 300
QY 382 ALSFGCCSYSD-----LGTNSLRHLDSFNCAIIMSANFMGLEEQLDPQSTLX 433
Db 301 ATASLRPRTFEDLHFLBELQIGHNRIRQL-----AERSFEGQLQLEVLTLDHNOLO 351
QY 434 RYTESAFSLSEKLYLDISYNTKIDPDGIFLGLSLMTLMAGNS----- 480
Db 352 EV-KVGAFLGLTVAVMNLISGNCRLNPEQVFRGLGKLSHLSGSCIGRIPTHFAGLS 410
QY 481 -----FKDNTLSNVFANT-----TNLFLDISKQLEQISWGVFTLRLQLLNNSHNNL 530
Db 411 GLRRLFLKDNQLVGIEBQSLWGLAELELDLTSNQLTHLPQGLGKLELYLLSHNRL 470
QY 531 LFLDSHYNQLYSISTLDCSNRRIETSKGLIQHFKSLAFNLTNNSVACICEHQKFLQ-- 589
Db 471 AELPADALGFLQRAFWMLDSHNRLEALPGSLASLGRIRRYANLNNSLRITTPQPPGIER 530
QY 590 -WVKEQKQFLVNVQMTCAFPVE-----MNTSLVLDENNSTC-----YMYKTI 632
Db 531 LMLEG-----NPMDCSCPLKALRDPALQNPQVPRFVQVCEGDDCCQPVYTYNNIT 582
QY 633 SVS 635

Db 583 CAS 585

RESULT 9

T15864 hypothetical protein C56E6.6 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15864

R/Pulton, L. submitted to the EMBL Data Library, November 1995

A/Description: The sequence of *C. elegans* coemid C56E6.

A/Reference number: S69019

A/Accession: T15864

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1066 <FULL>

A/Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810

C/Genetics:

A/Gene: C56E6.6

A/Intons: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

Query Match 7.3%; Score 315.5; DB 2; Length 1066;
Best Local Similarity 21.2%; Pred. No. 1.4e-11;
Matches 180; Conservative 128; Mismatches 217; Indels 323; Gaps 37;

56 KNIDSEFPLKIKSYFSFNSFSELOWLDSRCEI-----ETIE----- 93

171 RELDSTVQIVQVEDSSFEYVGHMSLDSTYRIRIYVFRGMKXNPAKTLKTLKLAEMNH 230

94 --DKAMGILHLSNLIITGNP-----I0SFSGSFGSLTS 126

231 ATPPALRLRLNLTNLNGNKNLRIDGVKCTDTVELFANNYLRHPIHGVLSGKQ 290

127 LENLVAVETKLASLE-----SFGQILTLKKLVANHFHSCKLPAVFSNLTMLVND 180

231 LEHLDISNKKIMSLKKPSSLSTYKEETSTVRLNLAGNRINNMEDYLIFFEMPLITYVD 350

181 LSYNYIQTIT-----VNDLQ--FLREN-----POV-----NLSDMSNPIDFIODQ 220

351 VSFNRIKRPISPRVFEKTKNLESLFLONNOIAHFPSLFRDLKRLHMLDN--NQIQKIDNF 408

221 AFQGI-KIHELTLRGN-----FNSSNMKTCLQNLAGLHVRHLIGEKDERNLEI 270

409 SLADI-PKLOHLSIAGNQDLITENMGSSSSSELKSLNLAHKXIHSSRSFSDLDNLO- 467

271 FEPSTMEGLCDVTIDEFRLTYNDFDDLVKHFCLANVGSMLAGV-SIKYLEDVPKHK 329

468 -----QRLSHNN-----IKTTSMTFSNLRIKRYL-DLSHN-- 498

330 WOSLSIIRCOLKQFPITLD-----PFLKSLTLTNMK-----G 361

499 -RIIKLPSALYOLPALDVLIHDHNNLNEIDRAPSPFSDLSLKLSHNAFRFPCEPFG 557

362 SISFKVALPSLYDLISRNALSFGS--CCSYS--DLGTNS-----LRH 401

558 SIS-----QVHQLDSSNQINBEIDFICARGIRKLSLASNSVEKINRKLQDATERLS 610

402 LDISFNGAL-IMSANFWGLELOHLDFOHSTLK-----RVTEFSAPLS--L 444

611 IDISHNGIIDVDADAFCECRKLSHIKLSHYINLMWKTGRVCIPWISHLTTPCFEFTKEHL 670

445 EKLTYLD-----ISYTNKIDF--DGIPLGLSTLNTLMAGN----- 479

671 ERTISYSYIIVDSQSLTSPGNLSILSPANKKVDISEGAEINLSLKIIDLSPNPTSWS 730

480 --SEKID--NTLSNV-FANT-----TNLTFLD 500

731 PTAFRDLSSHISINMANTGAFSPMKFSHRSIOSLANSCKKIYELSEKDLAPLTKVVALD 790

501 LSKQOLEQISWGVDTLHRLQOLMSNNLLFLDSSHYNOLYSL----- 544

791 ISHNMLKOISSMAFEPLIHLKQLVNSANPITHLTNEHIOOLYKLYNIPDMARPYQISIL 850

Qy 545 -----STLDCSFNRKETSGLIQLHFPKSLAFENLTNNSVACICENCKFLQ 569

Db 851 SNLPLHTTYVIDIKESALDRQFTYADTR--LRLHL--VAGRNLTIEVGAFATIRGF-- 904

Qy 590 WYKQKQPLVNVBQMTCAPEVMNTSLVLDENNSTCYMTKTIISVSVSIVV----- 642

Db 905 -----RVRIEIHNSIEBFPSR--IFDTLGISILSLSDNKLKLTTF 944

Qy 643 ----STVA 646

Db 945 NPROSTVA 952

RESULT 10

A29944 chaptain precursor - fruit fly (*Drosophila melanogaster*)

N/Alternate names: photoreceptor cell-specific membrane protein

C/Species: *Drosophila melanogaster*

C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004

C/Accession: A29944; A21123

R/Reinke, R.; Krantz, D.B.; Yen, D.; Zipursky, S.L.

Cell 52, 291-301, 1988

A/Title: Chaptain, a cell surface glycoprotein required for *Drosophila* photoreceptor cell

A/Reference number: A29944; MUID:88135762; PMID:3124963

A/Accession: A29944

A/Molecule type: DNA

A/Residues: 1-1134 <REI>

A/Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901

R/Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.

Cell 36, 15-26, 1984

A/Title: Neuronal development in the *Drosophila* retina: monoclonal antibodies as molecu

A/Reference number: A21123; MUID:84106810; PMID:6420071

A/Accession: A21123

A/Molecule type: protein

A/Residues: 31-43, 'HX', '46-49', 'H' <ZIP>

C/Genetics:

A/Gene: FlyBase:chp

A/Cross-references: FlyBase:FBgn0000313

A/Intons: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2

C/Suprafamily: Chaptain; leucine-rich alpha-2-glycoprotein repeat homology

C/Keywords: cell adhesion; glycoprotein; membrane protein

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-1134/Product: chaptain #status predicted <MUT>

F/80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>

F/103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F/128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F/152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F/177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F/201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F/226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F/250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F/279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F/303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F/326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F/351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>

F/375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F/401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F/428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F/453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>

F/477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F/502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

F/527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

F/551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>

F/577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>

F/601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>

F/625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>

F/649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>

F/673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>

F/708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>

F/733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>

F/757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>

F/781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>

F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
 F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.0%; Score 303.5; DB 1; Length 1134;
 Best Local Similarity 20.8%; Pred. No. 8.6e-11;

Matches 169; Conservative 122; Mismatches 275; Indels 247; Gaps 31;

44 LSKVDD-----IPST-----KNIDSFNPLKIKSYFSFN 75
 114 LTEIDDAFTGLERLMEILPONDVLEPSSKLNHLQKRLHDGYHHTIIOHDSFPG 173
 76 FSE-LQWIDLSRCEIETEDKAMHGLHLSNLIITGNPIQSPSPF-SGLTSLNVAV 133
 174 LEDSIQTLIRNENCISQLMHSFSGLLIETDLSGNNLFEIDPNVFDGMPRLRLILT 233
 134 ETKLASLSPFGIOLITLKKLVANRPHSCLPAYF---SNLNLVAVDLSYVIQTI 189
 234 DNILSEIPYDALGPKSKRTTLDISHNVWSLSGNETYEIKASTKTLNDLHLEYNHIEVL 293
 190 TVNDIQFRENPOVNLSDMSINPIDIQDAFOGKIKHETLR-----GNF 236
 224 PPNSSKRYF---DTVVRTF-PDGNPIHTLRBEDAFKARIREIMRQGLTNISPVAFDSLV 349
 237 NSSNIMKTCLQNLAGLHVAHRLI-----LGEFKDERNLIEPEPSIMEGLCVTIDEPL 289
 350 NSLIQILDSSGNLTLKHL-HKLFNPFVLRVISMEDNK-IKICKPTEFNAVAHYTL-LKL 405
 290 TYTNDFSDIYKHEKCLAVASAM-SLAGVISIKLEBV---PKAFK---WQSLSTIRCOL 340
 406 DLGG-RNDPTNLQTLRNMTRMRNRSLSISRLGSSVGPEDPKPGVELELDIQTIRASL 464
 341 KQPTLDLPFLKSL-----TLTNKKSISFKVALP----- 371
 465 SGIOSHAKRYRGLKRLDPSENGISSINDAFHEIGHSLISLMSHGYSGLSLPRLPH 524
 372 --SLSYDLSRNVALSFGCCSYSDI-----GT-----NSLRHLDLS 405
 525 LTSIQELDFSNNHISMSMDTSFHFKNLRLLEHDNRILEOVLKGTFOGDHSKLEISLR 584
 406 ENGALIMSAN-----FNGLEBELQHLDPQHSITLKAVTERPSA 440
 585 FNHLTISIQHTFFDELEALRKLHLDNKKIDKIERAFNNMLDELEYLSLRGNKINNLIAD-ES 643
 441 FLSTLEKL----- 447
 644 FQNLPEKLEILDMAFNQLPNNFEDYDQVGTLSNLNANVSHNOIRQLMTNSSSGNENEGG 703
 448 LY-----LDISYNTKIDFDGIFL-GLTSLNTLTKMAGNSFKDNTLSNVFANTTNLTFELD 500
 704 MYHSNLIKILDSHNNISIIHPGYFRPAEISLTLHLGYNLSL-NTRTRVFGMPLHQLD 762
 501 LSKQLEBISGVEPTLRLQLLMSHNNLLFLDSSHNNQLYSITLDCSRN----- 552
 763 LSYNMIHLELDFDAFNKTKQLQVFGHNYLSDIPDIPKPYQGRIVDFVSHNHLRGLEDN 822
 553 -----RIETSKGIIQHPFKS-----LAFNLTNNSVACICE---HOKF-LQW 590
 823 LFVNGMEKLDVSHNMKIPSSSLSLAALTLCGLHLSNNPISITISHMDLSNKRFRSLRY 882
 591 VKEQKQFLVNEQMTCAFPVEMNTSLVLDPNNS 623
 883 LDISYNYLLRIDDAVFAF---MPKLAVALDSLHN 912

RESULT 11

A41915

insulin-like growth factor-binding complex acid-labile chain precursor - human

N/Alternate names: Acid-labile Subunit (ALS)

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A41915

R/Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A/Title: Structure and functional expression of the acid-labile subunit of the insulin-1

A/Reference number: A41915; MUID:9257025; PMID:1379671

A/Accession: A41915

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-605 <LEO>

A/Experimental source: UNIPROT:P35858; GB:M86826; NID:G184807; PIDN:AAA36047.1; PID:G184808

A/Note: sequence extracted from NCBI backbone (NCBI:110171)

F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>

F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match 6.7%; Score 291.5; DB 2; Length 605;
 Best Local Similarity 22.0%; Pred. No. 2e-10;

Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;

39 CMDQKSKVPPDIPSTKNIDLSFNPLKIKSYFSNFSLEQWIDLSRCEIETEDKAMH 98
 60 CSSNLTRELPGVPGGQTQALWLDGNNLSVPPAFQNLISGIFNLQGGQGLSEPPQLL 119
 99 GLHLSNLIITGNPIQSPSPSGLSLENVAVETGLALESFPIQLITLKKLVANH 158
 120 GLENLCHLERNQRLSLAQTFAPHTPALASLGSNNRLSRLDEGLFEGLSLMDNLGW 179
 159 NFII-----SKLPAYFNNLTNLVHVDLSYNYIQTIVNDLQ 195
 180 NSLAVLPDAARFGISLELVLAGNRLAYLOPALFSGLAELRELDLSNNAIRAKAN--V 237
 196 FLRENPQVNLSDMSINPIDIQDAFOGIR-LHELTLRGNFNSNNIMKTCLQNLAGLV 254
 238 FVQPRLOKLYLDNRL--IAVAPGAFGLKALRWLDSH--RAAGLEDFEPGLGLRV 294
 255 HRLIGFKDERNLIEPEPSIMEGLCVTIDEPLTYTNDFSDIYKHEKCLAVASAMSLA 314
 295 LRL-----SHNIA 303
 315 GVSFKYLEVDKPKFMQSLSIIRCOLKQPTLDLPFLKSLTLTNKKSISFKVALPSSL 374
 304 SLR-----DLHFLBEL----- 319
 375 YLDSRNALSFSGCCSYSDIGTNSLRHLDSFNCAIITMSANFMGLBELQHLDPQHSITLKR 434
 320 -----QLGHNRIROL-----AERSFEGIGQLEVLTLHDNQOE 352
 435 VTERSAFLSEKLYLDISTYNTKIDPDGIFLGLTSLNTLTKMAGNS----- 480
 353 V-KAGAPFLGTLNVAVMNLGNCNLRLPBOVFRGLGKLHSLHLEGSCLGRIAPHTFTGLSG 411

Qy 481 -----FKONTLSNVFANT-----TNLTFDLDSKCOLEQISWGVDPDLRLQLLNMNSHNNL 531
Db 412 LRRFLKDNGLVGEBSIMGLABELLDLSNQTLPHRLFOGLKLEVLILSRRLA 471
Qy 532 FLDSHYNQVLSLTDSCFNRIETSKGILQHPKSLAFNLTNNSVACICEHOKPIQ-- 589
Db 472 ELFPADALGPLORAFMLDVSHNRLEBALPNSLAPLGRRLYLSLRNNSLRTFTTQPPGLERL 531
Qy 590 WYKQKQKQFLVNVQMTCAATPE-----NMNLSVLDFNNSTC-----YMYKTIIS 633
Db 532 WLEG-----NPMDCGCPKLALRDPALQNPASVAPRFVQALCEGDDCQPPATYNNITC 583
Qy 634 VSQVSVI 640
Db 584 ASPEEV 590

RESULT 12
T42218
alt-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomic 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T42218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NNK>
A:Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PID:BAA32460.1; PID:G3
A:Experimental source: strain Sprague-Dawley; brain
C:Gene: MEGF4
C:Superfamily: fruit fly slt protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 6.6%; Score 287.5; DB 2; Length 1531;
Best Local Similarity 21.0%; Pred. No. 1.3e-09;
Matches 161; Conservative 99; Mismatches 266; Indels 239; Gaps 26;
Qy 5 WLAATLIMALFFSCITPGLN-----PCIEV 31
Db 229 WLRQPTI-GLFTQCGSPASLRGLNVAEYKSEFSCGGGEAAQVPACTLSSGSCPMCS 287
Qy 32 VNPITYQCMQKLSKVPDDIPSTKNIDLSFNPPLKILKSYSPNSFELQMLDRCIEIT 91
Db 288 CNGIVDCRGKGLTALPAMLPETMEIRLELNGIKSIPGAFSPYKLRIDLSNNQIAE 347
Qy 92 IEDKAWHGHLSNLITGNPIQSPGSPGSLTLENLVAETKLASIESPFIQILTL 151
Db 348 IAPDAQGLSLNSLVYGNKITDLPRGVGGLYTIQLL-----LMA 390
Qy 152 KKLVAANPLHSCKLPAVESNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDML 211
Db 391 NKNIN-----CIRPDAFQDLQNLISLYDNKIOSLAKGFTSIR--AIQTLHMQ 438
Qy 212 NPIDFIQDAQFQIKLHELTLRGFNSSNMKT-----CL--QNLAGLHYHRLILGEFKDE 265
Db 439 NP--FTCD-----CNLMKLADPLKTNPIETTGARCAFPRLANKRIQOISKKFRCS 488
Qy 266 RNLEIFPESIMEGLCDVTIDEFRLTYNDPSDDIVKPH-CLAVWSAMSLAGVSI-KYLED 323
Db 489 AKQOYFPG-----TEDYHL--NSECTSDVACHKRCRASVVEGSGMLSKIPIER 537
Qy 324 VPKHFKWQSLIIRCOLKQPPITLDPFLKSLITLTMNGSISPKKVALPSLSYDLSNKL 383
Db 538 IP-----QSTTELRLNNEISILEATGL-----FKK--LSHKIKINTLSNKKV 577
Qy 384 S-----FSGCCSYSD--LGTNSLRHLDLSFNAGLIMSANFMGLIEHLDFQGSTLAKV 435

Db 578 SEIEDGPFEGATSVSEHLHTANQLES-----VRSQMFRLDGLRTLMNRNRSICI 628
Qy 436 TEPFASLEKLYLDISTNTKIDPDGIFLGITSLNTLKMAGNSPKDN----- 484
Db 629 HN-DSFTGLRNVALSLYDNHITTTISPAPDTLOALSTMLANPNCQOLAMLDMLR 687
Qy 485 -----TL 486
Db 688 KRKITVGNPRCONPDLRQIPLQDVAFPPDRCEGQEEVGCLEPPQCPQECADITVRC 747
Qy 487 SN-----VPANTNLTFDLDSKCOLEQISWGVDPDLRLQLLNMNSHNNLFLDSH 537
Db 748 SNKHQALPKGIPKAVTEL-YLDGNOFTLV--GQLSTFKYIQLVDLSNNKISSLSNSS 803
Qy 538 YNQLYSLTDSCFNRIETSKGILQHPKSLAFNLTNNSVA----- 579
Db 804 FTNMSQLTTLILSYNAQCIPPLAFQGLRSRLSLTSGNDVSTLOEGRPADVTSLSHAI 863
Qy 580 -----CICEHOKFLQWKEQKQFLVNVQMTCAATPEANNTSLVL 618
Db 864 GANPLVCDCHLRMLSSVVKGYK---EPGIARCAQPEPMGSKILL 905

RESULT 13
T10504
disease resistance protein Cf-2.1 - currant tomato
C:Species: Lycopersicon pimpinellifolium (currant tomato)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10504; T10515
R:Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A:Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
A:Reference number: Z17062; MUID:96190812; PMID:8608599
A:Accession: T10504
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1112 <DX>
A:Cross-references: UNIPROT:O41397; EMBL:U42444; NID:g1184074; PID:AACT5779.1; PID:g118
A:Experimental source: cultivar Cf 2
A:Accession: T10515
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1066, 'I', 1068-1085, 'E', 1087-1110, 'R', 1112 <DI2>
A:Cross-references: EMBL:U42445; NID:g1184076; PID:AACT5780.1; PID:g1184077
A:Experimental source: cultivar Cf 2

Query Match 6.5%; Score 283.5; DB 2; Length 1112;
Best Local Similarity 22.6%; Pred. No. 1.4e-09;
Matches 182; Conservative 109; Mismatches 285; Indels 231; Gaps 32;
Qy 11 LIMALFPGCTPGSLNPCIENVNIT--YQCMQKLSKVPDDIP--SSTKNIDLSFNPYLK 66
Db 385 LEMLYLYNNQLSGSPASIGLNANLSRLLYNNQLSGSPETIGYLSLTLYDLNNSN 444
Qy 67 ILKSYSFNSELQWLDLSRCEIETEDKAWHGHLSNLITGNPIQSPGSPGSLT 126
Db 445 GRTIPASFGMSLAFLEIYENQLASSVPEIGYLSLVLDLSNALNSIPASFGNLAN 504
Qy 127 LENLVAETKLASLSFPFGQITLKLVAANPLHSCKLPAVESNLTNLVHVDLSYNYI 186
Db 505 LSRNLNLYNNQLSGSPETIGYLSLVLDLSNALNG-SIPASFGNLANLSRLNLYNNQ 563
Qy 187 QITTVNDLOFLRENPQVNS-----LDM----- 209
Db 564 SGGIPEIGYLSLNDLGLSENALNSIPASIGLNANLSMLYLYNNQLSGSPETIGYLS 623
Qy 210 -----SLN--PIDFIQDAQFQIKLHELTLRGFNSS-----NTM 242
Db 624 SLTYLSLGNNSLNGLIPASFGNRLNQLIINDNNLIGEIPSVGNLTSLLEVLYMPRNL 683
Qy 243 K-----TCLQNLAGLHVHRLILGEFKDERNLEIFPESIMGLCDVTIDEFRLTYNDPSD 288
Db 684 KGVPCQCLGNISMLQVLSMSNSFSGEL-----PSSISNLTSLQIIDFG--RNNLEGA 734

QY 299 IYKFCICLANVSMGL-----AGVISIKYL-----EDVKKH-----K 329
 Db 735 IYKFCICLANVSMGL-----AGVISIKYL-----EDVKKH-----K 329
 QY 330 MOSLSIINCOQKQ--PPTL--DLPFLKSLITLTKNK--GSI--SFKVALPSLYLDSRA 382
 Db 793 LQVLDLGNQNLDTFPMMLGTLPBLRVLRLLTSNKLHGPRSSRAEIMFEDLRIIDLSRA 852
 QY 383 LSPSGCCSYSDLGTSNLRHLDSFNGAIIIMSANFMGLLEQLDFOHSTLKAETESAPL 442
 Db 853 FS-----QDLPTSLFHL-----KGM-----TVDKMEPESTE 881
 QY 443 SLEKLLYLDISTYNTKIDPDGIFLGLTSLNTLKKMAGSFKONTLSNVANTNLTFELDS 502
 Db 882 S-----YDDSVVVVVK-----GLELEIVRILSL-----YVIDLS 912
 QY 503 KQLEQISMGVFDTLHRQLQNLMSHNNLLFLDSHYNOQLSLSTIDCSFNRLETSGILQ 562
 Db 913 SNKEGHIPSVLDGLIARILANVSHNALQYIPSSLSGLSLESIDLSFNQLS-----G 966
 QY 563 HEPKSLA-----FENLTNNSV-ACICEHOKFLOW-----V 591
 Db 967 EIPQOLASLTFLPLNLSHNTLQSGIPQGPQRTESNSYEGANDLRCYPPVSKGCKDPV 1026
 QY 592 KEQKQFLVNEQMTCAPEVEMNTSLVDPNNSTCYMTKIIISVSVSV-IVST-----V 645
 Db 1027 SEKVYVALSDQ-----ESNBEFNDPFWKALMGSGICIGISMTYIILISTGNLML 1080
 QY 646 AFLIYHFPHILLAGCKKYSRGESIT 672
 Db 1081 ARILEKLEKIMOR--RKKQGGONY 1105

RESULT 14

B3665

slit protein 2 precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C/Accession: B3665

R/Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

A/Title: slit: an extracellular protein necessary for development of midline glia and co

A/Reference number: A3665; MUID:91099665; PMID:217636

A/Accession: B3665

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-146 <ROT>

A/Cross-references: GB:X53959

C/Genetics:

A/Genes: FlyBase:slit

C/Cross-references: FlyBase:FBgn0003425

A/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein 1

F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>

F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F/228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>

F/288-313/Domain: proteoglycan amino-terminal homology <PC2>

F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F/347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F/395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F/450-494/Domain: proteoglycan carboxyl-terminal homology <PAH3>

F/512-537/Domain: proteoglycan amino-terminal homology <PC3>

F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F/572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F/596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F/651-695/Domain: proteoglycan carboxyl-terminal homology <PC3>

F/708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F/846-890/Domain: proteoglycan carboxyl-terminal homology <PC4>
 F/1028-1061/Domain: EGF homology <EGF>
 F/1068-1099/Domain: EGF homology <EGF2>
 F/1115-1148/Domain: EGF homology <EGF1>

Query Match 6.3%; Score 273; DB 2; Length 1469;
 Best Local Similarity 21.6%; Pred. No. 9.4e-09;
 Matches 150; Conservative 86; Mismatches 241; Indels 218; Gaps 23;

QY 39 CMDQKSLVPPDIPSTKNIIDLSFNPILKLSYFSNFSBLOWDLSRCETIEDKAWH 98
 Db 308 CREKSLTSVPVTLPTDDTIDVLEQVFIETELPKSPSSFRRLRRIDLSNNNISRIADLDS 367
 QY 99 GLHLSNLILGNPIQSPSPSGSLTELEUVAVETLASLESPIQGLITLKKLVANH 158
 Db 368 GLKOLTTVLVGNKIKDIPSGVFKGLGSLRLILANAEI----- 406
 QY 159 NFHSCKLPAYFNSLTLNVHVDLSYNYIQTITVNDLQFLRENPOVNLSDMSINPIDFIO 218
 Db 407 ----SCIRKAPFRLDLSLSLSDYNNIQLANGTFDMKSMKTIVH----AKNF--FIC 456
 QY 219 DQAFQIK--LHEPLTRGNFNSNIMKTCLONLAGLHYHRLILGFKDERMLEPEPSIM 276
 Db 457 DQNRMLADVLAKNPIDISGARGESP-----RHRHRIISLRE----- 496
 QY 277 EGLCDVTIDBERLLTYTNDPSDIYKFCICLANVSMGLAGVISIKYLEDPK--HEKWSLS 334
 Db 497 ----KFKCSMGLRMKLSG--ECRMDSDCPACHCGCTVVD 531
 QY 335 IIRCOLKQPTLDPFLKSLTLTKNK--GSIQPKV--ALPSLYDLSHNASLFSGCC 389
 Db 532 CTGRKLRKIPR-DLP-LHTTELLANDDELGRISSDGLRGLPHLVKLEKRNQ----- 583
 QY 390 SYSDLGTNSLRLHDLSPNGAIIIMSANFMGLLEQLDFOHSTLKRVEFSAPLSLEKLY 449
 Db 584 --TGIEPNA-----PEGAGHIGELQGENKIKELISN--KMFGLGHQKPT 623
 QY 450 LDISTYNTKIDPDGIFLGLTSLNTLKKMAGSFKONTLSNVAN----- 492
 Db 624 LNVYDNOISCVMPSPFHLNLSLTSLNLSNPNFCNCHLWFAECVRKKSINGARCAP 683
 QY 493 ----TNNLFLSLSKOQLQISGV--- 513
 Db 684 SKVADVQIKDLPHSEPFKCSSENSGCCGADGCTCTGTGVVACSRNQLKEIPGIPAE 743
 QY 514 ----FDTLH-----RLQNLMSHNNLLFLDSHYNOQLSLSTIDCSFNRIR 555
 Db 744 TSELVLSNEIEQHYERIRHRLRSLTLDLSNNOITLISNTFPANLTKLSTLIISYNTQ 803
 QY 556 ----TSKGI-----LQHP-----KSLAFNLTNNSVACICEHOKFLOV 591
 Db 804 CLORHALSGLNLRVSVLSHGNRISMLPEGSFEDLKSLTHIALGSPNYCCDGLKWFSDWI 863
 QY 592 KEQKQFLVNEQ--MTCATPEVEMNTSLVDPNNST 624
 Db 864 K-----LDYVEPGIARCAEPQMDKILITPSSS 893

RESULT 15

A3665

slit protein 1 precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C/Accession: A3665; A31640; S13523

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A/Status: preliminary

